In [133]:
```
from google.colab import drive
drive.mount('/content/drive')
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call
drive.mount("/content/drive", force_remount=True).
```

In [135]:
```
cd '/content/drive/My Drive/CSE-544/Project/'
```

```
/content/drive/My Drive/CSE-544/Project
```

import libraries

In [0]:
```
import pandas as pd
from matplotlib import pyplot as plt
import matplotlib.dates as mdates
from matplotlib.dates import DateFormatter
import datetime, math
import numpy as np
import seaborn as sns
from scipy.stats import gamma, binom, poisson
from statistics import variance
```

Possible Counties(MA State) Contention:

All close to east coast and have high population densities. High number of confirmed cases and deaths as well (Except for Plymouth, Barnstable)

1. Suffolk
2. Middlesex
3. Essex
4. Norfolk
5. Plymouth
6. Barnstable

Task 1 and 2 (Cleaning)

In [137]:
```
#preprocessing occurs in multi steps

# load, basic process, save
def prepare_from_csv(filename):
  df = pd.read_csv(filename)
  df = df[df["State"] == 'MA'] # only MA state
  df = df.T # making date as index
  df.columns = df.iloc[1]
  df = df.drop(['countyFIPS', 'County Name', 'State', 'stateFIPS']) #unnecessa
ry for us
  # index to column, to preserve Date while saving (without index)
  df['Date'] = df.index

  # keeping column Date ahead
  cols = df.columns.tolist()
  cols = cols[-1:] + cols[:-1]
  df = df[cols]
  return df

def preprocess(df):
  # filtered counties
  cols = ['Date', 'Barnstable County', 'Essex County', 'Middlesex County', 'No
rfolk County','Plymouth County', 'Suffolk County']
  df = df[cols]
  df2 = df.copy()

  # reversing cumulative effect, making numbers occured each day
  for county in df.select_dtypes(include='int64').columns:
    vals = df[county].values
    df[county] = np.insert(vals[1:] - vals[:-1],0,vals[0])

  # data taken from 1st march, because before that almost no cases were there
  startdate = datetime.date(2020, 3, 1)
  df = df[pd.to_datetime(df['Date']) > pd.to_datetime(startdate)]
  df2 = df2[pd.to_datetime(df2['Date']) > pd.to_datetime(startdate)]

  return df, df2

# load, process, (run only once)
# confirmed = prepare_from_csv('CovidData/covid_confirmed_usafacts.csv')
# deaths = prepare_from_csv('CovidData/covid_deaths_usafacts.csv')

# # save (run only once)
# confirmed.to_csv('CovidData/MA_COVID_CONFIRMED.csv', index=False)
# deaths.to_csv('CovidData/MA_COVID_DEATHS.csv', index=False)

# load processed
confirmed = pd.read_csv('CovidData/MA_COVID_CONFIRMED.csv')
deaths = pd.read_csv('CovidData/MA_COVID_DEATHS.csv')

# filter counties, reverse cumulative effect, take data from 1st march
confirmed, confirmed2 = preprocess(confirmed)
deaths, deaths2 = preprocess(deaths)
```

```
/usr/local/lib/python3.6/dist-packages/ipykernel_launcher.py:28: SettingWithC
opyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/s
table/user_guide/indexing.html#returning-a-view-versus-a-copy
```

In [0]:
```
# just for temporary purpose to extract data

# how many weeks data do you want? check starting date for it!
# datetime.datetime(2020, 5, 6) - datetime.timedelta(weeks = 4)
```

In [0]:
```
# save it here

# startdate = datetime.date(2020, 4, 8)
# fourWeekDeaths = deaths[pd.to_datetime(deaths['Date']) > pd.to_datetime(star
tdate)]
# fourWeekConfirmed = confirmed[pd.to_datetime(confirmed['Date']) > pd.to_date
time(startdate)]

# fourWeekDeaths.to_csv('CovidData/' + 'lastfourWeekDeaths.csv', index=False)
# fourWeekConfirmed.to_csv('CovidData/' + 'lastfourWeekConfirmed.csv', index=F
alse)
```

functions definitions

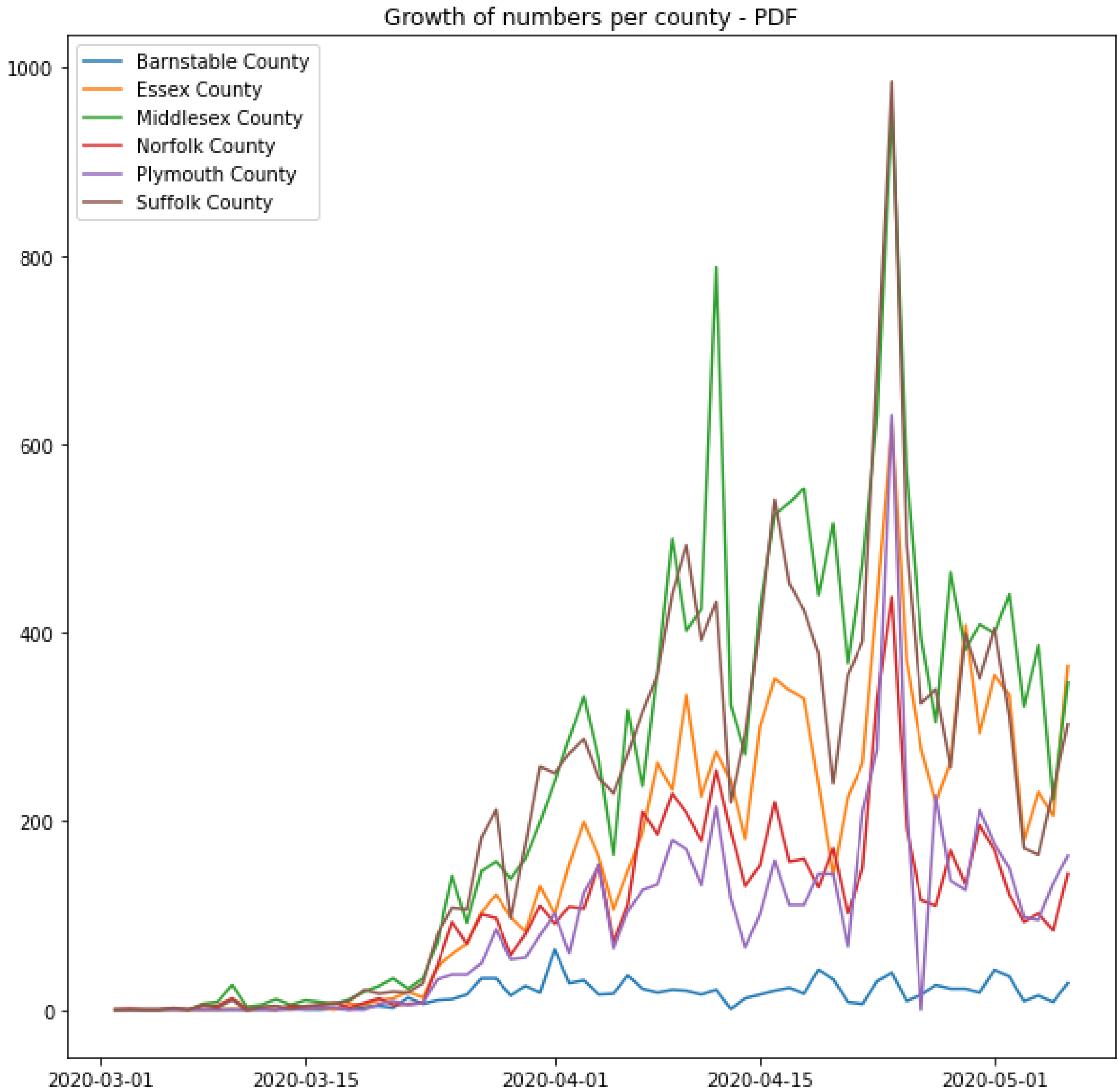
In [0]:
```
def applyTukeyRule(df, counties):

  # global list, carrying outliers per county (list of lists)
  outlier_list = []

  # iterate over counties
  for county in counties:

    Q1 = np.percentile(df[county], 25) # 1st quartile (25%)
    Q3 = np.percentile(df[county], 75) # 3rd quartile (75%)
    IQR = Q3 - Q1 # Interquartile range

    outlier_step = 2 * IQR

    # List of outliers for a single county
    outlier_list_county = df[(df[county] < Q1 - outlier_step) | (df[county] >
Q3 + outlier_step)].index

    # outlier "indices" for a county to the global list
    outlier_list.append(outlier_list_county)

    # dropping outlier record by each county iteration, so dates will remain s
ame for all counties
    # df = df.drop(outlier_list_county)
  return df, outlier_list

def show_outliers(df, counties):

  print("Before removing outliers, total records", len(df))
  df, outliersLoL = applyTukeyRule(df, counties) #list of list
  print("After removing outliers, total records", len(df))
  print('*'*20)

  print("Outliers per County")
  print('*'*20)
  for i, county in enumerate(counties):
    print(county, '=>', len(outliersLoL[i]))
  print('*'*20)

  print("Same is shown using boxplot of pandas")
  plt.figure(figsize=(10,10))
  df.boxplot(column=list(counties))
  plt.xticks(rotation=70)
  plt.title("Outliers per county")

  return df

def show_growth(df, counties):
  plt.figure(figsize=(10,10))
  for county in counties:
    plt.plot(df['Date'], df[county], label=county)
  plt.legend()
  plt.title('Growth of numbers per county - PDF')
  plt.show()

  plt.figure(figsize=(10,10))
```

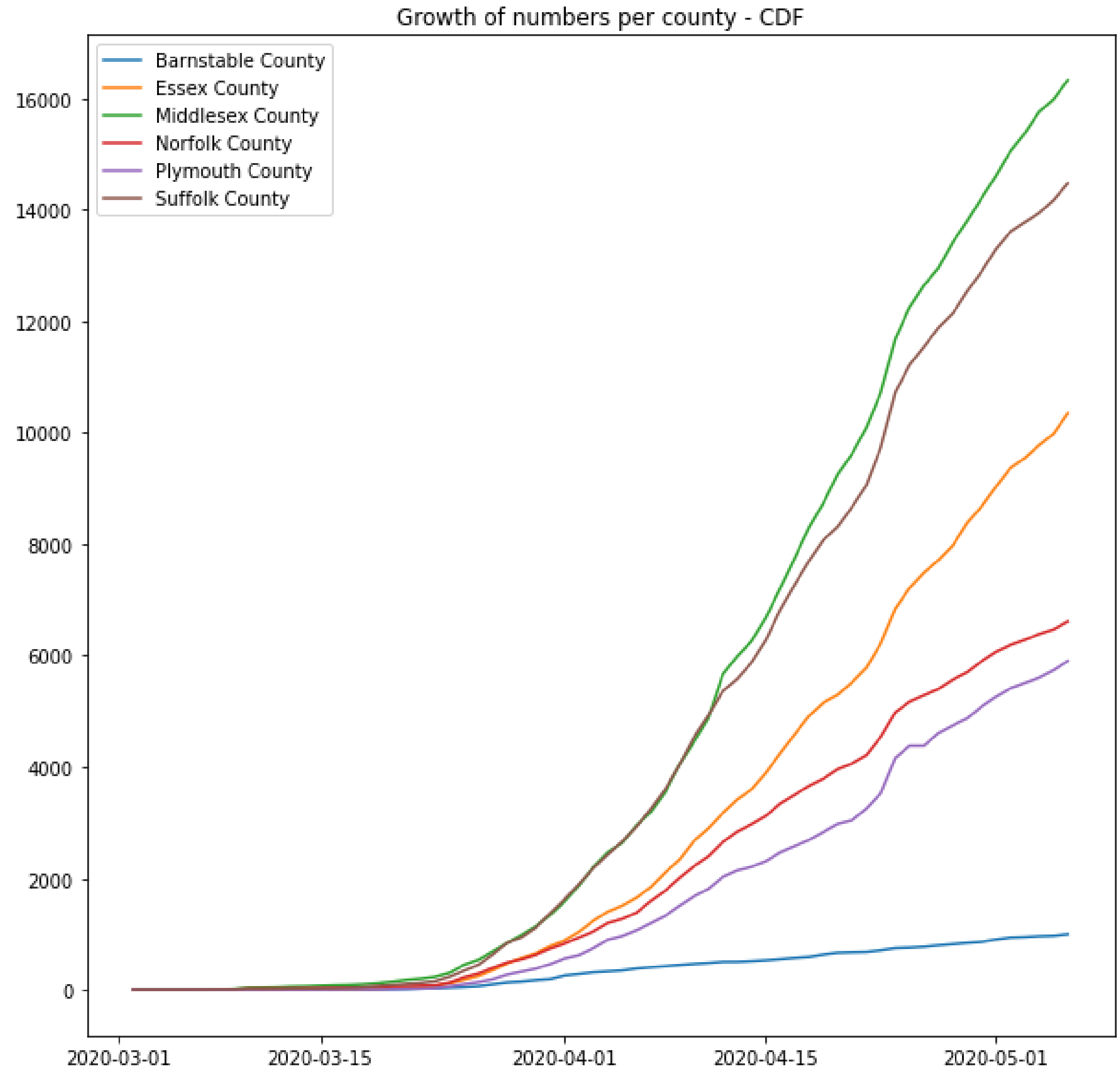
```
  for county in counties:
    plt.plot(df['Date'], df[county].cumsum(), label=county)
  plt.legend()
  plt.title('Growth of numbers per county - CDF')
  plt.show()


def process(df):
  df['Date'] = pd.to_datetime(df['Date'])

  df = df.sort_values('Date', ascending=True)

  print("Data is ranged from", df['Date'].min(), "to", df['Date'].max(), "wher
e total", df['Date'].max() - df['Date'].min(), "are there.")

  counties = df.select_dtypes(include='int64').columns
  show_growth(df, counties)
  df = show_outliers(df, counties)

def visualize(dfs, counties):

  print("Lets see growth of confirmed cases and deaths in each counties from 1
st March")
  confirmed_df = dfs[0]
  deaths_df = dfs[1]

  cols = 4
  rows = int(len(counties)/cols)-1

  fig, axes = plt.subplots(rows, cols, figsize=(15,10))
  fig.subplots_adjust(hspace=0.5)

  for ax, county in zip(axes.flatten(), counties):

    ax.plot(confirmed_df['Date'].dt.date, confirmed_df[county], label='confirm
ed')
    ax.plot(deaths_df['Date'].dt.date, deaths_df[county], label='deaths')
    ax.set_title(county)

    for tick in ax.get_xticklabels():
      tick.set_rotation(45)
    ax.legend()
  plt.show()
```

main work

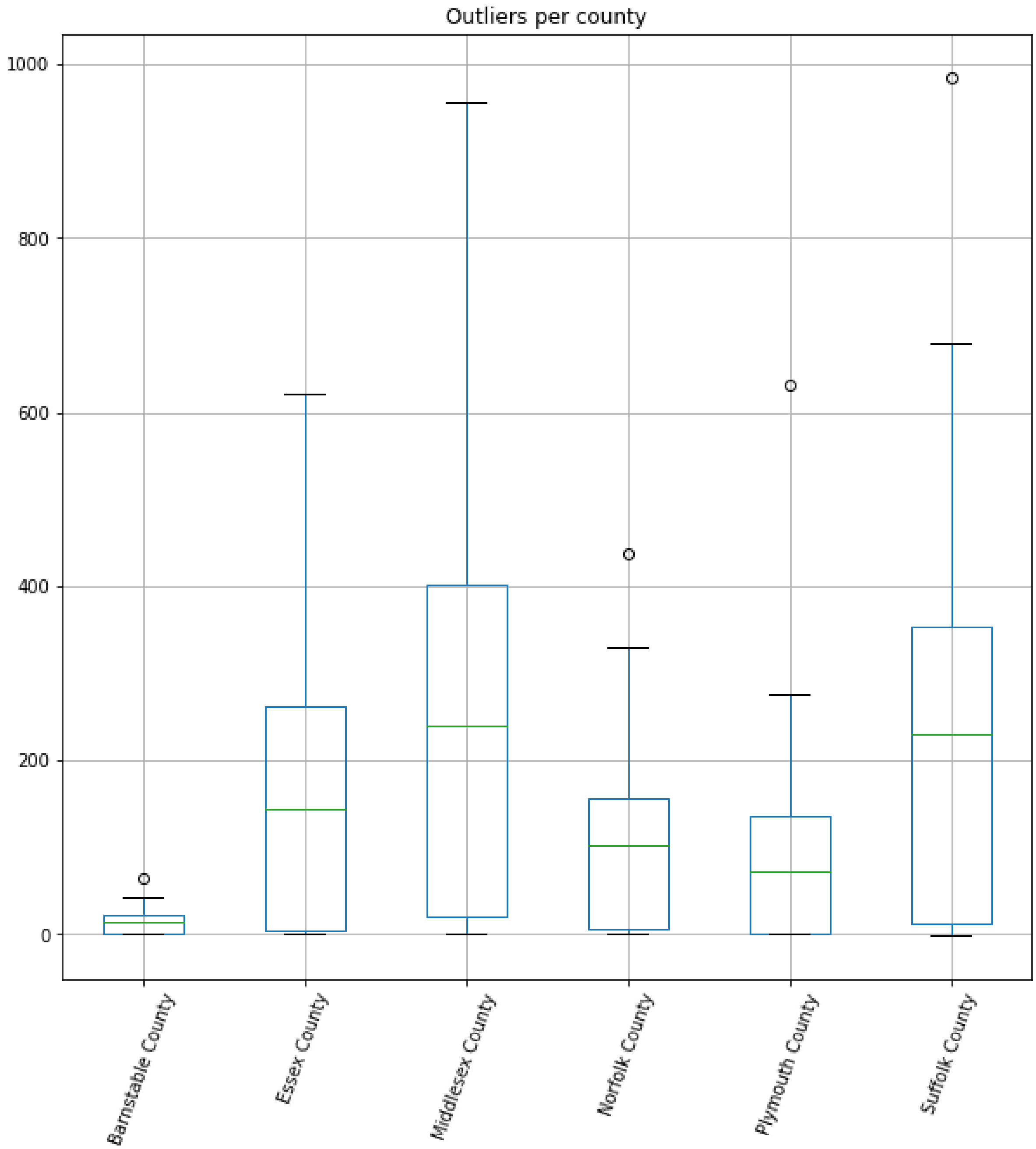
In [141]:
```
print("Confirmed")
print('*'*25)
print('*'*25)
process(confirmed)

print("Deaths")
print('*'*25)
print('*'*25)
process(deaths)
```

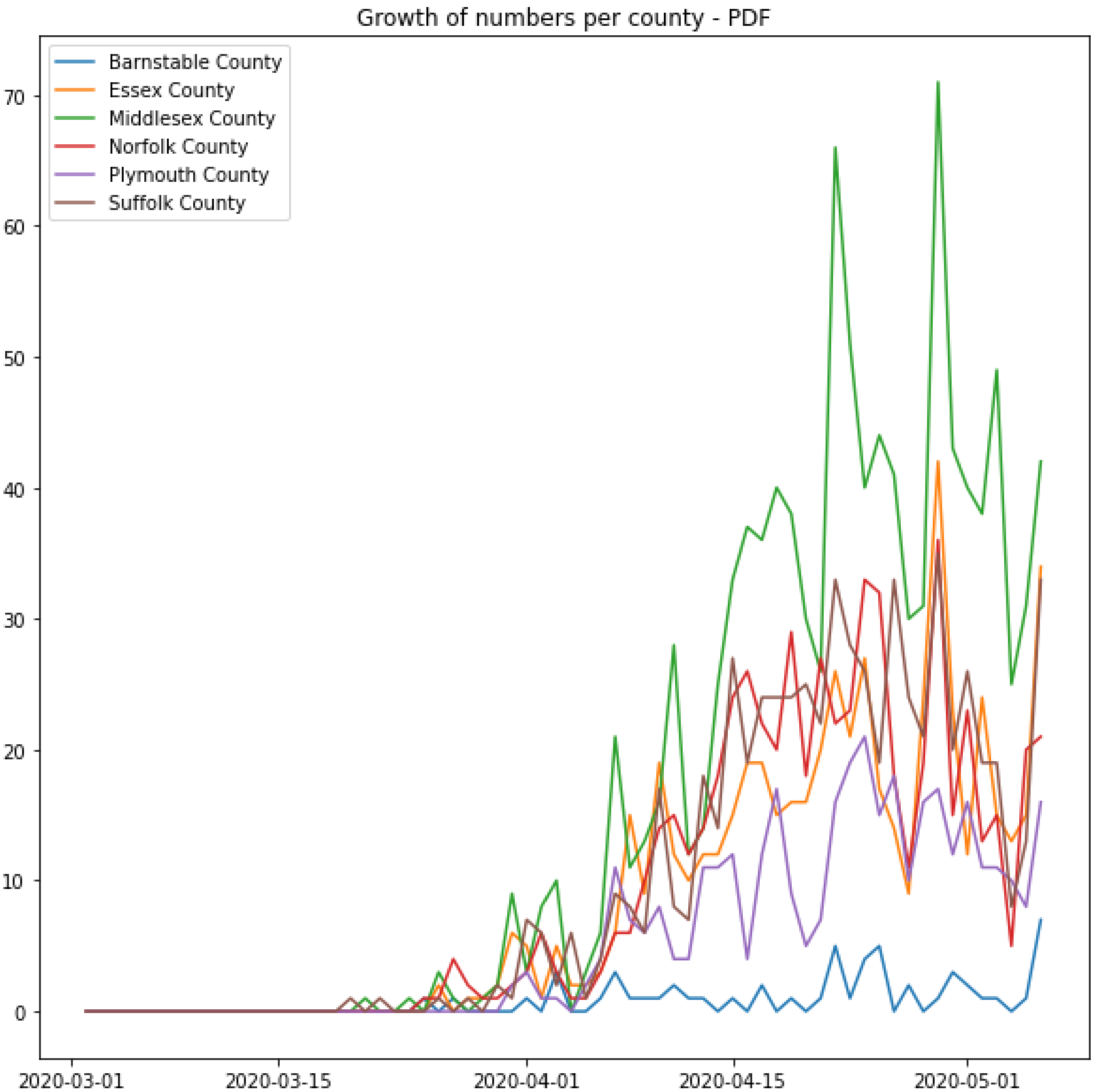
```
Confirmed
*************************
*************************
Data is ranged from 2020-03-02 00:00:00 to 2020-05-06 00:00:00 where total 65
days 00:00:00 are there.
```

