project-03-demo

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1 Project 3

1.1 B-IT Pattern Recognition

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```
In [1]: import numpy as np
        import timeit
        import time
        import matplotlib.pyplot as plt
        from mpl_toolkits.mplot3d import Axes3D
        %matplotlib inline

        from sklearn.cluster import KMeans
        from scipy.cluster.vq import kmeans, kmeans2

        import pattrex.plotting_mpl as plt_rex
        import pattrex.dimred as dim_rex
        import pattrex.fun_with_k_means as km_rex
        import pattrex.SpectralClustering as sc_rex
        import pattrex.SpectralClustering_AndrewNg as scan_rex
        from pattrex.demo_helper import read_whdata
        import pattrex.preprocessing as pre_rex
```

1.2 Task 3.1

1.2.1 Fun with k-means clustering