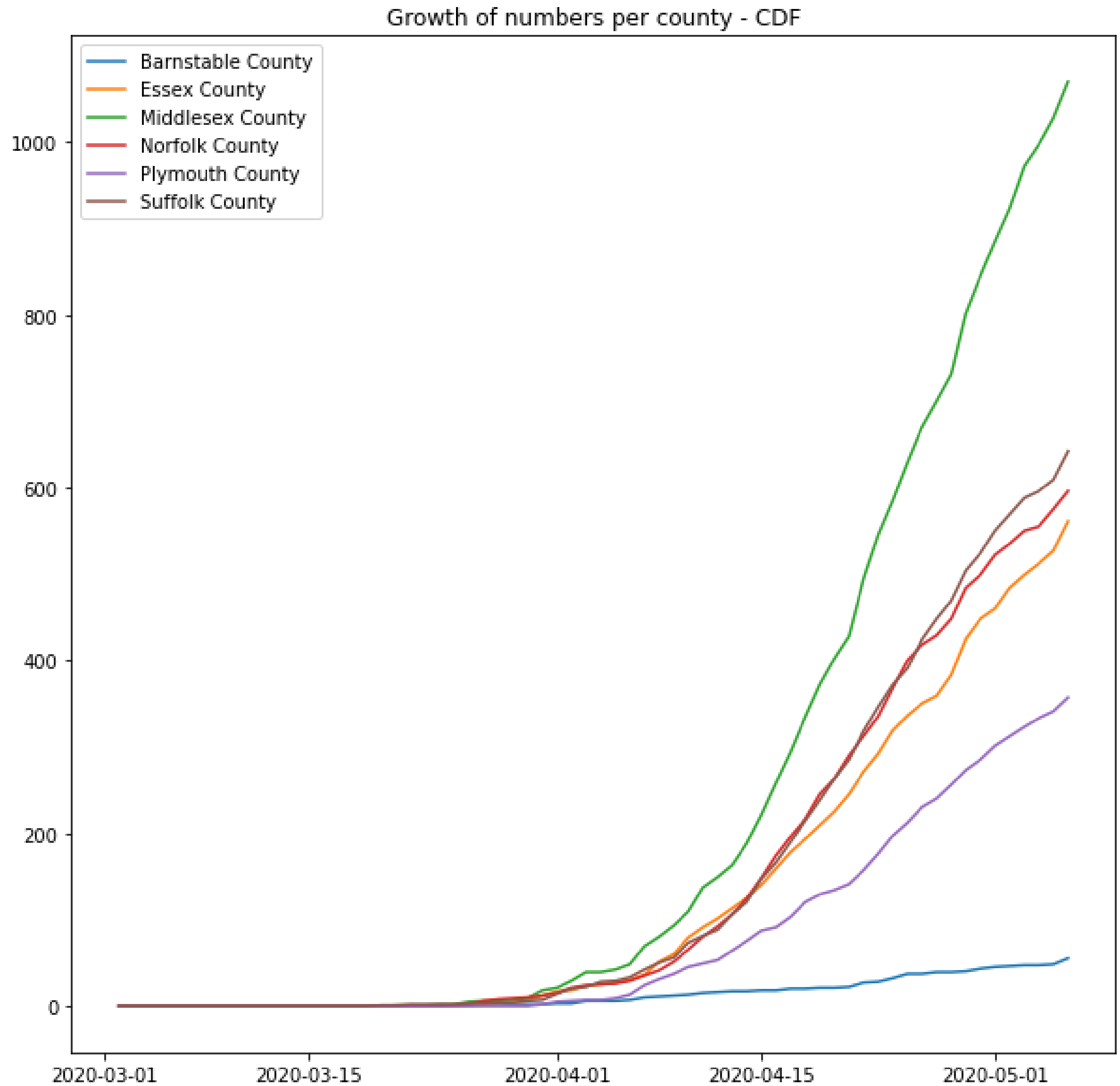




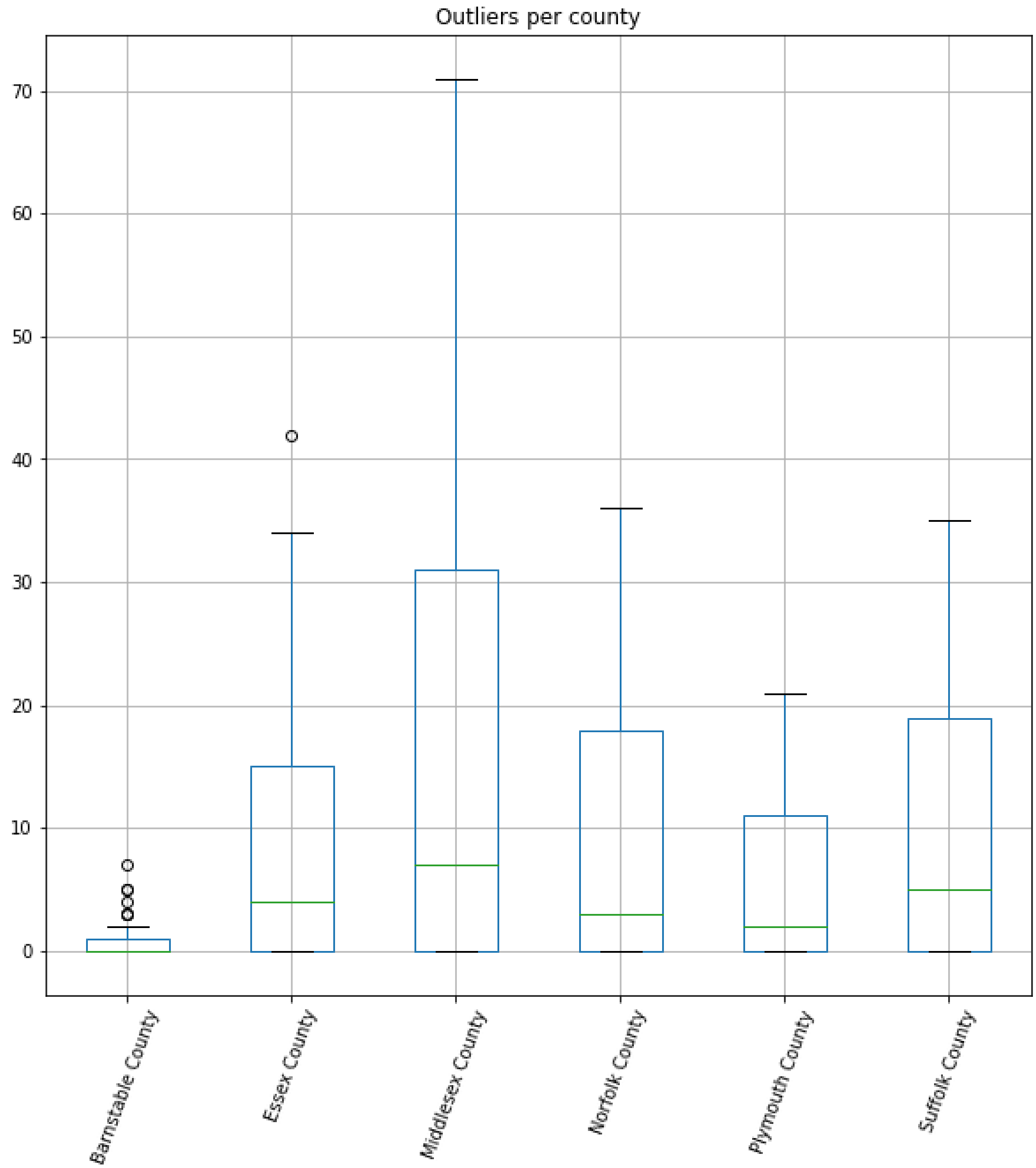

```
Before removing outliers, total records 66
After removing outliers, total records 66
********************
Outliers per County
********************
Barnstable County => 0
Essex County => 0
Middlesex County => 0
Norfolk County => 0
Plymouth County => 1
Suffolk County => 0
********************
Same is shown using boxplot of pandas
Deaths
*************************
*************************
Data is ranged from 2020-03-02 00:00:00 to 2020-05-06 00:00:00 where total 65
days 00:00:00 are there.
```


Outliers per county
1000
800
600
400
200
0
Barnstable County
Essex County
Middlesex County
Norfolk County
Plymouth County
Suffolk County


Growth of numbers per county - PDF
Barnstable County
Essex County
Middlesex County
Norfolk County
Plymouth County
Suffolk County
0
10
20
30
40
50
60
70
2020-03-01
2020-03-15
2020-04-01
2020-04-15
2020-05-01




```
Before removing outliers, total records 66
After removing outliers, total records 66
********************
Outliers per County
********************
Barnstable County => 4
Essex County => 0
Middlesex County => 0
Norfolk County => 0
Plymouth County => 0
Suffolk County => 0
********************
Same is shown using boxplot of pandas
```



Required Inference #1

Pre-processing

In [0]:
```
#confirmed = pd.read_csv('MA_COVID_CONFIRMED.csv')
# confirmed = confirmed.rename(columns={'Unnamed: 0':'Date'})
```

In [0]:
```
# deaths = pd.read_csv('MA_COVID_DEATHS.csv')
# deaths = deaths.rename(columns={'Unnamed: 0':'Date'})
```

In [0]:
```
#Bring the dates to a standard format
# STD_DATE_FORMAT = '%m/%d/%Y'
# DATA_DATE_FORMAT = '%m/%d/%y'
# confirmed.Date = pd.to_datetime(confirmed.Date, format=DATA_DATE_FORMAT).dt.strftime(STD_DATE_FORMAT)
# deaths.Date = pd.to_datetime(deaths.Date, format=DATA_DATE_FORMAT).dt.strftime(STD_DATE_FORMAT)
```

In [0]:
```
#MA Counties chosen for analysis
SELECTED_COUNTIES = ['Suffolk County', 'Middlesex County', 'Essex County', 'Norfolk County', 'Plymouth County', 'Barnstable County']
# confirmed=confirmed[['Date']+SELECTED_COUNTIES]
# deaths=deaths[['Date']+SELECTED_COUNTIES]
```

In [146]:
```
deaths.tail()
```

Out[146]:

	Date	Barnstable County	Essex County	Middlesex County	Norfolk County	Plymouth County	Suffolk County
101	2020-05-02	1	24	38	13	11	19
102	2020-05-03	1	15	49	15	11	19
103	2020-05-04	0	13	25	5	10	8
104	2020-05-05	1	15	31	20	8	13
105	2020-05-06	7	34	42	21	16	33

In [0]:
```
#Preprocessing data to have a consistent and standard format mm/dd/YYYY
def filter_dataframe(df, start_date_str):
  start_date = datetime.datetime.strptime(start_date_str,STD_DATE_FORMAT)
  delta = datetime.timedelta(days=27)
  end_date = start_date + delta
  end_date_str = end_date.strftime(STD_DATE_FORMAT)
  return df[(df.Date >= start_date_str) & (df.Date <= end_date_str)]
```

In [0]:
```
#Split 1 month data into 3 weeks : 1 week for train and test
def train_test_split(dframe):
  train_data = dframe.iloc[:dframe.shape[0]-7]
  test_data = dframe.iloc[dframe.shape[0]-7:]
  return (train_data, test_data)
```

Base data for monthly time series prediction

In [0]:
```
#Required dataset for Time Series Analysis of 1 month
reqd_df = filter_dataframe(confirmed, "04/01/2020")
reqd_death_df = filter_dataframe(deaths, "04/01/2020")
```

In [150]:
```
reqd_df.head()
```

Out[150]:

	Date	Barnstable County	Essex County	Middlesex County	Norfolk County	Plymouth County	Suffolk County
70	2020-04-01	64	101	242	91	102	251
71	2020-04-02	28	154	288	109	60	272
72	2020-04-03	31	199	332	107	124	287
73	2020-04-04	16	162	266	154	153	246
74	2020-04-05	17	106	164	72	65	229

In [151]:
```
reqd_death_df.head()
```

Out[151]:

	Date	Barnstable County	Essex County	Middlesex County	Norfolk County	Plymouth County	Suffolk County
70	2020-04-01	1	5	3	3	3	7
71	2020-04-02	0	1	8	6	1	6
72	2020-04-03	3	5	10	3	1	2
73	2020-04-04	0	2	0	1	0	6
74	2020-04-05	0	2	3	1	2	1

MAPE

In [0]:
```
#Calculate Mean Absolute Prediction Error %
# E(MAPE) = [Sum({|Y-Y_hat|/Y}) * 100]/n
def calc_mape(test_df, pred_df):
  residuals = abs(test_df.sub(pred_df))
  percent_diff = (residuals.div(test_df)) * 100
  percent_diff = percent_diff.replace(np.inf, 0)
  mape_perc = percent_diff.sum().div(test_df.shape[0])
  cumulative_mape = percent_diff.values.sum()/(test_df.shape[0]*test_df.shape[
1])
  return mape_perc, cumulative_mape
```

MSE

In [0]:
```
#Calculate Mean Squared Error
# E(MSE) = [Sum(|Y-Y_hat|)^2]/n
def calc_mse(test_df, pred_df):
  residuals = test_df.sub(pred_df)
  res_sq = residuals ** 2
  res_sq_sum = res_sq.sum()
  mse = res_sq_sum.div(test_df.shape[0])
  cumulative_mse = res_sq_sum.values.sum()/(test_df.shape[0]*test_df.shape[1])
  return mse, cumulative_mse
```

Exponentially Weighted Moving Avg

In [0]:
```
from math import pow
```

In [0]:
```
#EWMA
#required parameters: train_data, test_data, alpha
#train_data, test_data: rows-dates, cols-county

#The logic below calculates the EWMA prediction for t and then goes from t to
 t+7 iteratively
def calculate_ewma_coming_week(train_data, test_data, alpha):
  train_data_reqd = train_data.iloc[:train_data.shape[0]-1]
  train_len = train_data_reqd.shape[0]

  #Create a mask of [alpha, alpha(1-alpha), alpha(1-alpha)^2 ... alpha(1-alph
a)^i] to multiply with t-i values
  alpha_mask = [alpha * pow((1.0-alpha),train_len-1-i) for i in range(train_le
n)]
  element_mul = train_data_reqd[SELECTED_COUNTIES].mul(alpha_mask, axis=0)

  #Cumulative sum to get the predicted value for t without the first term
  dot_product = element_mul.sum(axis=0)

  #predicted_t with the first term added
  predicted_t = dot_product +  train_data_reqd.iloc[0][SELECTED_COUNTIES] * po
w((1.0-alpha),train_len)
  true_t = train_data.iloc[train_data.shape[0]-1][SELECTED_COUNTIES]


  ewma_df = pd.DataFrame(columns=SELECTED_COUNTIES)
  ewma_dt_series =  test_data.Date

  #prediction for next 7 days
  for ind in test_data.index:
    predicted_t1 = alpha * true_t + (1.0 - alpha) * predicted_t
    true_t = test_data.loc[ind][SELECTED_COUNTIES]
    predicted_t = predicted_t1
    ewma_df.loc[ind] = predicted_t

  ewma_df.insert(0,'Date',ewma_dt_series)
  return ewma_df
```

In [156]:
```
#Train Test Split for cases
train_cases, test_cases = train_test_split(reqd_df)
test_cases
```

Out[156]:

	Date	Barnstable County	Essex County	Middlesex County	Norfolk County	Plymouth County	Suffolk County
91	2020-04-22	6	262	473	150	210	391
92	2020-04-23	30	436	630	329	276	679
93	2020-04-24	39	622	957	438	631	985
94	2020-04-25	9	371	572	193	220	494
95	2020-04-26	16	277	395	116	0	325
96	2020-04-27	26	219	305	110	227	340
97	2020-04-28	22	264	464	169	137	257

In [157]:
```
#Train Test split for deaths
train_death, test_death = train_test_split(reqd_death_df)
test_death
```

Out[157]:

	Date	Barnstable County	Essex County	Middlesex County	Norfolk County	Plymouth County	Suffolk County
91	2020-04-22	5	26	66	22	16	33
92	2020-04-23	1	21	51	23	19	28
93	2020-04-24	4	27	40	33	21	26
94	2020-04-25	5	17	44	32	15	19
95	2020-04-26	0	14	41	18	18	33
96	2020-04-27	2	9	30	11	10	24
97	2020-04-28	0	24	31	19	16	21

1) alpha = 0.5

1.1) Cases

In [0]:
```
ewma_cases = calculate_ewma_coming_week(train_cases,test_cases,0.5)
```

In [159]:
```
ewma_cases
```

Out[159]:

	Date	Suffolk County	Middlesex County	Essex County	Norfolk County	Plymouth County	Barnstable County
91	2020-04-22	339.409661	433.777086	218.867452	130.855337	102.003332	19.556002
92	2020-04-23	365.204831	453.388543	240.433726	140.427669	156.001666	12.778001
93	2020-04-24	522.102415	541.694272	338.216863	234.713834	216.000833	21.389000
94	2020-04-25	753.551208	749.347136	480.108431	336.356917	423.500417	30.194500
95	2020-04-26	623.775604	660.673568	425.554216	264.678459	321.750208	19.597250
96	2020-04-27	474.387802	527.836784	351.277108	190.339229	160.875104	17.798625
97	2020-04-28	407.193901	416.418392	285.138554	150.169615	193.937552	21.899313

In [160]:
```
#MAPE
result = calc_mape(test_cases[SELECTED_COUNTIES], ewma_cases[SELECTED_COUNTIES
])
print('County-level MAPE:\n{}'.format(result[0]))
print('\nCumulative MAPE: \n{}'.format(result[1]))
```

```
County-level MAPE:
Suffolk County       49.834595
Middlesex County     37.328905
Essex County         36.912607
Norfolk County       57.588497
Plymouth County      46.266213
Barnstable County    88.353588
dtype: float64

Cumulative MAPE:
52.71406733438793
```

In [161]:
```
#MSE
result = calc_mse(test_cases[SELECTED_COUNTIES], ewma_cases[SELECTED_COUNTIES
])
print('County-level MSE:\n{}'.format(result[0]))
print('\nCumulative MSE: \n{}'.format(result[1]))
```

```
County-level MSE:
Suffolk County       73236.446470
Middlesex County     51309.083526
Essex County         24650.932823
Norfolk County       18102.396054
Plymouth County      50119.598818
Barnstable County      188.561354
dtype: float64

Cumulative MSE:
36267.83650743744
```

1.2) Deaths

In [0]:
```
ewma_deaths = calculate_ewma_coming_week(train_death,test_death,0.5)
```

In [163]:
```
ewma_deaths
```

Out[163]:

	Date	Suffolk County	Middlesex County	Essex County	Norfolk County	Plymouth County	Barnstable County
91	2020-04-22	23.114152	29.868278	18.038170	24.278209	7.542593	0.699759
92	2020-04-23	28.057076	47.934139	22.019085	23.139104	11.771297	2.849880
93	2020-04-24	28.028538	49.467069	21.509542	23.069552	15.385648	1.924940
94	2020-04-25	27.014269	44.733535	24.254771	28.034776	18.192824	2.962470
95	2020-04-26	23.007134	44.366767	20.627386	30.017388	16.596412	3.981235
96	2020-04-27	28.003567	42.683384	17.313693	24.008694	17.298206	1.990617
97	2020-04-28	26.001784	36.341692	13.156846	17.504347	13.649103	1.995309

In [164]:
```
#MAPE
result = calc_mape(test_death[SELECTED_COUNTIES], ewma_deaths[SELECTED_COUNTIE
S])
print('County-level MAPE:\n{}'.format(result[0]))
print('\nCumulative MAPE: \n{}'.format(result[1]))
```

```
County-level MAPE:
Suffolk County       21.560621
Middlesex County     21.973166
Essex County         40.482572
Norfolk County       35.191409
Plymouth County      33.485426
Barnstable County    52.012716
dtype: float64

Cumulative MAPE:
34.11765176436394
```

In [165]:
```
#MSE
result = calc_mse(test_death[SELECTED_COUNTIES], ewma_deaths[SELECTED_COUNTIES
])
print('County-level MSE:\n{}'.format(result[0]))
print('\nCumulative MSE: \n{}'.format(result[1]))
```

```
County-level MSE:
Suffolk County        43.854353
Middlesex County     229.400195
Essex County          53.974259
Norfolk County        62.203870
Plymouth County       32.322507
Barnstable County      7.171872
dtype: float64

Cumulative MSE:
71.48784265416835
```

2) alpha = 0.8

2.1) Cases

In [0]:
```
ewma_cases = calculate_ewma_coming_week(train_cases,test_cases,0.8)
```

In [167]:
```
ewma_cases
```

Out[167]:

	Date	Suffolk County	Middlesex County	Essex County	Norfolk County	Plymouth County	Barnstable County
91	2020-04-22	337.951165	395.427905	213.181624	114.410965	82.147117	13.008314
92	2020-04-23	380.390233	457.485581	252.236325	142.882193	184.429423	7.401663
93	2020-04-24	619.278047	595.497116	399.247265	291.776439	257.685885	25.480333
94	2020-04-25	911.855609	884.699423	577.449453	408.755288	556.337177	36.296067
95	2020-04-26	577.571122	634.539885	412.289891	236.151058	287.267435	14.459213
96	2020-04-27	375.514224	442.907977	304.057978	140.030212	57.453487	15.691843
97	2020-04-28	347.102845	332.581595	236.011596	116.006042	193.090697	23.938369

In [168]:
```
#MAPE
result = calc_mape(test_cases[SELECTED_COUNTIES], ewma_cases[SELECTED_COUNTIES
])
print('County-level MAPE:\n{}'.format(result[0]))
print('\nCumulative MAPE: \n{}'.format(result[1]))
```

```
County-level MAPE:
Suffolk County       43.211381
Middlesex County     38.629608
Essex County         35.788819
Norfolk County       55.386789
Plymouth County      60.247873
Barnstable County    84.025131
dtype: float64

Cumulative MAPE:
52.88160027517485
```

In [169]:
```
#MSE
result = calc_mse(test_cases[SELECTED_COUNTIES], ewma_cases[SELECTED_COUNTIES
])
print('County-level MSE:\n{}'.format(result[0]))
print('\nCumulative MSE: \n{}'.format(result[1]))
```

```
County-level MSE:
Suffolk County       67644.254826
Middlesex County     51130.383211
Essex County         22102.006376
Norfolk County       17426.363049
Plymouth County      55947.488755
Barnstable County      228.578196
dtype: float64

Cumulative MSE:
35746.5124022134
```

2.2 Deaths

In [0]:
```
ewma_deaths = calculate_ewma_coming_week(train_death,test_death,0.8)
```

In [171]:
```
ewma_deaths
```

Out[171]:

	Date	Suffolk County	Middlesex County	Essex County	Norfolk County	Plymouth County	Barnstable County
91	2020-04-22	22.558750	27.129534	19.198105	25.572264	6.813936	0.834614
92	2020-04-23	30.911750	58.225907	24.639621	22.714453	14.162787	4.166923
93	2020-04-24	28.582350	52.445181	21.727924	22.942891	18.032557	1.633385
94	2020-04-25	26.516470	42.489036	25.945585	30.988578	20.406511	3.526677
95	2020-04-26	20.503294	43.697807	18.789117	31.797716	16.081302	4.705335
96	2020-04-27	30.500659	41.539561	14.957823	20.759543	17.616260	0.941067
97	2020-04-28	25.300132	32.307912	10.191565	12.951909	11.523252	1.788213

In [172]:
```
#MAPE
result = calc_mape(test_death[SELECTED_COUNTIES], ewma_deaths[SELECTED_COUNTIE
S])
print('County-level MAPE:\n{}'.format(result[0]))
print('\nCumulative MAPE: \n{}'.format(result[1]))
```

```
County-level MAPE:
Suffolk County       25.280492
Middlesex County     22.410621
Essex County         39.083017
Norfolk County       35.475002
Plymouth County      35.406817
Barnstable County    77.368356
dtype: float64

Cumulative MAPE:
39.170717457668516
```

In [173]:
```
#MSE
result = calc_mse(test_death[SELECTED_COUNTIES], ewma_deaths[SELECTED_COUNTIES
])
print('County-level MSE:\n{}'.format(result[0]))
print('\nCumulative MSE: \n{}'.format(result[1]))
```

```
County-level MSE:
Suffolk County        56.797313
Middlesex County     266.063243
Essex County          59.490725
Norfolk County        62.459440
Plymouth County       32.506941
Barnstable County      8.801517
dtype: float64

Cumulative MSE:
81.01986310663062
```

Comments

---

1 month data from 1st April 2020 onwards was considered for the test.
If we look at the MAPE and MSE values for EWMA Prediction, the numbers are pretty high for number of confrmed cases. This is first of all due to the highly fluctuating nature of the data and how EWMA works. For EWMA, the highest weight is given to prediction of day before which is < 1, so if the data is increasing which was the general trend due to increase in testing around April.
On the other hand, the predictions for deaths were better, especially for MSE which could be due to a) Empiral factors resulting from less wildly fluctuating data such that the residual difference came to be low and b) An increase in testing does mean a pro-active approach towards treatment due to which the deaths would be on a downwards/approx. constant curve.
Also, results for alpha=0.8 were slightly worse than alpha=0.5. This is again due to the fact that there were wid fluctuations in the confirmed cases and the values from day before are given the most importance.

Autoregression

In [0]:
```
from numpy.linalg import inv
#Auto-Regression
#required parameters: train_data, test_data, alpha
#train_data, test_data: rows-dates, cols-county
def calculate_ar_coming_week(train_data, test_data):
  pred_list = []
  reqd_cols = [x for x in train_data.columns if x not in ['Date', 'Current']]
  train_feature_mat = train_data[reqd_cols].values
  grd_truth = train_data['Current']

  #Multi Linear regression optimization to estimate Beta
  for new_sample in range(test_data.shape[0]):
    train_feature_mat = train_feature_mat.astype(float)
    x_trans_x =  np.matmul(train_feature_mat.transpose(), train_feature_mat)
    x_trans_x_inv = inv(x_trans_x)
    inv_x_trans = np.matmul(x_trans_x_inv, train_feature_mat.transpose())
    beta_hat = np.matmul(inv_x_trans, grd_truth)
    test_feature_mat = test_data.iloc[new_sample][reqd_cols].values
    prediction = np.matmul(beta_hat, test_feature_mat)
    pred_list.append(prediction)
    train_feature_mat = np.concatenate((train_feature_mat, [test_feature_mat
]))
    grd_truth = np.append(grd_truth,test_data.iloc[0]['Current'])
  return pred_list
```

In [0]:
```
#Create Feature DataFrame out of t-param date records and save them in a
#dictionary keyed on County names

def create_ar_features(dframe, param):
  start_ind = param

  #Create rows as T_0, T_1..., T_param
  t_n_cols = ["T_"+str(i+1) for i in range(param)]
  ar_dframe_dic = dict()

  #Create Dataframe with previous values as features
  for county in SELECTED_COUNTIES:
    county_series = dframe[county]
    county_df = pd.DataFrame(columns=["Current"]+t_n_cols)
    county_df["Current"] = county_series[param:]

    for i,col in enumerate(t_n_cols):
      county_df[col] = county_series.iloc[(param-i-1):(county_series.shape[0]-
i-1)].values
    county_df.insert(0,'Date',dframe['Date'])
    county_df.insert(1,'T_0',1)
    ar_dframe_dic[county] = county_df
  return ar_dframe_dic
```

In [0]:
```
#AR(p) in action
def calc_ar_w_param(reqd_df, param):
  ar_dframe_dic = create_ar_features(reqd_df, param)
  result_df = pd.DataFrame(columns=['Date'] + SELECTED_COUNTIES)

  for county in SELECTED_COUNTIES:
    ar_train, ar_test = train_test_split(ar_dframe_dic[county])
    predictions = calculate_ar_coming_week(ar_train,ar_test)
    result_df['Date'] = ar_test.Date
    result_df[county] = predictions
  return result_df
```

1) AR(3)

1.1) Cases

In [0]:
```
ar_cases = calc_ar_w_param(reqd_df, 3)
```

In [178]:
```
ar_cases
```

Out[178]:

	Date	Suffolk County	Middlesex County	Essex County	Norfolk County	Plymouth County	Barnstable County
91	2020-04-22	347.774720	407.493383	227.474001	144.774769	114.931621	16.183521
92	2020-04-23	409.134352	469.890934	256.752170	164.939646	151.622097	19.729271
93	2020-04-24	544.294401	463.652309	352.831213	195.768038	103.174992	25.734200
94	2020-04-25	594.655738	573.833580	402.168734	207.376363	311.858692	21.301884
95	2020-04-26	308.743887	482.959652	264.998073	201.916526	86.066710	14.055793
96	2020-04-27	236.205367	562.800872	255.663817	216.351344	237.900142	19.616390
97	2020-04-28	356.852709	430.907084	236.740418	162.055693	166.319816	17.908203

In [179]:
```
#MAPE
result = calc_mape(test_cases[SELECTED_COUNTIES], ar_cases[SELECTED_COUNTIES])
print('County-level MAPE:\n{}'.format(result[0]))
print('\nCumulative MAPE: \n{}'.format(result[1]))
```

```
County-level MAPE:
Suffolk County       27.185697
Middlesex County     29.294370
Essex County         19.623664
Norfolk County       41.565845
Plymouth County      34.563027
Barnstable County    61.423757
dtype: float64

Cumulative MAPE:
35.609393268952594
```

In [180]:
```
#MSE
result = calc_mse(test_cases[SELECTED_COUNTIES], ar_cases[SELECTED_COUNTIES])
print('County-level MSE:\n{}'.format(result[0]))
print('\nCumulative MSE: \n{}'.format(result[1]))
```

```
County-level MSE:
Suffolk County       42865.292273
Middlesex County     49802.095351
Essex County         15568.074531
Norfolk County       14938.083870
Plymouth County      45704.437283
Barnstable County       85.397568
dtype: float64

Cumulative MSE:
28160.563479505927
```

1.2) Deaths

In [0]:
```
ar_deaths = calc_ar_w_param(reqd_death_df, 3)
```

In [182]:
```
ar_deaths
```

Out[182]:

	Date	Suffolk County	Middlesex County	Essex County	Norfolk County	Plymouth County	Barnstable County
91	2020-04-22	25.905443	28.464225	17.976441	24.712987	8.592114	1.058792
92	2020-04-23	27.179709	54.875008	24.160308	25.153554	11.963111	0.169577
93	2020-04-24	31.942328	37.030223	23.833126	23.289358	11.844345	0.079749
94	2020-04-25	33.662263	56.428767	25.213386	27.863581	16.305229	1.477084
95	2020-04-26	29.236899	56.164247	22.493000	30.404027	12.330891	4.975571
96	2020-04-27	27.609159	51.482781	16.596328	25.704638	18.004336	2.961476
97	2020-04-28	30.351032	46.642418	14.973219	17.455267	9.492470	2.410970

In [183]:
```
#MAPE
result = calc_mape(test_death[SELECTED_COUNTIES], ar_deaths[SELECTED_COUNTIES
])
print('County-level MAPE:\n{}'.format(result[0]))
print('\nCumulative MAPE: \n{}'.format(result[1]))
```

```
County-level MAPE:
Suffolk County       27.917629
Middlesex County     37.028105
Essex County         41.233093
Norfolk County       39.252500
Plymouth County      41.120844
Barnstable County    54.057835
dtype: float64

Cumulative MAPE:
40.101667540448226
```

In [184]:
```
#MSE
result = calc_mse(test_death[SELECTED_COUNTIES], ar_deaths[SELECTED_COUNTIES])
print('County-level MSE:\n{}'.format(result[0]))
print('\nCumulative MSE: \n{}'.format(result[1]))
```

```
County-level MSE:
Suffolk County        59.418226
Middlesex County     360.484777
Essex County          51.881697
Norfolk County        70.839585
Plymouth County       46.925769
Barnstable County     10.785078
dtype: float64

Cumulative MSE:
100.0558552829318
```

2) AR(5)

1.1) Cases

In [0]:
```
ar_cases = calc_ar_w_param(reqd_df, 5)
```

In [186]:
```
ar_cases
```

Out[186]:

	Date	Suffolk County	Middlesex County	Essex County	Norfolk County	Plymouth County	Barnstable County
91	2020-04-22	359.616842	409.977663	241.302355	147.233266	118.780944	21.427653
92	2020-04-23	446.691871	478.403392	332.049479	175.225993	149.724208	13.557058
93	2020-04-24	536.713027	457.309448	373.650125	218.165215	121.588355	28.356473
94	2020-04-25	514.079828	541.113933	346.319236	204.409128	297.147444	26.233832
95	2020-04-26	352.408289	457.104345	274.881053	197.603423	125.162228	16.048276
96	2020-04-27	134.554522	530.853731	160.737055	212.389116	92.042316	19.601530
97	2020-04-28	265.260863	430.149700	206.516143	151.735340	184.152561	13.489263

In [187]:
```
#MAPE
result = calc_mape(test_cases[SELECTED_COUNTIES], ar_cases[SELECTED_COUNTIES])
print('County-level MAPE:\n{}'.format(result[0]))
print('\nCumulative MAPE: \n{}'.format(result[1]))
```

```
County-level MAPE:
Suffolk County       23.412653
Middlesex County     27.438456
Essex County         18.209299
Norfolk County       39.761562
Plymouth County      42.694038
Barnstable County    84.901696
dtype: float64

Cumulative MAPE:
39.40295050767236
```

In [188]:
```
#MSE
result = calc_mse(test_cases[SELECTED_COUNTIES], ar_cases[SELECTED_COUNTIES])
print('County-level MSE:\n{}'.format(result[0]))
print('\nCumulative MSE: \n{}'.format(result[1]))
```

```
County-level MSE:
Suffolk County       42763.382819
Middlesex County     47658.663408
Essex County         11460.622611
Norfolk County       12793.188467
Plymouth County      46545.852581
Barnstable County      147.435406
dtype: float64

Cumulative MSE:
26894.857548737793
```

1.2) Deaths

In [0]:
```
ar_deaths = calc_ar_w_param(reqd_death_df, 5)
```

In [190]:
```
ar_deaths
```

Out[190]:

	Date	Suffolk County	Middlesex County	Essex County	Norfolk County	Plymouth County	Barnstable County
91	2020-04-22	25.720532	27.857098	19.858437	24.957347	12.059731	0.345856
92	2020-04-23	27.593486	56.043748	23.627403	26.904445	12.994361	0.286697
93	2020-04-24	31.305744	39.589902	23.074560	25.931849	8.168888	-0.363957
94	2020-04-25	33.637790	33.608070	21.760366	25.776400	10.769638	1.783760
95	2020-04-26	29.543109	65.904369	21.958248	29.949514	12.330947	6.580371
96	2020-04-27	31.387289	61.099273	19.472315	27.415229	18.787728	1.338281
97	2020-04-28	31.654441	52.703334	16.384119	20.223425	13.675082	2.840718

In [191]:
```
#MAPE
result = calc_mape(test_death[SELECTED_COUNTIES], ar_deaths[SELECTED_COUNTIES
])
print('County-level MAPE:\n{}'.format(result[0]))
print('\nCumulative MAPE: \n{}'.format(result[1]))
```

```
County-level MAPE:
Suffolk County       30.421396
Middlesex County     46.677515
Essex County         40.515740
Norfolk County       41.905764
Plymouth County      39.920143
Barnstable County    52.988978
dtype: float64

Cumulative MAPE:
42.07158951701823
```

In [192]:
```
#MSE
result = calc_mse(test_death[SELECTED_COUNTIES], ar_deaths[SELECTED_COUNTIES])
print('County-level MSE:\n{}'.format(result[0]))
print('\nCumulative MSE: \n{}'.format(result[1]))
```

```
County-level MSE:
Suffolk County        67.944427
Middlesex County     520.986833
Essex County          44.813848
Norfolk County        75.204279
Plymouth County       49.842052
Barnstable County     14.766715
dtype: float64

Cumulative MSE:
128.92635902628646
```

Comments

The trends seen for EWMA repeat in Auto-regression as well. Although, overall the MAPE and MSE for confirmed case look a bit better than EWMA, the general picture looks the same.
This can probably be attributed to the fact that rather than consider all the previous months' values, only 3 or 5 previous data points are being considered.
Here too, the prediction metrics for deaths show a better result due to low variance in the data for a better part of April.
Also, the weights calculated are based on minimizing the loss rather than choosing an alpha value which should lead to better results.

Required Inference #2

In [0]:
```
#Preprocessing data to have a consistent and standar format mm/dd/YYYY
def filter_dataframe(df, start_date_str):
 start_date = datetime.datetime.strptime(start_date_str,STD_DATE_FORMAT)
 delta = datetime.timedelta(days=7)
 end_date = start_date + delta
 end_date_str = end_date.strftime(STD_DATE_FORMAT)
 return df[(df.Date >= start_date_str) & (df.Date <= end_date_str)]
```

In [0]:
```
#Classifying data into second last week and last week
confirmed_2ndlast_week = filter_dataframe(confirmed, "03/22/2020")
confirmed_final_week =  filter_dataframe(confirmed, "03/29/2020")
deaths_2ndlast_week = filter_dataframe(deaths, "03/22/2020")
deaths_final_week =  filter_dataframe(deaths, "03/29/2020")
```

In [0]:
```
confirmed_temp_last_week = confirmed_final_week[SELECTED_COUNTIES].diff()
confirmed_temp_second_last_week = confirmed_2ndlast_week[SELECTED_COUNTIES].di
ff()
deaths_temp_last_week = deaths_final_week[SELECTED_COUNTIES].diff()
deaths_temp_second_last_week = deaths_2ndlast_week[SELECTED_COUNTIES].diff()

confirmed_temp_last_week['Total'] = confirmed_temp_last_week.sum(axis = 1)
confirmed_temp_second_last_week['Total'] = confirmed_temp_second_last_week.sum
(axis=1)
deaths_temp_last_week['Total'] = deaths_temp_last_week.sum(axis=1)
deaths_temp_second_last_week['Total'] = deaths_temp_second_last_week.sum(axis=
1)

confirmed_last_week = confirmed_temp_last_week['Total'][1:]
confirmed_second_last_week = confirmed_temp_second_last_week['Total'][1:]
deaths_last_week = deaths_temp_last_week['Total'][1:]
deaths_second_last_week = deaths_temp_second_last_week['Total'][1:]
```

INFERENCES FOR NUMBER OF DEATHS

Z TEST

In [196]:
```
def z_test(deaths1, deaths2):
  mean_deaths_last_week = deaths1.mean()
  mean_deaths_secondlast_week = deaths2.mean()
  variance_secondlast_week = deaths2.var()
  z_stat = abs((mean_deaths_last_week - mean_deaths_secondlast_week) / math.sq
rt( variance_secondlast_week/ len(deaths1)))
  if z_stat > 1.96:
    print("Mean deaths for second last week and last week are different becaus
e of the z statistic value",z_stat,"is greater than alpha at 0.05")
  else:
    print("Mean deaths for second last week and last week are same because of
 the z statistic value",z_stat,"is less than alpha at 0.05")

z_test(deaths_last_week, deaths_second_last_week)
```

```
Mean deaths for second last week and last week are same because of the z stat
istic value 0.6405126152203484 is less than alpha at 0.05
```

Conclusion - \ With the assumption that variance should be known and test is applicable only if n is large and the data is normally distributed, we can conclude that this test is infact applicable because all the assumptions hold true.

1 SAMPLE T TEST

In [197]:
```
def t_test_1sample(deaths1, deaths2):
  mean_deaths_secondlast_week = deaths2.mean()
  mean_deaths_last_week = deaths1.mean()
  variance_secondlast_week = deaths2.var()
  t_stat = abs((mean_deaths_secondlast_week - mean_deaths_last_week) / math.sq
rt(variance_secondlast_week/ len(deaths1)))
  if t_stat > 2.447:
    print("Mean deaths for second last week and last week are different becaus
e of the t statistic value",t_stat,"is greater than alpha at 0.05")
  else:
    print("Mean deaths for second last week and last week are same because of
 the t statistic value",t_stat,"is less than alpha at 0.05")


t_test_1sample(deaths_last_week, deaths_second_last_week)
```

```
Mean deaths for second last week and last week are same because of the t stat
istic value 0.6405126152203484 is less than alpha at 0.05
```

Conclusion - \ T test is applicable because it has no such assumptions but is useful when n is small. \ Hence this test is also applicable here.

2 SAMPLE UNPAIRED T TEST

In [198]:
```
def t_test_2sample_unpaired(deaths1, deaths2):
  mean_deaths_last_week = deaths1.mean()
  mean_deaths_secondlast_week = deaths2.mean()
  variance_last_week = deaths1.var()
  variance_secondlast_week = deaths1.var()
  t_stat = abs((mean_deaths_last_week - mean_deaths_secondlast_week) / math.sq
rt( variance_last_week/ 7 + variance_secondlast_week/ len(deaths1)))
  if t_stat > 1.96:
    print("Mean deaths for second last week and last week are different becaus
e of the t statistic value",t_stat,"is greater than alpha at 0.05")
  else:
    print("Mean deaths for second last week and last week are same because of
 the t statistic value",t_stat,"is less than alpha at 0.05")


t_test_2sample_unpaired(deaths_last_week, deaths_second_last_week)
```

```
Mean deaths for second last week and last week are same because of the t stat
istic value 0.12887589588356851 is less than alpha at 0.05
```

Conclusion - In 2 sample unpaired T test both the distributions must be independent. \ In this case the mean number of deaths in second last week are independent on mean number of deaths in the last week. \ Hence this test is also applicable.

2 SAMPLE PAIRED T TEST

In [199]:
```
def t_test_2sample_paired(deaths1, deaths2):
  mean_deaths_last_week = deaths1.mean()
  mean_deaths_secondlast_week = deaths2.mean()
  variance_last_week = deaths1.var()
  variance_secondlast_week = deaths2.var()
  difference = mean_deaths_last_week - mean_deaths_secondlast_week

  t_stat = abs(difference/ math.sqrt(variance_last_week/len(deaths1)))
  if t_stat > 1.96:
    print("Mean deaths for second last week and last week are different becaus
e of the t statistic value",t_stat,"is greater than alpha at 0.05")
  else:
    print("Mean deaths for second last week and last week are same because of
 the t statistic value",t_stat,"is less than alpha at 0.05")

t_test_2sample_paired(deaths_last_week, deaths_second_last_week)
```

```
Mean deaths for second last week and last week are same because of the t stat
istic value 0.1822580398215255 is less than alpha at 0.05
```

Conclusion - In 2 sample paired T test both the distributions must be dependent. \ In this case the mean number of deaths in second last week are not dependent on the mean number of deaths in the last week. \ Hence this test is not applicable.

1 SAMPLE WALDS TEST

In [200]:
```
def walds_test_1sample(deaths1, deaths2):
  mean_deaths_last_week = deaths1.mean()
  mean_deaths_secondlast_week = deaths2.mean()
  variance_last_week = deaths1.var()
  variance_secondlast_week = deaths2.var()
  walds_stat = abs((mean_deaths_secondlast_week - mean_deaths_last_week)/math.
sqrt(mean_deaths_secondlast_week/len(deaths1)))
  if walds_stat > 1.96:
    print("Mean deaths for second last week and last week are different becaus
e of the walds statistic value",walds_stat,"is greater than alpha at 0.05")
  else:
    print("Mean deaths for second last week and last week are same because of
 the walds statistic value",walds_stat,"is less than alpha at 0.05")


walds_test_1sample(deaths_last_week, deaths_second_last_week)
```

```
Mean deaths for second last week and last week are different because of the w
alds statistic value 2.8284271247461903 is greater than alpha at 0.05
```

Conclusion - \ In this the estimator must be asymptotically normal. \ Here the assumptions holds true and hence this test is applicable here.

2 SAMPLE WALDS TEST

In [201]:
```
def walds_test_2sample(deaths1, deaths2):
  mean_deaths_last_week = deaths1.mean()
  mean_deaths_secondlast_week = deaths2.mean()
  variance_last_week = deaths1.var()
  variance_secondlast_week = deaths2.var()
  walds_stat = abs((mean_deaths_secondlast_week - mean_deaths_last_week)/math.
sqrt((mean_deaths_secondlast_week/len(deaths2)) + (mean_deaths_last_week/len(d
eaths1))))
  if walds_stat > 1.96:
    print("Mean deaths for second last week and last week are different becaus
e of the walds statistic value",walds_stat,"is greater than alpha at 0.05")
  else:
    print("Mean deaths for second last week and last week are same because of
 the t statistic value",walds_stat,"is less than alpha at 0.05")


walds_test_2sample(deaths_last_week, deaths_second_last_week)
```

```
Mean deaths for second last week and last week are same because of the t stat
istic value 1.4142135623730951 is less than alpha at 0.05
```

Conclusion - \ In this both distributions must be independent and both the estimators must be asymptotically normal. Both these assumptions hold true in this case, hence this test is applicable.

INFERENCE FOR NUMBER OF CASES

Z TEST

In [202]:
```
def z_test(cases1, cases2):
  mean_cases_last_week = cases1.mean()
  mean_cases_secondlast_week = cases2.mean()
  variance_last_week = cases1.var()
  variance_secondlast_week = cases2.var()
  z_stat = abs((mean_cases_last_week - mean_cases_secondlast_week) / math.sqrt
( variance_secondlast_week/ len(cases1)))
  if z_stat > 1.96:
    print("Mean cases for second last week and last week are different because
of the z statistic value",z_stat,"is greater than alpha at 0.05")
  else:
    print("Mean cases for second last week and last week are same because of t
he z statistic value",z_stat,"is less than alpha at 0.05")


z_test(confirmed_last_week, confirmed_second_last_week)
```

```
Mean cases for second last week and last week are same because of the z stati
stic value 0.4177339723905385 is less than alpha at 0.05
```

Conclusion - \ With the assumption that variance should be known and test is applicable only if n is large and the data is normally distributed, we can conclude that this test is infact applicable because all the assumptions hold true.

1 SAMPLE T TEST

In [203]:
```
def t_test_1sample(cases1, cases2):
  mean_cases_secondlast_week = cases2.mean()
  mean_cases_last_week = cases1.mean()
  variance_secondlast_week = cases2.var()
  t_stat = abs((mean_cases_secondlast_week - mean_cases_last_week) / math.sqrt
(variance_secondlast_week/ len(cases1)))
  if t_stat > 2.447:
    print("Mean cases for second last week and last week are different because
of the t statistic value",t_stat,"is greater than alpha at 0.05")
  else:
    print("Mean cases for second last week and last week are same because of t
he t statistic value",t_stat,"is less than alpha at 0.05")

t_test_1sample(confirmed_last_week, confirmed_second_last_week)
```

```
Mean cases for second last week and last week are same because of the t stati
stic value 0.4177339723905385 is less than alpha at 0.05
```

Conclusion - \ T test is applicable because it has no such assumptions but is useful when n is small. \ Hence this test is also applicable here.

2 SAMPLE UNPAIRED T TEST

In [204]:
```
def t_test_2sample_unpaired(cases1, cases2):
  mean_cases_secondlast_week = cases2.mean()
  mean_cases_last_week = cases1.mean()
  variance_secondlast_week = cases2.var()
  variance_last_week = cases1.var()
  t_stat = abs((mean_cases_last_week - mean_cases_secondlast_week) / math.sqrt
( variance_last_week/ len(cases2) + variance_secondlast_week/ len(cases1)))
  if t_stat > 1.96:
    print("Mean cases for second last week and last week are different because
of the t statistic value",t_stat,"is greater than alpha at 0.05")
  else:
    print("Mean cases for second last week and last week are same because of t
he t statistic value",t_stat,"is less than alpha at 0.05")


t_test_2sample_unpaired(confirmed_last_week, confirmed_second_last_week)
```

```
Mean cases for second last week and last week are same because of the t stati
stic value 0.2754365511142155 is less than alpha at 0.05
```

Conclusion - In 2 sample unpaired T test both the distributions must be independent. \ In this case the mean number of deaths in second last week are independent on mean number of deaths in the last week. \ Hence this test is also applicable.

2 SAMPLE PAIRED T TEST

In [205]:
```
def t_test_2sample_paired(cases1, cases2):
  mean_cases_secondlast_week = cases2.mean()
  mean_cases_last_week = cases1.mean()
  variance_secondlast_week = cases2.var()
  variance_last_week = cases1.var()
  t_stat = abs((mean_cases_last_week - mean_cases_secondlast_week) / math.sqrt
( variance_last_week/ len(cases1)))
  if t_stat > 1.96:
    print("Mean cases for second last week and last week are different because
of the t statistic value",t_stat,"is greater than alpha at 0.05")
  else:
    print("Mean cases for second last week and last week are same because of t
he t statistic value",t_stat,"is less than alpha at 0.05")

t_test_2sample_paired(confirmed_last_week, confirmed_second_last_week)
```

```
Mean cases for second last week and last week are same because of the t stati
stic value 0.36635557893726833 is less than alpha at 0.05
```

Conclusion - In 2 sample paired T test both the distributions must be dependent. \ In this case the mean number of deaths in second last week are not dependent on the mean number of deaths in the last week. \ Hence this test is not applicable.

1 SAMPLE WALDS TEST

In [206]:
```
def walds_test_1sample(cases1, cases2):
  mean_cases_secondlast_week = cases2.mean()
  mean_cases_last_week = cases1.mean()
  variance_secondlast_week = cases2.var()
  variance_last_week = cases1.var()
  walds_stat = abs((mean_cases_secondlast_week - mean_cases_last_week)/math.sq
rt(mean_cases_secondlast_week/len(cases1)))
  if walds_stat > 1.96:
    print("Mean cases for second last week and last week are different because
of the walds statistic value",walds_stat,"is greater than alpha at 0.05")
  else:
    print("Mean cases for second last week and last week are same because of t
he walds statistic value",walds_stat,"is less than alpha at 0.05")


walds_test_1sample(confirmed_last_week, confirmed_second_last_week)
```

```
Mean cases for second last week and last week are different because of the wa
lds statistic value 9.476482128292727 is greater than alpha at 0.05
```

Conclusion - \ In this the estimator must be asymptotically normal. \ Here the assumptions holds true and hence this test is applicable here.

2 SAMPLE WALDS TEST

In [207]:
```
def walds_test_2sample(cases1, cases2):
  mean_cases_secondlast_week = cases2.mean()
  mean_cases_last_week = cases1.mean()
  variance_secondlast_week = cases2.var()
  variance_last_week = cases1.var()
  walds_stat = abs((mean_cases_secondlast_week - mean_cases_last_week)/math.sq
rt((mean_cases_secondlast_week/len(cases2)) + (mean_cases_last_week/len(cases1
))))
  if walds_stat > 1.96:
    print("Mean cases for second last week and last week are different because
of the walds statistic value",walds_stat,"is greater than alpha at 0.05")
  else:
    print("Mean cases for second last week and last week are same because of t
he walds statistic value",walds_stat,"is less than alpha at 0.05")


walds_test_2sample(confirmed_last_week, confirmed_second_last_week)
```

```
Mean cases for second last week and last week are different because of the wa
lds statistic value 7.706911912567196 is greater than alpha at 0.05
```

Conclusion - \ In this both distributions must be independent and both the estimators must be asymptotically normal. Both these assumptions hold true in this case, hence this test is applicable.

Required Inference #3

Prepare Data

In [0]:
```
confirmed_last_week = confirmed.tail(7)
confirmed_second_last_week = confirmed.tail(14).head(7)
deaths_last_week = deaths.tail(7)
deaths_second_last_week = deaths.tail(14).head(7)
```

In [0]:
```
```

In [209]:
```
confirmed.tail()
```

Out[209]:

	Date	Barnstable County	Essex County	Middlesex County	Norfolk County	Plymouth County	Suffolk County
101	2020-05-02	35	334	441	122	150	311
102	2020-05-03	9	180	322	93	98	171
103	2020-05-04	15	231	387	102	95	164
104	2020-05-05	8	206	223	84	134	232
105	2020-05-06	28	365	347	144	163	303

In [0]:
```
def calc_cdf(SeriesA, SeriesB=[], draw=False):
  # Calculates cdf for seriesA and seriesB with optional plot.
  # Input - One or Two series
  # Output - Sorted SeriesA, Series A cdf, [if two series] Sorted Series B, Se
ries B cdf


  na = len(SeriesA)
  SeriesA_sorted = sorted(SeriesA)

  delta = .1
  X_seriesA = [min(SeriesA_sorted)-delta]
  Y_seriesA = [0]

  for i in range(0, na):
      X_seriesA = X_seriesA + [SeriesA_sorted[i], SeriesA_sorted[i]]
      Y_seriesA = Y_seriesA + [Y_seriesA[len(Y_seriesA)-1], Y_seriesA[len(Y_se
riesA)-1]+(1/na)]
  X_seriesA = X_seriesA + [max(SeriesA_sorted)+delta]
  Y_seriesA = Y_seriesA + [1]
  if SeriesB:
    nb = len(SeriesB)
    SeriesB_sorted = sorted(SeriesB)
    X_seriesB = [min(SeriesB_sorted)-delta]
    Y_seriesB = [0]
    for i in range(0, nb):
        X_seriesB = X_seriesB + [SeriesB_sorted[i], SeriesB_sorted[i]]
        Y_seriesB = Y_seriesB + [Y_seriesB[len(Y_seriesB)-1], Y_seriesB[len(Y_
seriesB)-1]+(1/nb)]
    X_seriesB = X_seriesB + [max(SeriesB_sorted)+delta]
    Y_seriesB = Y_seriesB + [1]


  # The above portion of cdf calculation is taken from the code that professor
shared.
  # https://www3.cs.stonybrook.edu/~anshul/courses/cse544_s20/eCDF.py
  if draw:
    plt.figure('eCDF')
    plt.plot(X_seriesA, Y_seriesA ,label='eCDF')
    if SeriesB:
      plt.plot(X_seriesB, Y_seriesB ,label='eCDF 2')
    plt.xlabel('x')
    plt.ylabel('Pr[X<=x]')
    plt.title('eCDF of Series A and Series B')
    plt.legend(loc="upper left")
    plt.grid()
    plt.show()


  # Returns X_seriesA (sorted Series A), Y_seriesA (cdf of seriesA), X_seriesB
(sorted Series B), Y_seriesB (cdf of series B)
  if SeriesB:
    return X_seriesA, Y_seriesA, X_seriesB, Y_seriesB
  else:
    return X_seriesA, Y_seriesA, _, _
```

```
def post_process_cdf(a, b=[], c=[], d=[]):
  # Post process cdf data from calc cdf. Contains multiple values.
  # This is required because the calc_cdf function give multiple value for plo
tting purposes.
  # This cdf and sorted data is used further for KS tests.

  if a:

    a = a[::2]
    a = a[1:]
  if b:
    b = b[::2]
    b = b[1:]
  if c:
    c = c[::2]
    c = c[1:]
  if d:
    d = d[::2]
    d = d[1:]

  return a, b, c, d

def find_nearest(a,v):
  # Given an array a, find nearest value v in it and return its index.

  idx = np.searchsorted(a, v, side="left")
  if idx > 0 and (v > a[idx-1]) and (v < a[idx]):
      return (idx-1)
  else:
      return (idx)


plt.rcParams["figure.figsize"] = (20,10)
def calc_KS(X1, X1cdf, Y1, Y1cdf,show_table=False):
  # Calculates D value of the of two series X1, Y1 with cdf value as X1cdf and
Y1cdf respectively.

  nx = len(X1)
  ny = len(Y1)
  if nx <= ny:
    X = X1
    Y = Y1
    FX = X1cdf
    FY = Y1cdf
  else:
    X = Y1
    FX = Y1cdf
    Y = X1
    FY = X1cdf
  # Remember FX is me, the smaller(in terms of length) distribution [X], FY is
the other distribution.
  # Fx is where me(X) stands in the other distribution(Y)
  x = []
  Fx = []
  Fy_left = []
```

```
    Fy_right = []
    F_left_diff = []
    F_right_diff = []

    for i in range(len(X)):

      x.append(X[i])
      if X[i]<min(Y):
        Fx.append(0)
      elif X[i]>max(Y):
        Fx.append(1)

      else:
        index_of_nearest = find_nearest(Y,X[i])
        Fx.append(FY[index_of_nearest])
      if i==0:
        Fy_left.append(0)
        Fy_right.append(FX[i])
      else:
        Fy_left.append(FX[i-1])
        Fy_right.append(FX[i])

      if X[i] not in Y:
        F_left_diff.append(abs(Fy_left[i]-Fx[i]))
        F_right_diff.append(abs(Fy_right[i]-Fx[i]))
      else:

        #Get the index of the element in the other distribution for edge cases
        i_y = Y.index(X[i])

        #There are total 9 cases to cover considering combinatation of (i=0, i!=
0, i==n-1) for both x and y.
        if i == 0:
          if i_y ==0:
            # if i = 0 and i_y = 0, left = 0 [L:1/9]
            F_left_diff.append(0)
          else:
            # if i = 0 and i_y != 0, and i_y==(ny-1) : left is simply the other
 cdf. [L:3/9]
            F_left_diff.append(abs(FY[i_y-1]))

          if i_y+1>=len(Y):
            # if i= 0 and i_y==n-1, right = 1 - my cdf [R:1/9]
            F_right_diff.append(abs(1-FX[i]))
          else:
            # if i= 0, i_y = 0 or i_y = != (ny-1) ; right = base case[R: 3/9]
            F_right_diff.append(abs(FX[i+1]-FY[i_y+1]))
        else:

          if i_y==0:
            # i!=0 , i_y=0 ; left = whatever current distribution had since the
 other hasnt staretd: [L:5/9]
            F_left_diff.append(abs(FX[i-1]))
          else:
            # i!=0, i_y can be any non-zero; left = proper case; [L:9/9]
            F_left_diff.append(abs(FX[i-1]-FY[i_y-1]))
```

```
        if i+1>=len(X) and i_y+1>=len(Y):
          # i= nx-1 and i_y= ny -1; right: both have ended, so right = 0; [R:
4/9]
          F_right_diff.append(0)
        elif i+1>=len(X):
          # i==nx-1 and i_y!=0; right = 1 - other cdf ; [R:6/9]
          F_right_diff.append(abs(1-FY[i_y]))

        elif i_y+1>=len(Y):
          # i_y=ny-1 and i!=0; right = 1 - my cdf since current ended; [R:7/9]
          F_right_diff.append(abs(1-FX[i]))

        else:
          # i!=0, i_y!=ny-1, right = proper case: [R:9/9]
          F_right_diff.append(abs(FX[i+1]-FY[i_y+1]))


  d = pd.DataFrame(pd.Series(x))
  d.columns = ['x']
  d['Fx'] = Fx
  d['Fy_left'] = Fy_left
  d['Fy_right'] = Fy_right
  d['F_left_diff'] = F_left_diff

  d['F_right_diff'] = F_right_diff
  if show_table:
    print(d)
  # print("D: {}".format(max(F_left_diff + F_right_diff)))

  m = max(F_left_diff + F_right_diff)

  try:
    ai = F_left_diff.index(m)
  except:
    ai = F_right_diff.index(m)
  x1,x2 = x[ai], x[ai]
  y1,y2 = Fy_right[ai], Fx[ai]


  # Returns m as maxium value(D), (x1,y1) and (x2,y2) points between which the
re is maximum difference.
  return m, x1, x2, y1, y2

def KS( listA, listB, C, draw=False,message=""):
  if message:
    print(message)
  A, Acdf, B, Bcdf = calc_cdf(listA, listB, draw=draw)
  A, Acdf, B, Bcdf = post_process_cdf(A, Acdf, B, Bcdf)
  D, x1, x2, y1, y2 = calc_KS(A, Acdf, B, Bcdf,show_table=False)
  if D >= C:
    print("Rejecting null hypothesis because D value = {} greater than or equa
l to {}.".format(D, C))
    result = "Reject"
  else:
    print("Accepting null hypothesis because D value = {} less than {}.".forma
t(D, C))
```

```
        result = "Accept"
    return D, result
```

1 - sample KS

In [0]:
```
def calc_poisson_cdf(param, x):
  v = 0
  for i in range(x+1):
    v+= math.exp(-param) * math.pow(param, i)/math.factorial(i)
  return v

def calc_geometric_cdf(param,x) :
  return 1 - math.pow((1-param), x)

def calc_1_sample_KS(X1, X1cdf, name, params, show_table=False):
  # Calculates D value of the of two series X1, Y1 with cdf value as X1cdf and Y1cdf respectively.


  nx = len(X1)
  # print("Distribution: {}, Params: {} ".format(name, params))
  X = X1
  FX = X1cdf
  x = []
  Fx = []
  Fy_left = []
  Fy_right = []
  F_left_diff = []
  F_right_diff = []

  for i in range(len(X)):
    x.append(X[i])
    if name=="Binomial":
      if X[i]<0:
        Fx.append(0)
      elif X[i]>params['n']:
        Fx.append(1)
      else:
        nearest = binom.cdf(X[i], params['n'], params['p'])
        Fx.append(nearest)
    elif name=="Poisson":
      if X[i]<0:
        Fx.append(0)
      else:
        nearest = poisson.cdf(X[i],params['lambda'])
        Fx.append(nearest)
    elif name=="Geometric":
      if X[i]<0:
        Fx.append(0)
      else:
        nearest = calc_geometric_cdf(params['p'], X[i])
        Fx.append(nearest)

    if i==0:
      Fy_left.append(0)
      Fy_right.append(FX[i])
    else:
      Fy_left.append(FX[i-1])
      Fy_right.append(FX[i])
```

```
    F_left_diff.append(abs(Fy_left[i]-Fx[i]))
    F_right_diff.append(abs(Fy_right[i]-Fx[i]))


  d = pd.DataFrame(pd.Series(x))
  d.columns = ['x']
  d['Fx'] = Fx
  d['Fy_left'] = Fy_left
  d['Fy_right'] = Fy_right
  d['F_left_diff'] = F_left_diff
  d['F_right_diff'] = F_right_diff
  if show_table:
    print(d)
  # print("D: {}".format(max(F_left_diff + F_right_diff)))

  m = max(F_left_diff + F_right_diff)
  return m
```

In [0]:
```
def format_params(d):
  for k in list(d.keys()):
    v = float("{:.2f}".format(d[k]))
    d[k]=v
  return d

def KS_1_sample(county_name, county_data_second_last_week, county_data_last_we
ek , C):

  if county_data_second_last_week.mean() == 0:
    print("County: {} - No Data for this county.\n".format(county))
    return -1, "Mean=0"
  else:
    print("County: {}\n".format(county))
    poisson_lambda_mme = county_data_second_last_week.mean()
    geometric_p_mme = 1/county_data_second_last_week.mean()
    binomial_p_mme = 1 - (county_data_second_last_week.var()/county_data_secon
d_last_week.mean())
    binomial_n_mme = county_data_second_last_week.mean()/binomial_p_mme
    uniform_a_mle = min(county_data_second_last_week)
    uniform_b_mle = max(county_data_second_last_week)

    distribution_and_args={
        # "Binomial":{'p':float("{:.2f}".format(binomial_p_mme)), 'n': math.ce
il(binomial_n_mme)},
        "Binomial":{'p':binomial_p_mme, 'n': math.ceil(binomial_n_mme)},
        # "Geometric":{'p':float("{:.2f}".format(geometric_p_mme))},
        "Geometric":{'p':geometric_p_mme},
        # "Poisson":{"lambda":float("{:.2f}".format(poisson_lambda_mme))
        "Poisson":{"lambda":poisson_lambda_mme}


    }
    A, Acdf, B, Bcdf = calc_cdf(county_data_last_week.tolist(), draw=False)
    A, Acdf, B, Bcdf = post_process_cdf(A, Acdf, c = [], d= [])

    counties=[]
    distData = {}
    for d in list(distribution_and_args.keys()):
      D = calc_1_sample_KS(A, Acdf, d,distribution_and_args[d], show_table=Fal
se)
      print("Null hypthesis: Last week data follow a {} distribution with para
meters {}\n".format(d,distribution_and_args[d]))
      if D >= C:
        print("Rejecting null hypothesis because D value = {} greater than or
 equal to {}.".format(D, C))
        result = "Reject"
      else:
        print("Accepting null hypothesis because D value = {} less than {}.".f
ormat(D, C))
        result = "Accept"
      print("-------------------------\n")
      testResult = {"Params":format_params(distribution_and_args[d]),"Result":
result, "D":D}
      distData[d]=testResult
    return D, distData
```

In [0]:
```
county_names=list(filter(lambda x: "County" in x, deaths_last_week.columns.to_
list()))
```

In [214]:
```
binomial_params = []
binomial_D = []
binomial_result = []
geometric_params = []
geometric_D = []
geometric_result = []
poisson_params = []
poisson_D = []
poisson_result = []
for county in county_names:
  print("######################################################################"
)
  D, distData = KS_1_sample(county, deaths_second_last_week[county],deaths_las
t_week[county],0.05)
  if D==-1:
    binomial_params.append(distData)
    geometric_params.append(distData)
    poisson_params.append(distData)
    binomial_D.append("-")
    binomial_result.append("-")
    poisson_D.append("-")
    poisson_result.append("-")
    geometric_D.append("-")
    geometric_result.append("-")
  else:
    binomial_params.append("{}".format(distData["Binomial"]["Params"]));
    binomial_D.append("{:.2f}".format(distData["Binomial"]["D"]));
    binomial_result.append("{} null".format(distData["Binomial"]["Result"]));

    geometric_params.append("{}".format(distData["Geometric"]["Params"]));
    geometric_D.append("{:.2f}".format(distData["Geometric"]["D"]));
    geometric_result.append("{} null".format(distData["Geometric"]["Result"
]));

    poisson_params.append("{}".format(distData["Poisson"]["Params"]));
    poisson_D.append("{:.2f}".format(distData["Poisson"]["D"]));
    poisson_result.append("{} null".format(distData["Poisson"]["Result"]));

one_sample=pd.DataFrame(county_names)
one_sample.columns = ['County']
one_sample['Binomial Params'] = pd.DataFrame(binomial_params);
one_sample['Binomial D'] = pd.DataFrame(binomial_D);
one_sample['Binomial Result'] = pd.DataFrame(binomial_result);
one_sample['Poisson Params'] = pd.DataFrame(poisson_params);
one_sample['Poisson D'] = pd.DataFrame(poisson_D);
one_sample['Poisson Result'] = pd.DataFrame(poisson_result);
one_sample['Geometric Params'] = pd.DataFrame(geometric_params);
one_sample['Geometric D'] = pd.DataFrame(geometric_D);
one_sample['Geometric Result'] = pd.DataFrame(geometric_result);

one_sample
```

```
######################################################################
County: Barnstable County

Null hypthesis: Last week data follow a Binomial distribution with parameters
{'p': -1.0512820512820515, 'n': -1}

Rejecting null hypothesis because D value = 1 greater than or equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Geometric distribution with parameter
s {'p': 0.5384615384615384}

Rejecting null hypothesis because D value = 0.3956043956043956 greater than o
r equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Poisson distribution with parameters
{'lambda': 1.8571428571428572}

Rejecting null hypothesis because D value = 0.30319441518848894 greater than
or equal to 0.05.
--------------------------

######################################################################
County: Essex County

Null hypthesis: Last week data follow a Binomial distribution with parameters
{'p': -4.212121212121212, 'n': -5}

Rejecting null hypothesis because D value = 1 greater than or equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Geometric distribution with parameter
s {'p': 0.045454545454545456}

Rejecting null hypothesis because D value = 0.4277848303492515 greater than o
r equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Poisson distribution with parameters
{'lambda': 22.0}

Rejecting null hypothesis because D value = 0.4945369713782102 greater than o
r equal to 0.05.
--------------------------

######################################################################
County: Middlesex County

Null hypthesis: Last week data follow a Binomial distribution with parameters
{'p': -3.424242424242424, 'n': -12}

Rejecting null hypothesis because D value = 1 greater than or equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Geometric distribution with parameter
s {'p': 0.022727272727272728}
```

```
Rejecting null hypothesis because D value = 0.43714765822176205 greater than
or equal to 0.05.
-------------------------

Null hypthesis: Last week data follow a Poisson distribution with parameters
{'lambda': 44.0}

Rejecting null hypothesis because D value = 0.3771928634445671 greater than o
r equal to 0.05.
-------------------------

####################################################################
County: Norfolk County

Null hypthesis: Last week data follow a Binomial distribution with parameters
{'p': -2.5116279069767438, 'n': -9}

Rejecting null hypothesis because D value = 1 greater than or equal to 0.05.
-------------------------

Null hypthesis: Last week data follow a Geometric distribution with parameter
s {'p': 0.04069767441860465}

Rejecting null hypothesis because D value = 0.384570917198205 greater than or
equal to 0.05.
-------------------------

Null hypthesis: Last week data follow a Poisson distribution with parameters
{'lambda': 24.571428571428573}

Rejecting null hypothesis because D value = 0.582455151150163 greater than or
equal to 0.05.
-------------------------

####################################################################
County: Plymouth County

Null hypthesis: Last week data follow a Binomial distribution with parameters
{'p': 0.2586206896551726, 'n': 65}

Rejecting null hypothesis because D value = 0.6058424097642939 greater than o
r equal to 0.05.
-------------------------

Null hypthesis: Last week data follow a Geometric distribution with parameter
s {'p': 0.06034482758620689}

Rejecting null hypothesis because D value = 0.39221767001977936 greater than
or equal to 0.05.
-------------------------

Null hypthesis: Last week data follow a Poisson distribution with parameters
{'lambda': 16.571428571428573}

Rejecting null hypothesis because D value = 0.5562920850107532 greater than o
r equal to 0.05.
```

```
-------------------------

####################################################################
County: Suffolk County

Null hypthesis: Last week data follow a Binomial distribution with parameters
{'p': -0.3154121863799284, 'n': -84}

Rejecting null hypothesis because D value = 1 greater than or equal to 0.05.
-------------------------

Null hypthesis: Last week data follow a Geometric distribution with parameter
s {'p': 0.03763440860215054}

Rejecting null hypothesis because D value = 0.281982958762351 greater than or
equal to 0.05.
-------------------------

Null hypthesis: Last week data follow a Poisson distribution with parameters
{'lambda': 26.571428571428573}

Rejecting null hypothesis because D value = 0.5979854338380407 greater than o
r equal to 0.05.
-------------------------
```

Out[214]:

	County	Binomial Params	Binomial D	Binomial Result	Poisson Params	Poisson D	Poisson Result	Geometric Params	Geometric D
0	Barnstable County	{'p': -1.05, 'n': -1.0}	1.00	Reject null	{'lambda': 1.86}	0.30	Reject null	{'p': 0.54}	0.40
1	Essex County	{'p': -4.21, 'n': -5.0}	1.00	Reject null	{'lambda': 22.0}	0.49	Reject null	{'p': 0.05}	0.43
2	Middlesex County	{'p': -3.42, 'n': -12.0}	1.00	Reject null	{'lambda': 44.0}	0.38	Reject null	{'p': 0.02}	0.44
3	Norfolk County	{'p': -2.51, 'n': -9.0}	1.00	Reject null	{'lambda': 24.57}	0.58	Reject null	{'p': 0.04}	0.38
4	Plymouth County	{'p': 0.26, 'n': 65.0}	0.61	Reject null	{'lambda': 16.57}	0.56	Reject null	{'p': 0.06}	0.39
5	Suffolk County	{'p': -0.32, 'n': -84.0}	1.00	Reject null	{'lambda': 26.57}	0.60	Reject null	{'p': 0.04}	0.28

Confirmed Cases

In [215]:
```
binomial_params = []
binomial_D = []
binomial_result = []
geometric_params = []
geometric_D = []
geometric_result = []
poisson_params = []
poisson_D = []
poisson_result = []
for county in county_names:
  print("######################################################################"
)
  D, distData = KS_1_sample(county, confirmed_second_last_week[county],confirm
ed_last_week[county],0.05)
  if D==-1:
    binomial_params.append(distData)
    geometric_params.append(distData)
    poisson_params.append(distData)
    binomial_D.append("-")
    binomial_result.append("-")
    poisson_D.append("-")
    poisson_result.append("-")
    geometric_D.append("-")
    geometric_result.append("-")
  else:
    binomial_params.append("{}".format(distData["Binomial"]["Params"]));
    binomial_D.append("{:.2f}".format(distData["Binomial"]["D"]));
    binomial_result.append("{} null".format(distData["Binomial"]["Result"]));

    geometric_params.append("{}".format(distData["Geometric"]["Params"]));
    geometric_D.append("{:.2f}".format(distData["Geometric"]["D"]));
    geometric_result.append("{} null".format(distData["Geometric"]["Result"
]));

    poisson_params.append("{}".format(distData["Poisson"]["Params"]));
    poisson_D.append("{:.2f}".format(distData["Poisson"]["D"]));
    poisson_result.append("{} null".format(distData["Poisson"]["Result"]));

one_sample=pd.DataFrame(county_names)
one_sample.columns = ['County']
one_sample['Binomial Params'] = pd.DataFrame(binomial_params);
one_sample['Binomial D'] = pd.DataFrame(binomial_D);
one_sample['Binomial Result'] = pd.DataFrame(binomial_result);
one_sample['Poisson Params'] = pd.DataFrame(poisson_params);
one_sample['Poisson D'] = pd.DataFrame(poisson_D);
one_sample['Poisson Result'] = pd.DataFrame(poisson_result);
one_sample['Geometric Params'] = pd.DataFrame(geometric_params);
one_sample['Geometric D'] = pd.DataFrame(geometric_D);
one_sample['Geometric Result'] = pd.DataFrame(geometric_result);

one_sample
```

```
######################################################################
County: Barnstable County

Null hypthesis: Last week data follow a Binomial distribution with parameters
{'p': -2.9817073170731705, 'n': -7}

Rejecting null hypothesis because D value = 1 greater than or equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Geometric distribution with parameter
s {'p': 0.042682926829268296}

Rejecting null hypothesis because D value = 0.29458216629401257 greater than
or equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Poisson distribution with parameters
{'lambda': 23.428571428571427}

Rejecting null hypothesis because D value = 0.41791668072366306 greater than
or equal to 0.05.
--------------------------

######################################################################
County: Essex County

Null hypthesis: Last week data follow a Binomial distribution with parameters
{'p': -49.307277628032345, 'n': -7}

Rejecting null hypothesis because D value = 1 greater than or equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Geometric distribution with parameter
s {'p': 0.0026954177897574125}

Rejecting null hypothesis because D value = 0.38481377642476866 greater than
or equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Poisson distribution with parameters
{'lambda': 371.0}

Rejecting null hypothesis because D value = 0.6867683038411022 greater than o
r equal to 0.05.
--------------------------

######################################################################
County: Middlesex County

Null hypthesis: Last week data follow a Binomial distribution with parameters
{'p': -90.06594691857849, 'n': -5}

Rejecting null hypothesis because D value = 1 greater than or equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Geometric distribution with parameter
s {'p': 0.0018893387314439945}
```

```
Rejecting null hypothesis because D value = 0.4343144490047046 greater than o
r equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Poisson distribution with parameters
{'lambda': 529.2857142857143}

Rejecting null hypothesis because D value = 0.9999560537900697 greater than o
r equal to 0.05.
--------------------------

####################################################################
County: Norfolk County

Null hypthesis: Last week data follow a Binomial distribution with parameters
{'p': -71.78629032258063, 'n': -2}

Rejecting null hypothesis because D value = 1 greater than or equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Geometric distribution with parameter
s {'p': 0.004704301075268817}

Rejecting null hypothesis because D value = 0.39684138166185945 greater than
or equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Poisson distribution with parameters
{'lambda': 212.57142857142858}

Rejecting null hypothesis because D value = 0.8654342892798084 greater than o
r equal to 0.05.
--------------------------

####################################################################
County: Plymouth County

Null hypthesis: Last week data follow a Binomial distribution with parameters
{'p': -168.57395962093122, 'n': -1}

Rejecting null hypothesis because D value = 1 greater than or equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Geometric distribution with parameter
s {'p': 0.004326328800988875}

Rejecting null hypothesis because D value = 0.3988493662417869 greater than o
r equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Poisson distribution with parameters
{'lambda': 231.14285714285714}

Rejecting null hypothesis because D value = 0.8910577562805204 greater than o
r equal to 0.05.
--------------------------
```

```
########################################################################
County: Suffolk County

Null hypthesis: Last week data follow a Binomial distribution with parameters
{'p': -130.69483568075117, 'n': -3}

Rejecting null hypothesis because D value = 1 greater than or equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Geometric distribution with parameter
s {'p': 0.002012072434607646}

Rejecting null hypothesis because D value = 0.44232505637169806 greater than
or equal to 0.05.
--------------------------

Null hypthesis: Last week data follow a Poisson distribution with parameters
{'lambda': 497.0}

Rejecting null hypothesis because D value = 0.9999884868253803 greater than o
r equal to 0.05.
--------------------------
```

Out[215]:

	County	Binomial Params	Binomial D	Binomial Result	Poisson Params	Poisson D	Poisson Result	Geometric Params	Geometric D
0	Barnstable County	{'p': -2.98, 'n': -7.0}	1.00	Reject null	{'lambda': 23.43}	0.42	Reject null	{'p': 0.04}	0.29
1	Essex County	{'p': -49.31, 'n': -7.0}	1.00	Reject null	{'lambda': 371.0}	0.69	Reject null	{'p': 0.0}	0.38
2	Middlesex County	{'p': -90.07, 'n': -5.0}	1.00	Reject null	{'lambda': 529.29}	1.00	Reject null	{'p': 0.0}	0.43
3	Norfolk County	{'p': -71.79, 'n': -2.0}	1.00	Reject null	{'lambda': 212.57}	0.87	Reject null	{'p': 0.0}	0.40
4	Plymouth County	{'p': -168.57, 'n': -1.0}	1.00	Reject null	{'lambda': 231.14}	0.89	Reject null	{'p': 0.0}	0.40
5	Suffolk County	{'p': -130.69, 'n': -3.0}	1.00	Reject null	{'lambda': 497.0}	1.00	Reject null	{'p': 0.0}	0.44

KS - One sample

We performed 1 sample KS test on the death of the last week of some counties trying to see if it follows binomial, poisson or geometric. Based on the results, the data does not follow any of the distribution. Based on the results, however one can see that there is a pattern in the moving average. For the sake of simplicity we use the pandas rolling function to calculate moving average. The results of this are given in the creative inference.

As a result of this inference, using 1-sample KS test we can say that the deaths and the confirmed cases does not follow Binomial, Geometric, Poisson distribution for both death and confirmed cases.

2 sample KS - Deaths

In [216]:
```
two_sample_D = []
two_sample_result = []
for county in county_names:
  print("------------------------")
  D, result = KS( deaths_second_last_week[county].tolist(),deaths_last_week[co
unty].tolist(),0.05, message="County: {}".format(county))
  two_sample_D.append(D)
  two_sample_result.append(result)
two_sample=pd.DataFrame(county_names)
two_sample.columns = ['County']
two_sample['D'] = pd.DataFrame(two_sample_D);
two_sample['Result'] = pd.DataFrame(two_sample_result);
two_sample
```

```
------------------------
County: Barnstable County
Rejecting null hypothesis because D value = 0.2857142857142857 greater than o
r equal to 0.05.
------------------------
County: Essex County
Rejecting null hypothesis because D value = 0.2857142857142857 greater than o
r equal to 0.05.
------------------------
County: Middlesex County
Rejecting null hypothesis because D value = 0.2857142857142858 greater than o
r equal to 0.05.
------------------------
County: Norfolk County
Rejecting null hypothesis because D value = 0.4285714285714286 greater than o
r equal to 0.05.
------------------------
County: Plymouth County
Rejecting null hypothesis because D value = 0.5714285714285714 greater than o
r equal to 0.05.
------------------------
County: Suffolk County
Rejecting null hypothesis because D value = 0.5714285714285714 greater than o
r equal to 0.05.
```

Out[216]:

	County	D	Result
0	Barnstable County	0.285714	Reject
1	Essex County	0.285714	Reject
2	Middlesex County	0.285714	Reject
3	Norfolk County	0.428571	Reject
4	Plymouth County	0.571429	Reject
5	Suffolk County	0.571429	Reject

2- sample - KS - confirmed

In [217]:
```
two_sample_D = []
two_sample_result = []
for county in county_names:
  print("------------------------")
  D, result = KS( confirmed_second_last_week[county].tolist(),confirmed_last_w
eek[county].tolist(),0.05, message="County: {}".format(county))
  two_sample_D.append(D)
  two_sample_result.append(result)
two_sample=pd.DataFrame(county_names)
two_sample.columns = ['County']
two_sample['D'] = pd.DataFrame(two_sample_D);
two_sample['Result'] = pd.DataFrame(two_sample_result);
two_sample
```

```
------------------------
County: Barnstable County
Rejecting null hypothesis because D value = 0.2857142857142857 greater than o
r equal to 0.05.
------------------------
County: Essex County
Rejecting null hypothesis because D value = 0.5714285714285714 greater than o
r equal to 0.05.
------------------------
County: Middlesex County
Rejecting null hypothesis because D value = 0.5714285714285714 greater than o
r equal to 0.05.
------------------------
County: Norfolk County
Rejecting null hypothesis because D value = 0.42857142857142855 greater than
or equal to 0.05.
------------------------
County: Plymouth County
Rejecting null hypothesis because D value = 0.5714285714285714 greater than o
r equal to 0.05.
------------------------
County: Suffolk County
Rejecting null hypothesis because D value = 0.5714285714285714 greater than o
r equal to 0.05.
```

Out[217]:

	County	D	Result
0	Barnstable County	0.285714	Reject
1	Essex County	0.571429	Reject
2	Middlesex County	0.571429	Reject
3	Norfolk County	0.428571	Reject
4	Plymouth County	0.571429	Reject
5	Suffolk County	0.571429	Reject

KS 2- sample

The null hypothesis for the KS test is that the data follows the same distribution. Visibly the KS-test rejects this hypothesis showing that the last week and the second does not follow the same distribution. We carry out the permutation test to further strengthen this hypthesis.

Permutation Test - Deaths

In [0]:
```
import random
def get_random_split(xuy, len_x, len_y, n):
  #  Randomly split X U Y into X' and Y' of length(X) and length(Y) respective
ly. n is the number of permutations.

  X = []
  Y = []
  for i in range(n):
    random.shuffle(xuy)
    x = xuy[:len_x]
    y = xuy[len_x:]
    X.append(x)
    Y.append(y)
  return X, Y


def I(A, B):
  if A > B:
    return 1
  else:
    return 0

def calc_p_val(X, Y, n):
  # Calculate p_value of two series X and Y for n permutations.
  _XUY = X + Y
  mean_x = sum(X)/len(X)
  mean_y = sum(Y)/len(Y)
  T_obs = abs(mean_x - mean_y)
  Xi, Yi = get_random_split(_XUY, len(X), len(Y), n)
  summation_i = 0
  for i in range(n):
    xi,yi = Xi[i], Yi[i]
    mean_x = sum(xi)/len(xi)
    mean_y = sum(yi)/len(yi)
    Ti = abs(mean_x - mean_y)
    summation_i += I(Ti, T_obs)
    # print("I(Ti, T_obs): ", I(Ti, T_obs))
  p_value = summation_i/n
  return p_value

def test_hypothesis(p_value, alpha, message):
  # Test hypothesis for p_value with alpha as alpha with message containing de
tails of the test.

  if p_value <= alpha:
    print("{}Rejecting null hypothesis. p value: {}".format(message, p_value))
    result = "Reject"
  else:
    print("{}Accepting null hypothesis. p value: {} ".format(message, p_value
))
    result = "Accept"
  return result
```

In [219]:
```
p_values = []
results = []
alpha = 0.05
n=5040
for county in county_names:
  print("------------------------")
  p_value = calc_p_val(deaths_last_week[county].tolist(),deaths_second_last_we
ek[county].tolist(), n)
  p_values.append(p_value)
  result = test_hypothesis(p_value, alpha, "County:{} for {} permutations: ".f
ormat(county,n))
  results.append(result)
p_test=pd.DataFrame(county_names)
p_test.columns = ['County']
p_test['p-value'] = pd.DataFrame(p_values);
p_test['result'] = pd.DataFrame(results);
p_test
```

```
------------------------
County:Barnstable County for 5040 permutations: Accepting null hypothesis. p
value: 0.7287698412698412
------------------------
County:Essex County for 5040 permutations: Accepting null hypothesis. p valu
e: 0.5910714285714286
------------------------
County:Middlesex County for 5040 permutations: Accepting null hypothesis. p v
alue: 0.37857142857142856
------------------------
County:Norfolk County for 5040 permutations: Accepting null hypothesis. p val
ue: 0.06170634920634921
------------------------
County:Plymouth County for 5040 permutations: Rejecting null hypothesis. p va
lue: 0.02361111111111111
------------------------
County:Suffolk County for 5040 permutations: Accepting null hypothesis. p val
ue: 0.08928571428571429
```

Out[219]:

	County	p-value	result
0	Barnstable County	0.728770	Accept
1	Essex County	0.591071	Accept
2	Middlesex County	0.378571	Accept
3	Norfolk County	0.061706	Accept
4	Plymouth County	0.023611	Reject
5	Suffolk County	0.089286	Accept

p test confirmed cases

In [220]:
```
p_values = []
results = []
alpha = 0.05
n=5040
for county in county_names:
  print("------------------------")
  p_value = calc_p_val(confirmed_last_week[county].tolist(),confirmed_second_l
ast_week[county].tolist(), n)
  p_values.append(p_value)
  result = test_hypothesis(p_value, alpha, "County:{} for {} permutations: ".f
ormat(county,n))
  results.append(result)
p_test=pd.DataFrame(county_names)
p_test.columns = ['County']
p_test['p-value'] = pd.DataFrame(p_values);
p_test['result'] = pd.DataFrame(results);
p_test
```

```
------------------------
County:Barnstable County for 5040 permutations: Accepting null hypothesis. p
value: 0.8093253968253968
------------------------
County:Essex County for 5040 permutations: Accepting null hypothesis. p valu
e: 0.14424603174603173
------------------------
County:Middlesex County for 5040 permutations: Accepting null hypothesis. p v
alue: 0.05734126984126984
------------------------
County:Norfolk County for 5040 permutations: Accepting null hypothesis. p val
ue: 0.11488095238095238
------------------------
County:Plymouth County for 5040 permutations: Accepting null hypothesis. p va
lue: 0.3200396825396825
------------------------
County:Suffolk County for 5040 permutations: Rejecting null hypothesis. p val
ue: 0.02896825396825397
```

Out[220]:

	County	p-value	result
0	Barnstable County	0.809325	Accept
1	Essex County	0.144246	Accept
2	Middlesex County	0.057341	Accept
3	Norfolk County	0.114881	Accept
4	Plymouth County	0.320040	Accept
5	Suffolk County	0.028968	Reject

The null hypothesis for the p-test is that the distributions are not same. The results show that they are indeed not same. The 2-sample KS test also claims this. Hence, both the tests show that the data from the previous week and the last week are not from the same distribution.

Required Inference #4

Prepare required dataframes for Task 4

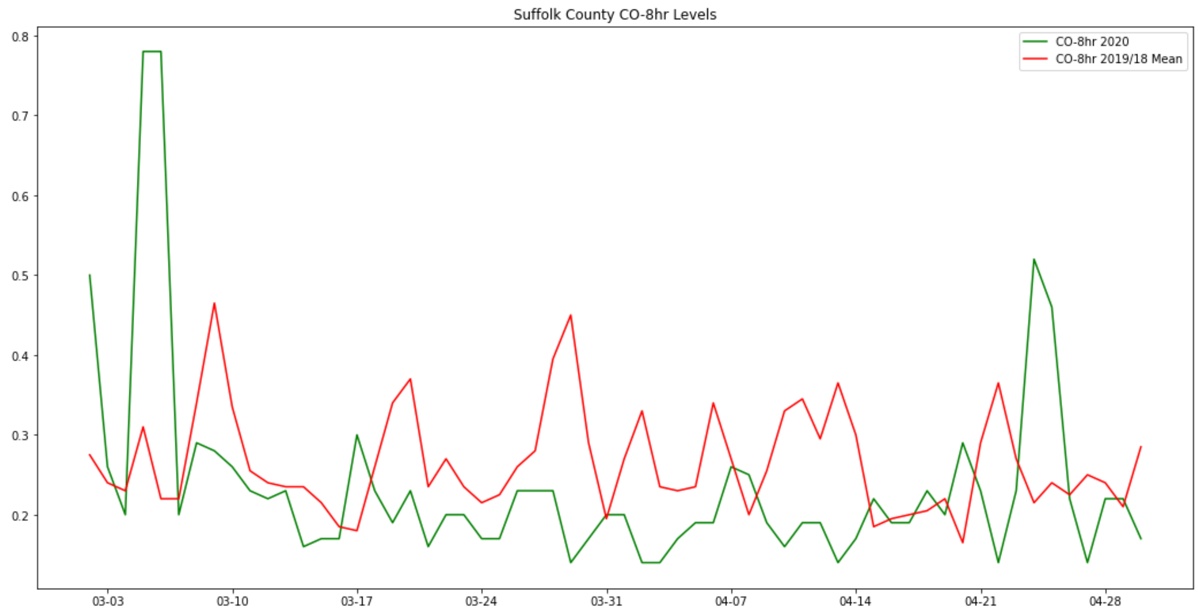
In [0]:
```
start_date = datetime.date(2020, 3, 1)
end_date = datetime.date(2020, 4, 30)
confirmed_march_april = confirmed[(confirmed['Date'] >= pd.to_datetime(start_d
ate)) & (confirmed['Date'] <=  pd.to_datetime(end_date))]
deaths_march_april = deaths[(deaths['Date'] >= pd.to_datetime(start_date)) & (
deaths['Date'] <=  pd.to_datetime(end_date))]

def prepare_airnow_df(year):
  df = pd.read_csv('AirNow/AirNow_Massachusetts_{}_WithCounties.csv'.format(ye
ar))
  df = df.drop('Unnamed: 0', axis=1)
  df['Valid date'] = pd.to_datetime(df['Valid date'])
  df['Valid date'].dt.strftime('%Y-%m-%d')
  df = df.set_index('Valid date')
  df['AQSID'] = df['AQSID'].map(lambda x: x % 10**9)
  df['county'] = df['county'].map(lambda x: x + ' County')
  return df

def impute_missing_dates(df, year, dates):
  idx = pd.date_range('03-01-{}'.format(year), '04-30-{}'.format(year))
  df = df.reindex(idx, fill_value=None)
  df = df.resample('D').interpolate()
  df = df.fillna(method='ffill')
  df = df[df.index.isin(dates)]
  return df

airnow_2020 = prepare_airnow_df('2020')
airnow_2019 = prepare_airnow_df('2019')
airnow_2018 = prepare_airnow_df('2018')
airnow_2017 = prepare_airnow_df('2017')
```

Calulate Pearson correlations for certain metrics and plot graphs as required.

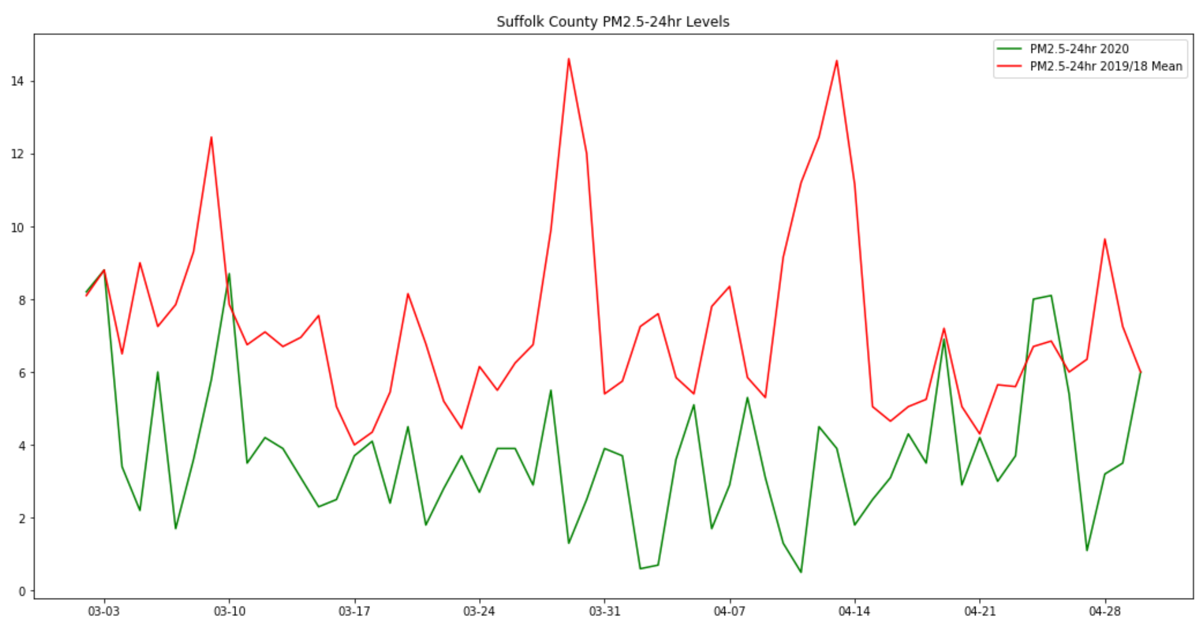
In [222]:
```
def calculate_pearson_correlation(x, y):
  n = len(x)
  x_mean = sum(x) / len(x)
  y_mean = sum(y) / len(y)
  numerator = sum([(x[i] - x_mean) * (y[i] - y_mean) for i in range(n)])
  denominator1 = sum([(xi - x_mean)**2 for xi in x]) ** 0.5
  denominator2 = sum([(yi - y_mean)**2 for yi in y]) ** 0.5
  denominator = denominator1 * denominator2
  return numerator / denominator

def calculate_correlation_and_plot(county, station, parameter):
  xc = confirmed_march_april[county].tolist()
  filtered20 = airnow_2020[(airnow_2020['AQSID'] == station) & (airnow_2020['p
arameter name'] == parameter)]
  filtered20 = impute_missing_dates(filtered20, '2020', confirmed_march_april[
'Date'].dt.strftime('2020-%m-%d').values.tolist())
  filtered19 = airnow_2019[(airnow_2019['AQSID'] == station) & (airnow_2019['p
arameter name'] == parameter)]
  filtered19 = impute_missing_dates(filtered19, '2019', confirmed_march_april[
'Date'].dt.strftime('2019-%m-%d').values.tolist())
  filtered18 = airnow_2018[(airnow_2018['AQSID'] == station) & (airnow_2018['p
arameter name'] == parameter)]
  filtered18 = impute_missing_dates(filtered18, '2018', confirmed_march_april[
'Date'].dt.strftime('2018-%m-%d').values.tolist())
  filtered17 = airnow_2017[(airnow_2017['AQSID'] == station) & (airnow_2017['p
arameter name'] == parameter)]
  filtered17 = impute_missing_dates(filtered17, '2017', confirmed_march_april[
'Date'].dt.strftime('2017-%m-%d').values.tolist())

  filtered_mean1918 = np.mean(np.vstack((filtered19['value'], filtered18['valu
e'])), axis=0)
  print('Pearson Correlation: {} Cases vs {} 2020               : '.format(coun
ty, parameter), calculate_pearson_correlation(xc, filtered20['value']))
  print('Pearson Correlation: {} Cases vs {} Mean of 2019, 2018: '.format(coun
ty, parameter), calculate_pearson_correlation(xc, filtered_mean1918))

  plt.figure(figsize=(18,9))
  plt.plot(filtered20.index, filtered20['value'].tolist(), label='{} 2020'.for
mat(parameter), color='green')
  plt.plot(filtered20.index, filtered_mean1918, label='{} 2019/18 Mean'.format
(parameter), color='red')
  plt.title('{} {} Levels'.format(county, parameter))
  plt.legend()
  ax = plt.gca()
  date_form = DateFormatter("%m-%d")
  ax.xaxis.set_major_formatter(date_form)
  ax.xaxis.set_major_locator(mdates.WeekdayLocator(interval=1))
  plt.show()

  print('\n' * 2 + '*' * 20 + '\n'*2)

correlations_metrics_options = [('Suffolk County', 250250042, 'CO-8hr'),
                                ('Suffolk County', 250250042, 'PM2.5-24hr'),
                                ('Essex County', 250092006, 'PM2.5-24hr'),
                                ('Plymouth County', 250230005, 'PM2.5-24hr')]
```

```
for option in correlations_metrics_options:
  calculate_correlation_and_plot(option[0], option[1], option[2])
```

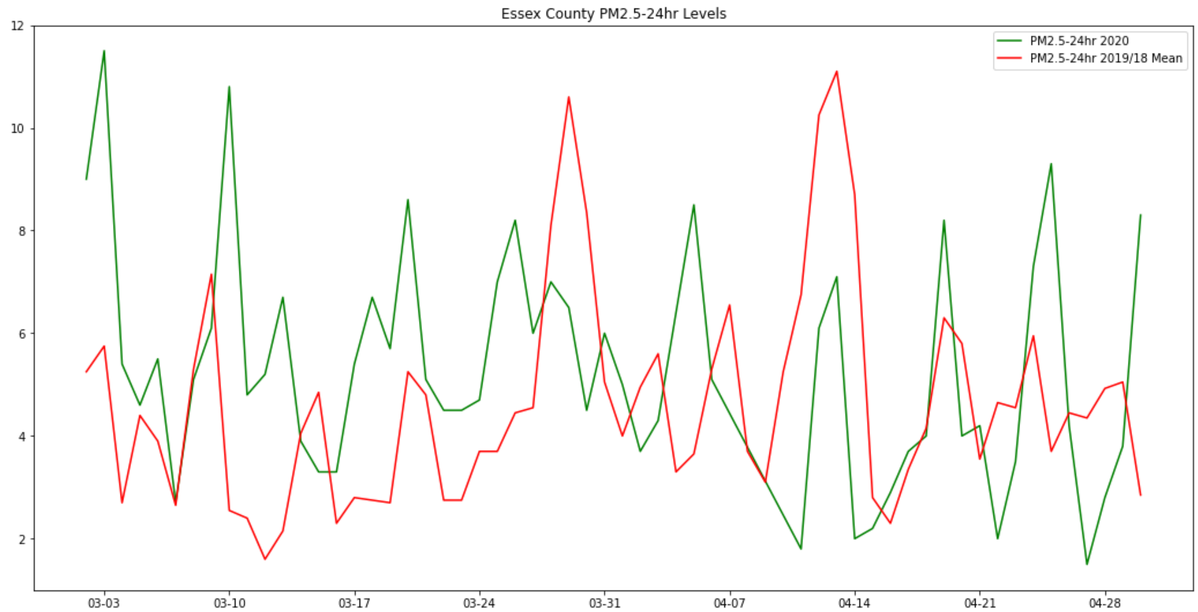
```
Pearson Correlation: Suffolk County Cases vs CO-8hr 2020              :  -0.0
4462455726611543
Pearson Correlation: Suffolk County Cases vs CO-8hr Mean of 2019, 2018:  -0.1
29609943934291
```



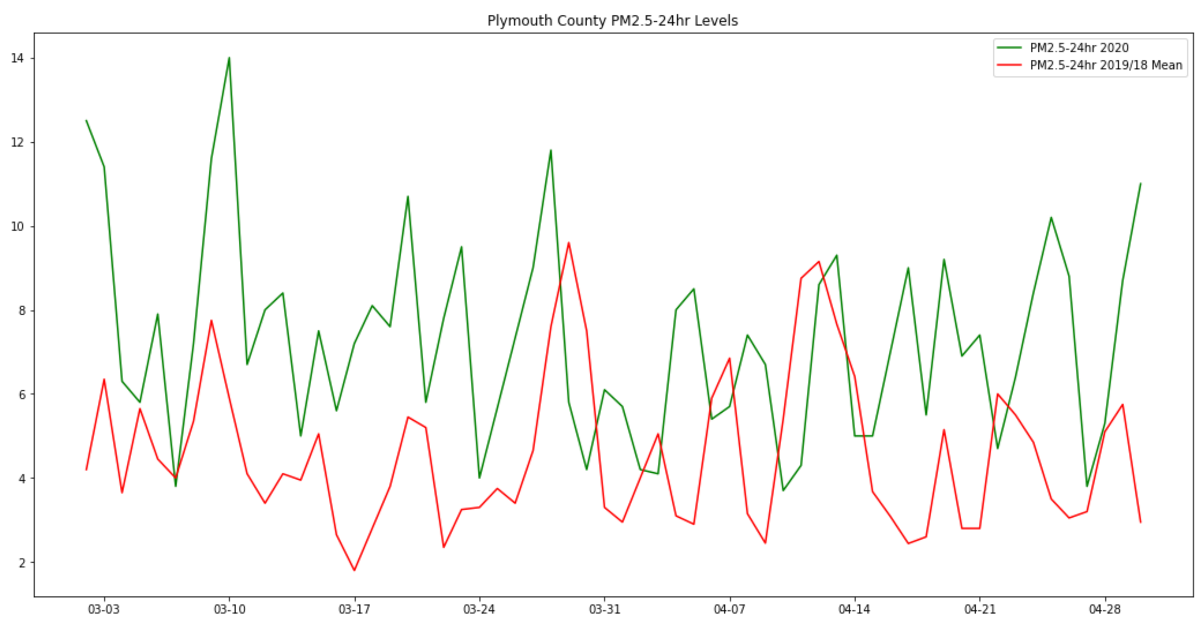

```
********************


Pearson Correlation: Suffolk County Cases vs PM2.5-24hr 2020             :
0.061902922246009656
Pearson Correlation: Suffolk County Cases vs PM2.5-24hr Mean of 2019, 2018:
-0.08324564001187174
```



```
*******************

Pearson Correlation: Essex County Cases vs PM2.5-24hr 2020            :  -
0.23170721893452534
Pearson Correlation: Essex County Cases vs PM2.5-24hr Mean of 2019, 2018:  0.
19667521171516353
```




```
*******************

Pearson Correlation: Plymouth County Cases vs PM2.5-24hr 2020            :
-0.08254956761862675
Pearson Correlation: Plymouth County Cases vs PM2.5-24hr Mean of 2019, 2018:
0.08667637955756387
```



****

Pearson Correlation Review Analysis

NOTE: We only plot for years and stations where there was data to make meaningful inferences.

CO Levels: This data was available only for Suffolk County.

Notice that the Pearson Correlation for number of cases vs Carbon Monoxide levels for 2019 and 2018 mean is very close to 0 but that is the case with 2020 levels as well.

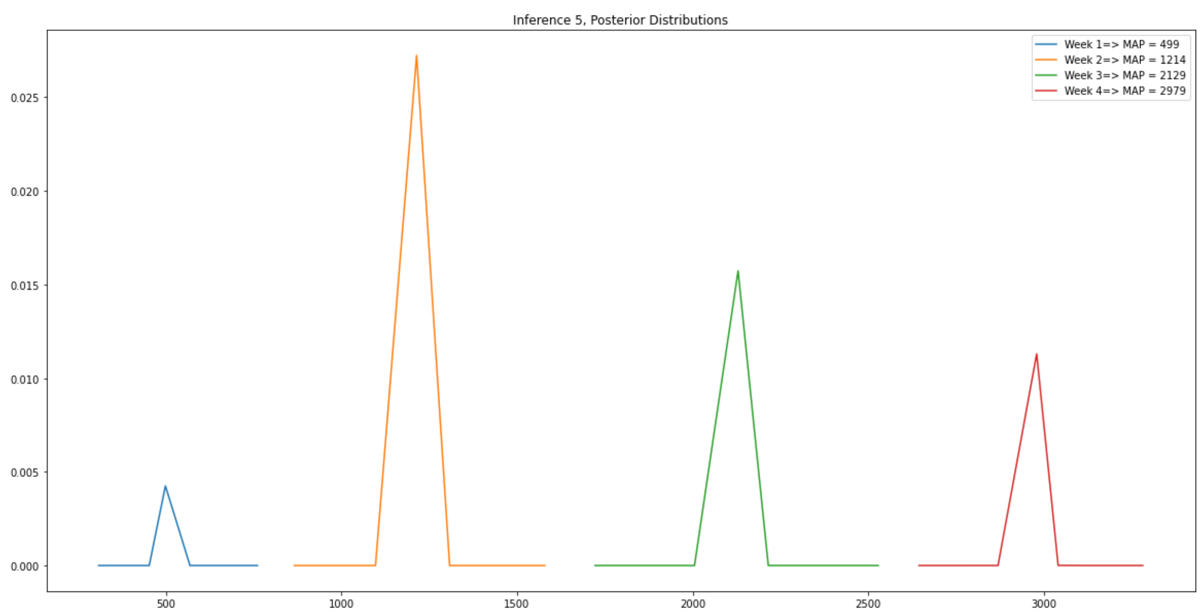
Lead Levels: We can see a similar trend with Lead levels as well for Suffolk and Plymouth counties. But for Essex even though the magintudes of the correlation are comparative to others but they are in opposite directions.

Graphs: The graphs are indicative of the drop one can see in the levels over the months of March and April and slight drop over time. Also note that the values for 2020 are below the mean of previous 2 years significantly (barring a few spikes) in general but we can not significantly say that impact can be attributed to the increasing number of confirmed cases.

This puts into perspective the possible impact of COVID-19 on the Air Pollution parameters.

Required Inference #5 (Done)

In [223]:
```
deaths4weeks = deaths2.iloc[-28:] # filtering last 28 days - 4 weeks
deaths4weeks = np.array_split(deaths4weeks.sum(1), 4) # dividing into 4 differ
ent weeks

post_list = []
map_list = []

# possion data with exponential prior gives gamma posterior (same distribution
in subsequent iterations)
# gamma distribution will have alpha = sum(x) + 1 and beta = n + (mean(data))^
-1
# proof shared in drive

for data in deaths4weeks:
  alpha = sum(data) + 1
  beta = len(data) + (1/np.mean(data))
  posterior = [gamma.pdf(x, a=alpha, scale=1/beta) for x in data]
  post_list.append(posterior)
  map_list.append(list(data)[np.argmax(posterior)]) # map is x values where po
sterior is highest

for i, (data, post) in enumerate(zip(deaths4weeks, post_list)):
  plt.plot(data, post, label='Week '+str(i+1) + '=> MAP = ' + str(map_list[i
]))
plt.legend()
plt.title('Inference 5, Posterior Distributions')
plt.show()
```



If we implement gamma pdf function by ourselves, it gives overflow error

In [0]:
```
# def gamma_dist(x, alpha, beta):
#   # https://en.wikipedia.org/wi ki/Gamma_distribution
#   return ((beta**(-alpha))*(x**(alpha-1))*(np.exp((-x/beta))))/scipy.math.fa
ctorial(alpha-1)

# deaths4weeks = deaths2.iloc[-28:] # filtering last 28 days - 4 weeks
# deaths4weeks = np.array_split(deaths4weeks.sum(1), 4) # dividing into 4 diff
erent weeks

# for data in deaths4weeks:
#   alpha = sum(data) + 1
#   beta = len(data) + (1/np.mean(data))
#   # posterior = [gamma.pdf(x, a=alpha, scale=1/beta) for x in data]  # direc
t scipy function for gamma (https://docs.scipy.org/doc/scipy/reference/generat
ed/scipy.stats.gamma.html)
#   posterior = [gamma_dist(x, alpha, 1/beta) for x in data]           # our f
unction giving overflow error
#   post_list.append(posterior)
#   map_list.append(list(data)[np.argmax(posterior)]) # map is x values where
 posterior is highest

# for i, (data, post) in enumerate(zip(deaths4weeks, post_list)):
#   plt.plot(data, post, label='Week '+str(i+1) + '=> MAP = ' + str(map_list
[i]))
# plt.legend()
# plt.title('Inference 5, Posterior Distributions')
# plt.show()
```

Creative Inference #1

We look to apply KS Test to see how similar are distributions for Carbon Monoxide and Lead levels from station in Suffolk County, and Lead levels for Essex and Plymouth counties for years 2020 and previous years.

In [225]:
```
def calculate_KS_for(county, station, parameter):
  filtered20 = airnow_2020[(airnow_2020['AQSID'] == station) & (airnow_2020['p
arameter name'] == parameter)]
  filtered20 = impute_missing_dates(filtered20, '2020', confirmed_march_april[
'Date'].dt.strftime('2020-%m-%d').values.tolist())
  filtered19 = airnow_2019[(airnow_2019['AQSID'] == station) & (airnow_2019['p
arameter name'] == parameter)]
  filtered19 = impute_missing_dates(filtered19, '2019', confirmed_march_april[
'Date'].dt.strftime('2019-%m-%d').values.tolist())
  filtered18 = airnow_2018[(airnow_2018['AQSID'] == station) & (airnow_2018['p
arameter name'] == parameter)]
  filtered18 = impute_missing_dates(filtered18, '2018', confirmed_march_april[
'Date'].dt.strftime('2018-%m-%d').values.tolist())

  critical_value = 0.05
  print("H0: The data for the metric in 2020 and 2019 come from the same distr
ibution.")
  print('KS Test: {} for {} 2020 vs 2019: '.format(county, parameter))
  KS(filtered20['value'].tolist(), filtered19['value'].tolist(), critical_valu
e)
  print('\n' * 1 + '*' * 20 + '\n'*1)
  print("H0: The data for the metric in 2019 and 2018 come from the same distr
ibution.")
  print('KS Test: {} for {} 2019 vs 2018: '.format(county, parameter))
  KS(filtered19['value'].tolist(), filtered18['value'].tolist(), critical_valu
e)

  print('\n' * 2 + '*' * 20 + '\n'*2)

KS_metrics_options = [('Suffolk County', 250250042, 'CO-8hr'),
                      ('Suffolk County', 250250042, 'PM2.5-24hr'),
                      ('Essex County', 250092006, 'PM2.5-24hr'),
                      ('Plymouth County', 250230005, 'PM2.5-24hr')]

for option in KS_metrics_options:
  calculate_KS_for(option[0], option[1], option[2])
```

```
H0: The data for the metric in 2020 and 2019 come from the same distribution.
KS Test: Suffolk County for CO-8hr 2020 vs 2019:
Rejecting null hypothesis because D value = 0.4666666666666675 greater than o
r equal to 0.05.

********************

H0: The data for the metric in 2019 and 2018 come from the same distribution.
KS Test: Suffolk County for CO-8hr 2019 vs 2018:
Rejecting null hypothesis because D value = 0.2333333333333333 greater than o
r equal to 0.05.


********************


H0: The data for the metric in 2020 and 2019 come from the same distribution.
KS Test: Suffolk County for PM2.5-24hr 2020 vs 2019:
Rejecting null hypothesis because D value = 0.7333333333333342 greater than o
r equal to 0.05.

********************

H0: The data for the metric in 2019 and 2018 come from the same distribution.
KS Test: Suffolk County for PM2.5-24hr 2019 vs 2018:
Rejecting null hypothesis because D value = 0.4333333333333338 greater than o
r equal to 0.05.


********************


H0: The data for the metric in 2020 and 2019 come from the same distribution.
KS Test: Essex County for PM2.5-24hr 2020 vs 2019:
Rejecting null hypothesis because D value = 0.13333333333333375 greater than
or equal to 0.05.

********************

H0: The data for the metric in 2019 and 2018 come from the same distribution.
KS Test: Essex County for PM2.5-24hr 2019 vs 2018:
Rejecting null hypothesis because D value = 0.5500000000000004 greater than o
r equal to 0.05.


********************


H0: The data for the metric in 2020 and 2019 come from the same distribution.
KS Test: Plymouth County for PM2.5-24hr 2020 vs 2019:
Rejecting null hypothesis because D value = 0.21666666666666734 greater than
or equal to 0.05.

********************

H0: The data for the metric in 2019 and 2018 come from the same distribution.
KS Test: Plymouth County for PM2.5-24hr 2019 vs 2018:
```

```
Rejecting null hypothesis because D value = 0.6000000000000002 greater than o
r equal to 0.05.


********************
```

NOTE: We only calculate for years and stations where there was data to make meaningful inferences.

In order to compare the distributions for certain metrics we perform the KS test to see if the values for 2020 and 2019 are similar and as a baseline if we see 2019 and 2018 comparison.

Our Null hypothesis is that they follow datasets we are comparing come from the same distribution. In all of the cases we can see that we reject the Null hypothesis. This does NOT give us much insight.

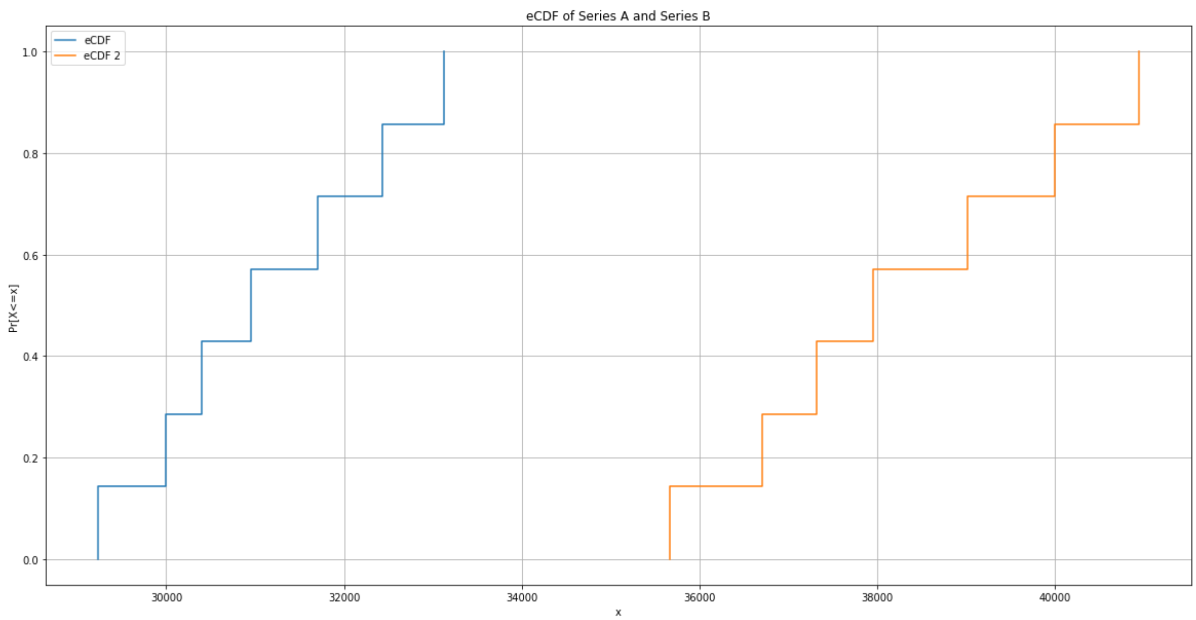
An important metric to compare the KS-statistic values which are smaller for the test for 2018 and 2019 in comparison to the test for comparing 2020 and 2019 in the case of Suffolk county.

We observe the opposite trend for Essex and Plymouth counties.

Creative inference #2

In [226]:
```
age = pd.read_csv('extractedData/Age.csv')
sex = pd.read_csv('extractedData/Sex.csv')
sex_data=sex.tail(7)
KS( sex_data['Male'].tolist(), sex_data['Female'].tolist(), 0.05, message="Mal
e Vs Female",draw=True)
n = 2000
alpha = 0.05
p_value = calc_p_val(sex_data['Male'].tolist(), sex_data['Female'].tolist(), n
)
p_values.append(p_value)
result = test_hypothesis(p_value, alpha, "Males Vs Female for {} permutations:
".format(n))
```

```
Male Vs Female
```




```
Rejecting null hypothesis because D value = 0.9999999999999998 greater than o
r equal to 0.05.
Males Vs Female for 2000 permutations: Rejecting null hypothesis. p value: 0.
0
```

The null hypothesis for KS Test is that Male and Female distribution is the same distribution. The results show that they are not the same distribution.

The null hypothesis of permutation test is that the male and female cases distribution is same. The hypothesis is rejected and hence it rejects that the distribution of deaths of male and female is not different and hence it is same.

Creative Inference #3

Difference in Pollution means before and after Stay-at-Home directive

In [0]:
```
air_qual = pd.read_csv('AirNow/AirNow_Massachusetts_2020_WithCounties.csv')
```

In [0]:
```
air_qual = air_qual[['Valid date', 'site name', 'parameter name', 'reporting units', 'value', 'AQI', 'county']]
```

In [0]:
```
STD_DATE_FORMAT = '%m/%d/%Y'
DATA_DATE_FORMAT = '%m/%d/%y'
air_qual['Valid date'] = pd.to_datetime(air_qual['Valid date'], format=DATA_DATE_FORMAT).dt.strftime(STD_DATE_FORMAT)
```

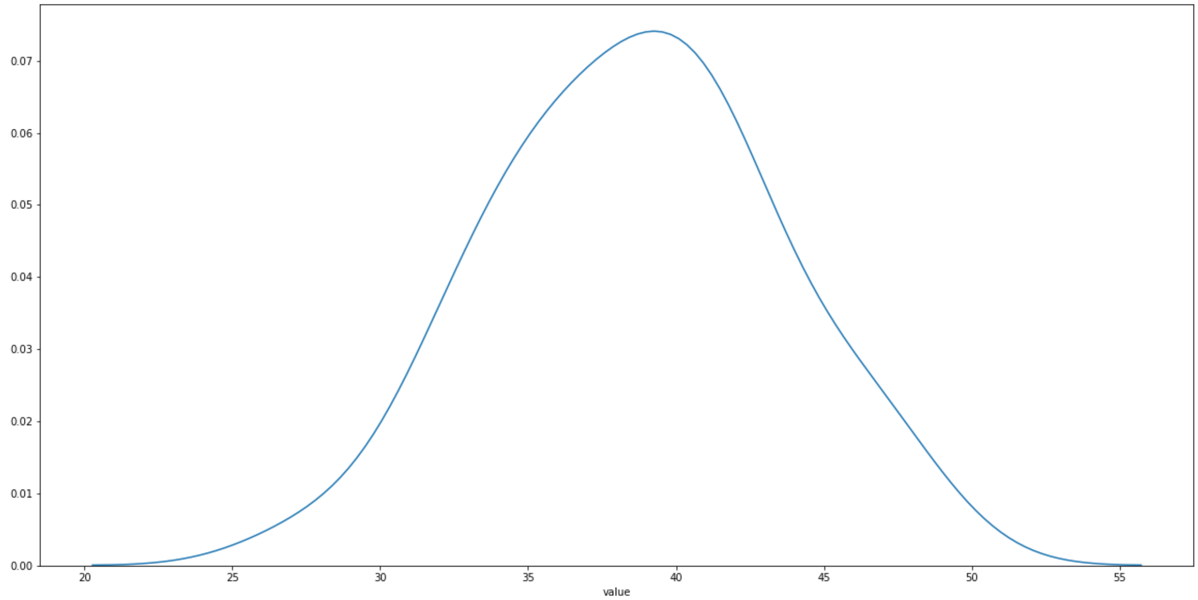
In [0]:
```
import matplotlib.pyplot as plt
import seaborn as sns

#Remove outliers from pollution data by Tukey's Rule
def remove_outliers(air_qual_reqd):
  x = np.copy(air_qual_reqd['value'].values)
  x.sort()
  q_1 = x[len(x)//4]
  q_3 = x[3*len(x)//4]
  iqr = q_3-q_1

  iqr_1 = q_1 - 1.5 * iqr
  iqr_3 = q_3 + 1.5 * iqr
  outliers = x[(x<iqr_1) | (x>iqr_3)]
  print("{} outliers found, {}".format(len(outliers),outliers))
  air_qual_reqd = air_qual_reqd[~air_qual_reqd['value'].isin(outliers)]
  #plt.hist(air_qual_reqd.value, histtype='step')
  #Plot the sample distribution
  sns.distplot(air_qual_reqd.value, hist=False)
  plt.pause(1)
  plt.show
```

In [0]:
```
def t_test_2sample_unpaired(sample1, sample2):
  #Critical values from https://www.itl.nist.gov/div898/handbook/eda/section3/
eda3672.htm
  critical_val_dict = {20:-1.725,19:-1.729,18:-1.734,17:-1.740,}
  mean_sample1 = sample1.mean()
  mean_sample2 = sample2.mean()
  variance_sample1 = sample1.var()
  variance_sample2 = sample2.var()
  t_stat = (mean_sample1 - mean_sample2) / math.sqrt( variance_sample1/len(sam
ple1) + variance_sample2/len(sample2))
  dfreedom = min(len(sample1), len(sample2))-1
  if dfreedom in critical_val_dict:
    t_critical = critical_val_dict[dfreedom]
  else:
    raise Exception("Not enough sample points to compare after removing outlie
rs")
  print('Value of t-stat for critical value {} at n-1 = {} & alpha 0.05 = {}'.
format(t_critical, dfreedom, t_stat))
  if t_stat < t_critical:
    return False
  else:
    return True
```

In [0]:
```
import math

#County:Site dictionary to obtain pollution data from Dataset
county_site_dict = {'Middlesex':'ChelmsfordNR', 'Suffolk':'Boston - Roxbury',
'Bristol': 'Fall River', 'Essex': 'Haverhill', 'Plymouth':'Brockton'}
pollution_param = ['OZONE-8HR', 'PM2.5-24hr']

def calc_pollution_significance(county):
  if county in county_site_dict:
    for param in pollution_param:
      print(param)
      site = county_site_dict[county]
      air_qual_reqd = air_qual[(air_qual['county']==county) & (air_qual['site
 name']==site) & (air_qual['parameter name']==param)]
      remove_outliers(air_qual_reqd)
      prior_data = air_qual_reqd[(air_qual_reqd['Valid date'] >= '03/01/2020'
)][:20]
      after_data = air_qual_reqd[(air_qual_reqd['Valid date'] >= '04/05/2020'
)][:20]
      try:
        result = t_test_2sample_unpaired(prior_data['value'], after_data['valu
e'])
        if not result:
          print('H0 is rejected, Mean before stay-at-home is not greater than
 after stay-at-home order')
        else:
          print("Can't reject H0, Mean before stay-at-home could be greater th
an after stay-at-home order")
        print('\n')
      except:
        print('Not enough data points to calculate significance')
```

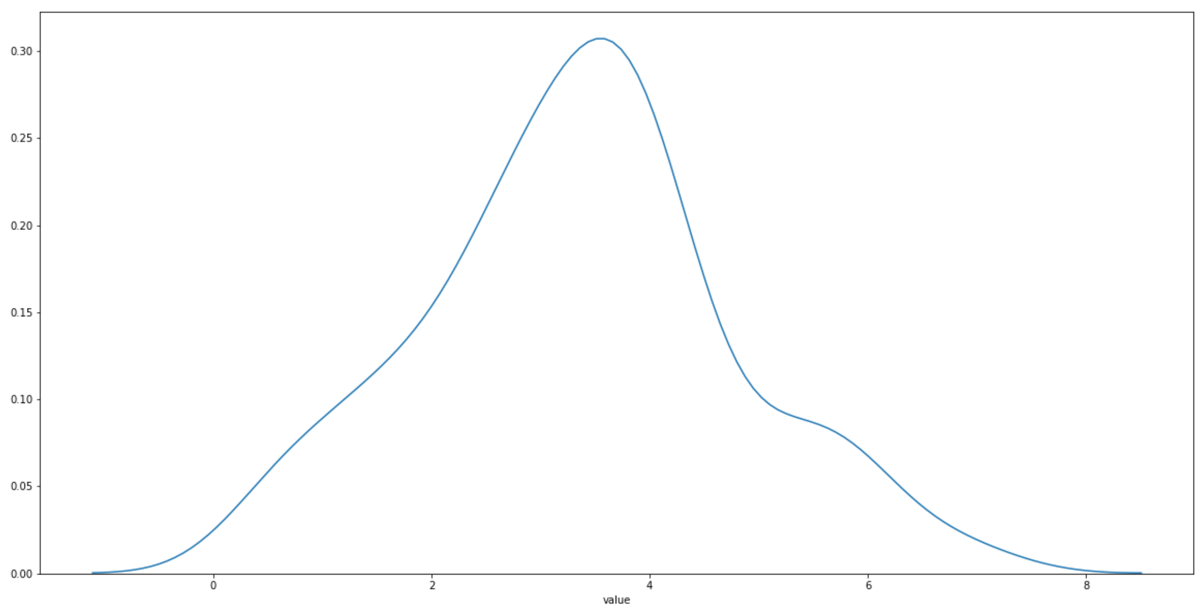
In [233]:
```
import time
pollution_counties_list = ['Suffolk', 'Middlesex', 'Essex', 'Bristol', 'Plymou
th']
for county in pollution_counties_list:
  print(county)
  calc_pollution_significance(county)
```

```
Suffolk
OZONE-8HR
1 outliers found, [55.]
```



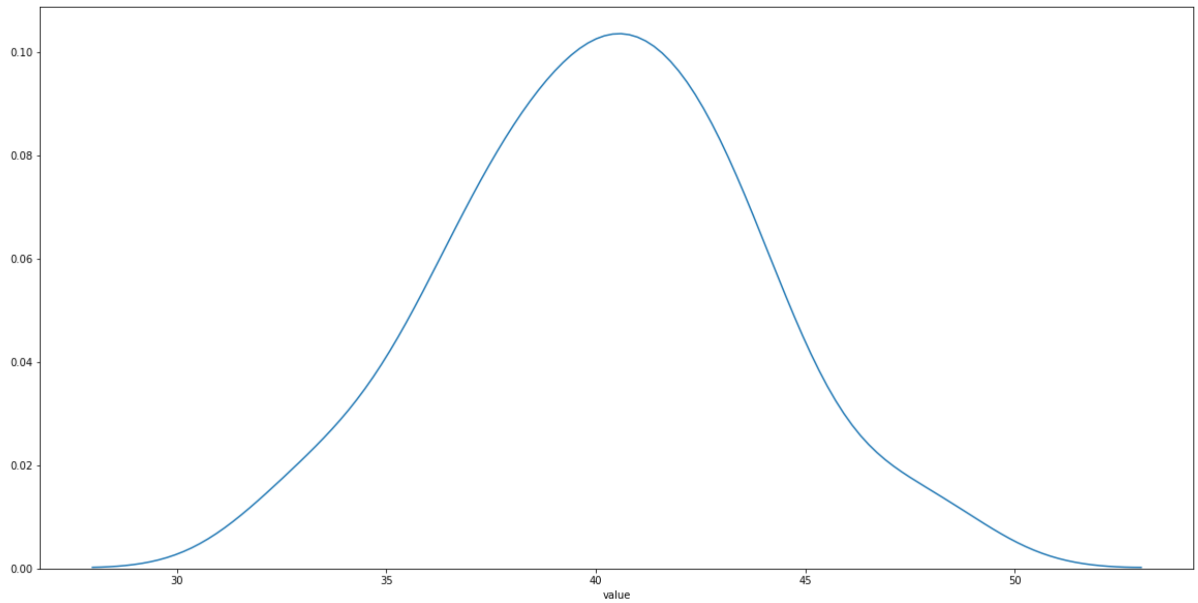

```
Value of t-stat for critical value -1.729 at n-1 = 19 & alpha 0.05 = -2.03370
09569766686
H0 is rejected, Mean before stay-at-home is not greater than after stay-at-ho
me order
```

```
PM2.5-24hr
5 outliers found, [8.  8.1 8.2 8.7 8.8]
```



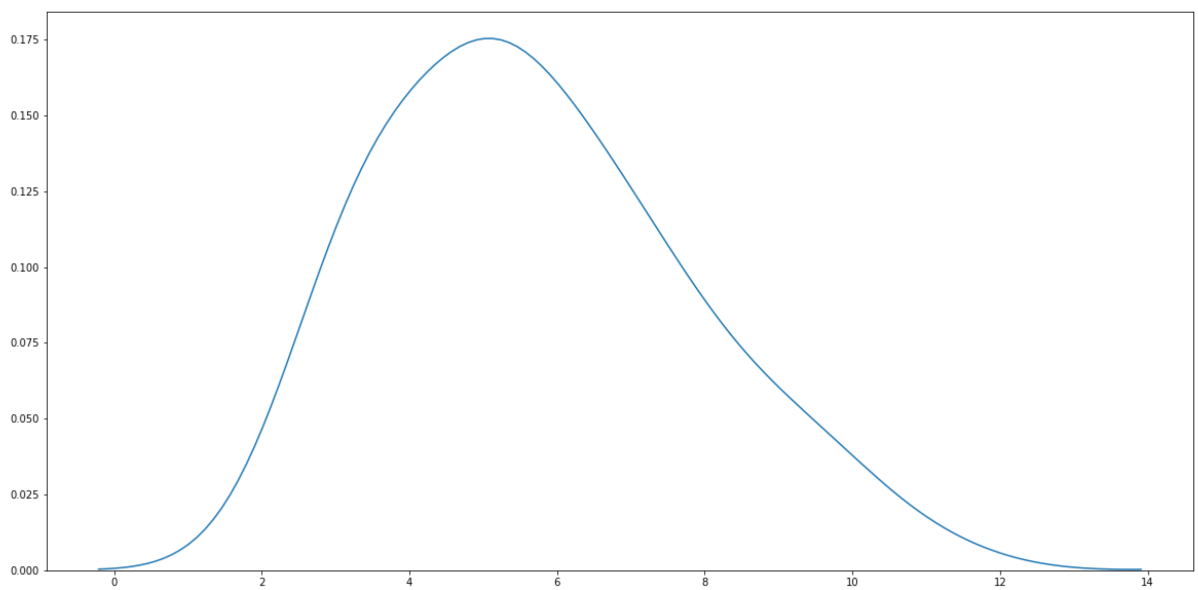
```
Value of t-stat for critical value -1.729 at n-1 = 19 & alpha 0.05 = 1.153701
446227327
Can't reject H0, Mean before stay-at-home could be greater than after stay-at
-home order
```

```
Middlesex
OZONE-8HR
3 outliers found, [22. 29. 52.]
```

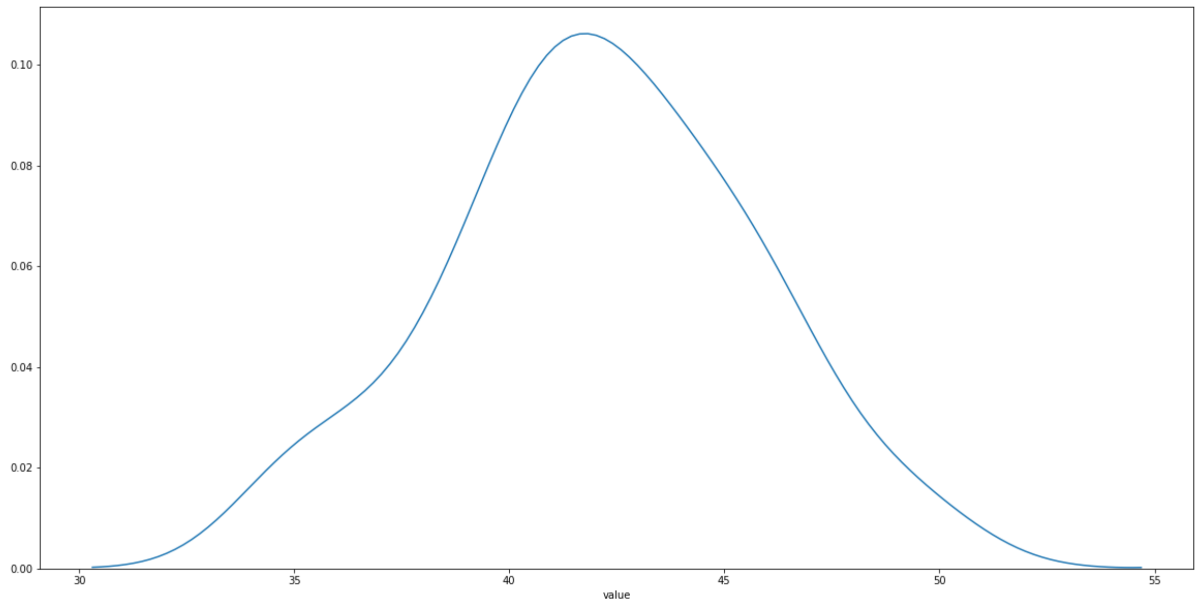



```
Value of t-stat for critical value -1.729 at n-1 = 19 & alpha 0.05 = -2.24768
650807746
H0 is rejected, Mean before stay-at-home is not greater than after stay-at-ho
me order
```

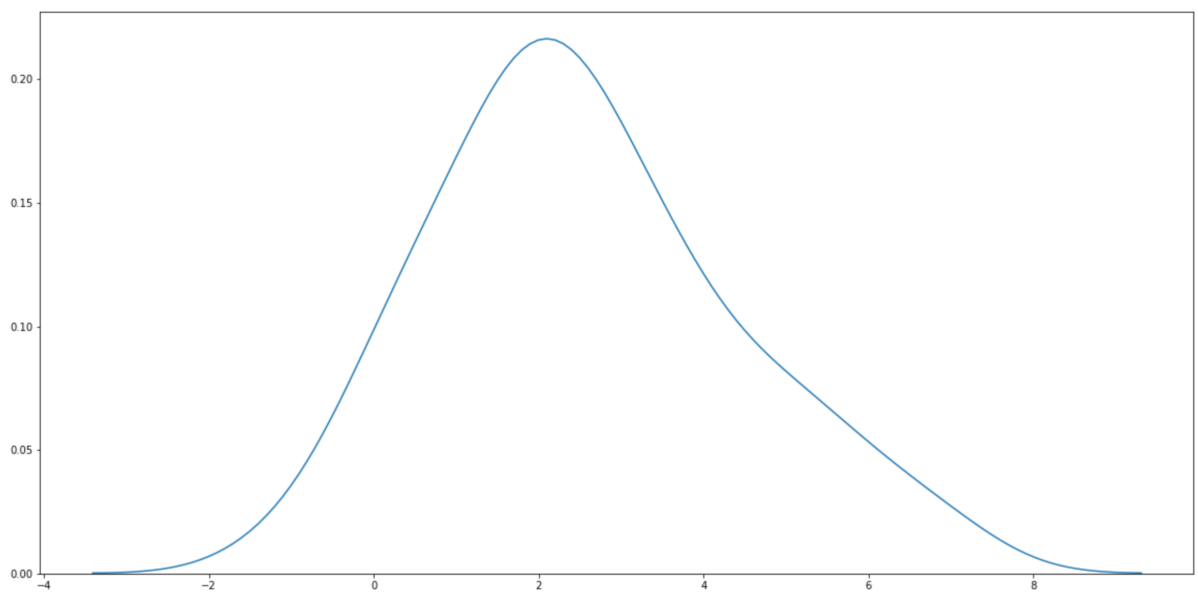
```
PM2.5-24hr
2 outliers found, [11.3 12.3]
```



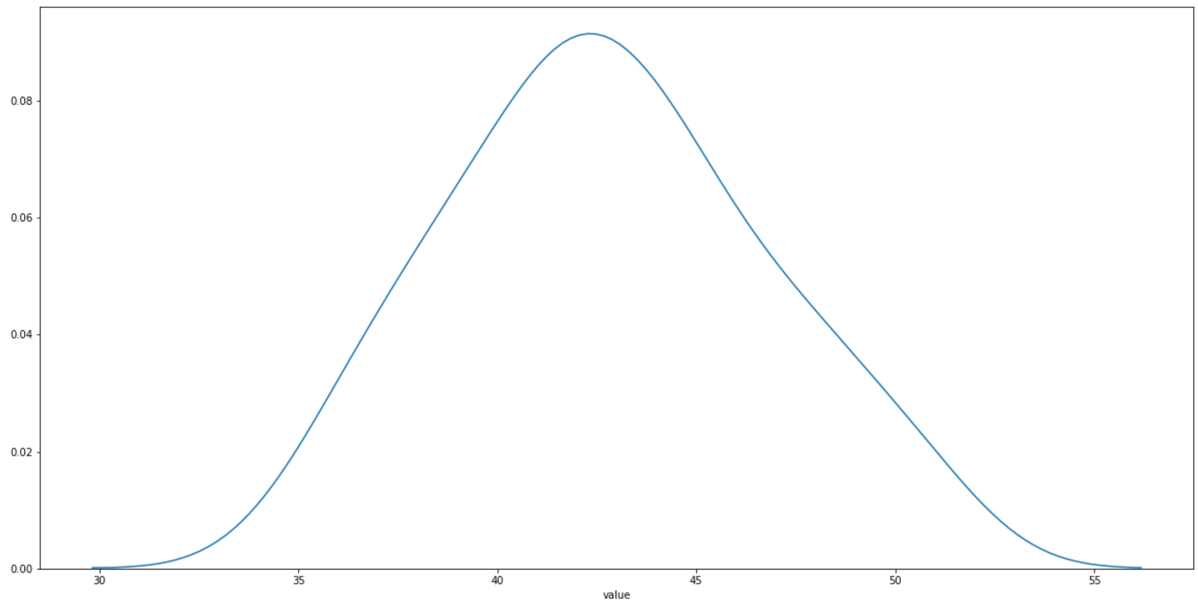
```
Value of t-stat for critical value -1.729 at n-1 = 19 & alpha 0.05 = -0.77585
78263001827
Can't reject H0, Mean before stay-at-home could be greater than after stay-at
-home order


Essex
OZONE-8HR
2 outliers found, [32. 54.]
```



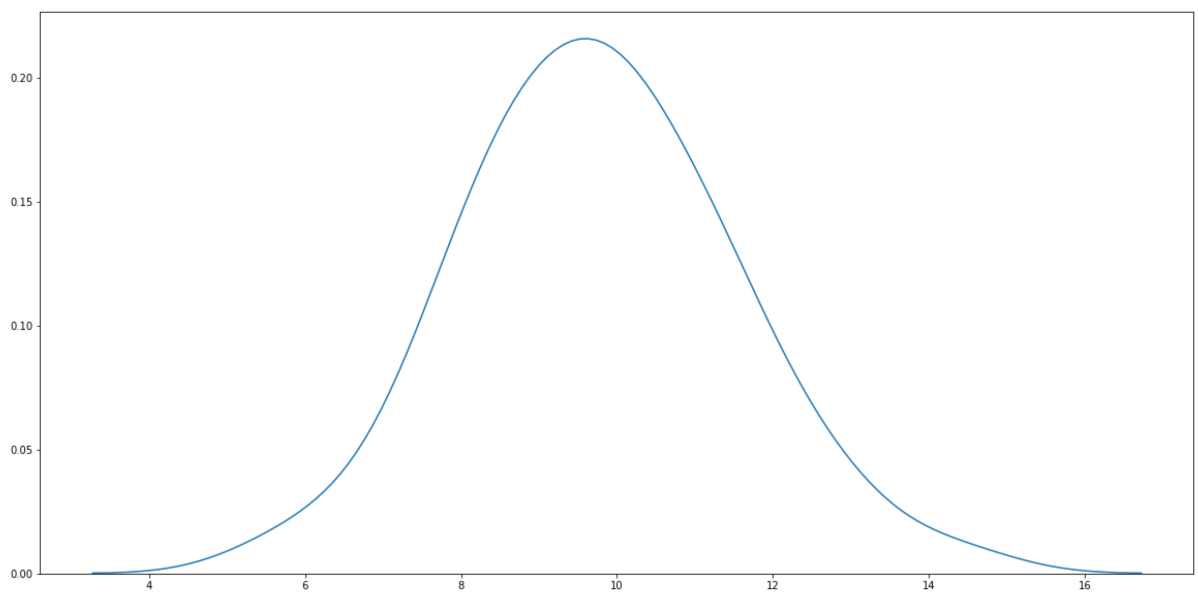

```
Value of t-stat for critical value -1.729 at n-1 = 19 & alpha 0.05 = -1.82512
18407216985
H0 is rejected, Mean before stay-at-home is not greater than after stay-at-ho
me order


PM2.5-24hr
2 outliers found, [7.9 8.5]
```



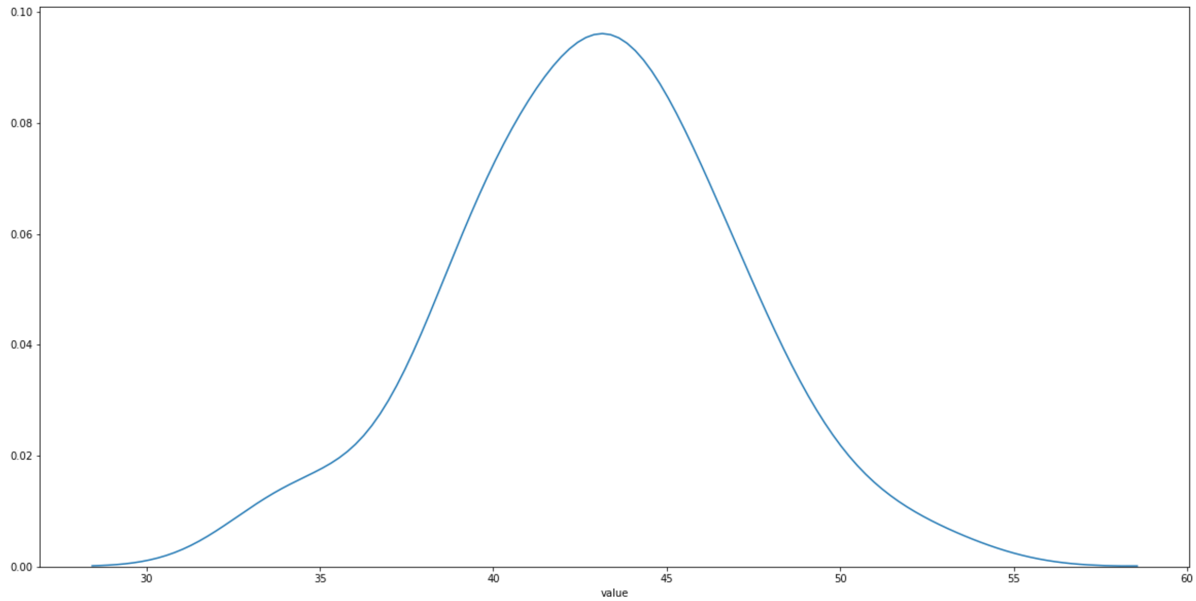
```
Value of t-stat for critical value -1.729 at n-1 = 19 & alpha 0.05 = 0.255996
0557948599
Can't reject H0, Mean before stay-at-home could be greater than after stay-at
-home order


Bristol
OZONE-8HR
0 outliers found, []
```



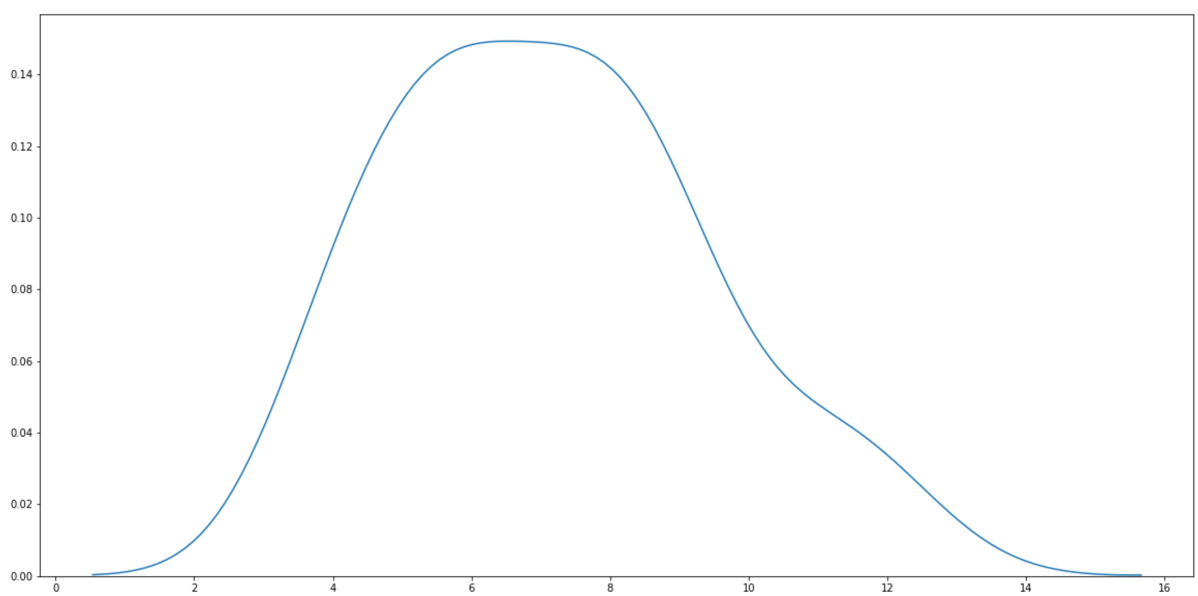

```
Value of t-stat for critical value -1.729 at n-1 = 19 & alpha 0.05 = -2.39679
30416912835
H0 is rejected, Mean before stay-at-home is not greater than after stay-at-ho
me order


PM2.5-24hr
5 outliers found, [ 3.2  4.1 15.5 17.1 20.5]
```



```
Value of t-stat for critical value -1.729 at n-1 = 19 & alpha 0.05 = 0.739496
5702623602
Can't reject H0, Mean before stay-at-home could be greater than after stay-at
-home order


Plymouth
OZONE-8HR
0 outliers found, []
```




```
Value of t-stat for critical value -1.729 at n-1 = 19 & alpha 0.05 = -2.96683
98292705853
H0 is rejected, Mean before stay-at-home is not greater than after stay-at-ho
me order


PM2.5-24hr
1 outliers found, [14.]
```



```
Value of t-stat for critical value -1.729 at n-1 = 19 & alpha 0.05 = 1.878056
7879764116
Can't reject H0, Mean before stay-at-home could be greater than after stay-at
-home order
```

In [234]:
```
try:
  result = t_test_2sample_unpaired(prior_data['value'], after_data['value'])
  if not result:
    print('H0 is rejected', 'Mean before stay-at-home is not greater than afte
r stay-at-home order')
  else:
    print("Can't reject H0")
except:
  print('Not enough data points to calculate significance')
```

```
Not enough data points to calculate significance
```

Comments

As per https://ballotpedia.org/States_with_lockdown_and_stay-at-home_orders_in_response_to_the_coronavirus_(COVID-19)_pandemic,_2020#Orders_by_state (https://ballotpedia.org/States_with_lockdown_and_stay-at-home_orders_in_response_to_the_coronavirus_(COVID-19)_pandemic,_2020#Orders_by_state)

Governor of Massachusetts gave a stay at home order starting March 24.
Here,we are hypothesising that the air quality would get better due to people staying at home and commute getting scarce. Hence, the Ozone and PM2.5, which is particulate data were compared for 20 days before and after the order was given.
The before and after data is from the start of March and April months respectively.
The hypothesis here is that mean value of the particulate matters in air before the announcement were more than after.
The data is taken from AirNow, and for the consideration period outliers were removed for each County, and then the data was plotted before applying hypothesis testing.
Since the data seems approximately Normal, and also 20 records were considered for each sample,Unpaired T-test was applied to compare the sample mean estimators.
As per the results, the ground level Ozone doesn't seem to be impacted which maybe due to the fact that it takes a long time in general for the Ozone concentration to change which is a general longer term climate consideration.
On the other hand, the hypothesis for PM2.5 can't be rejected which maybe due to the fact that due to fewer people gathering together and most of all travelling, the quantity of particulate matter might be going down.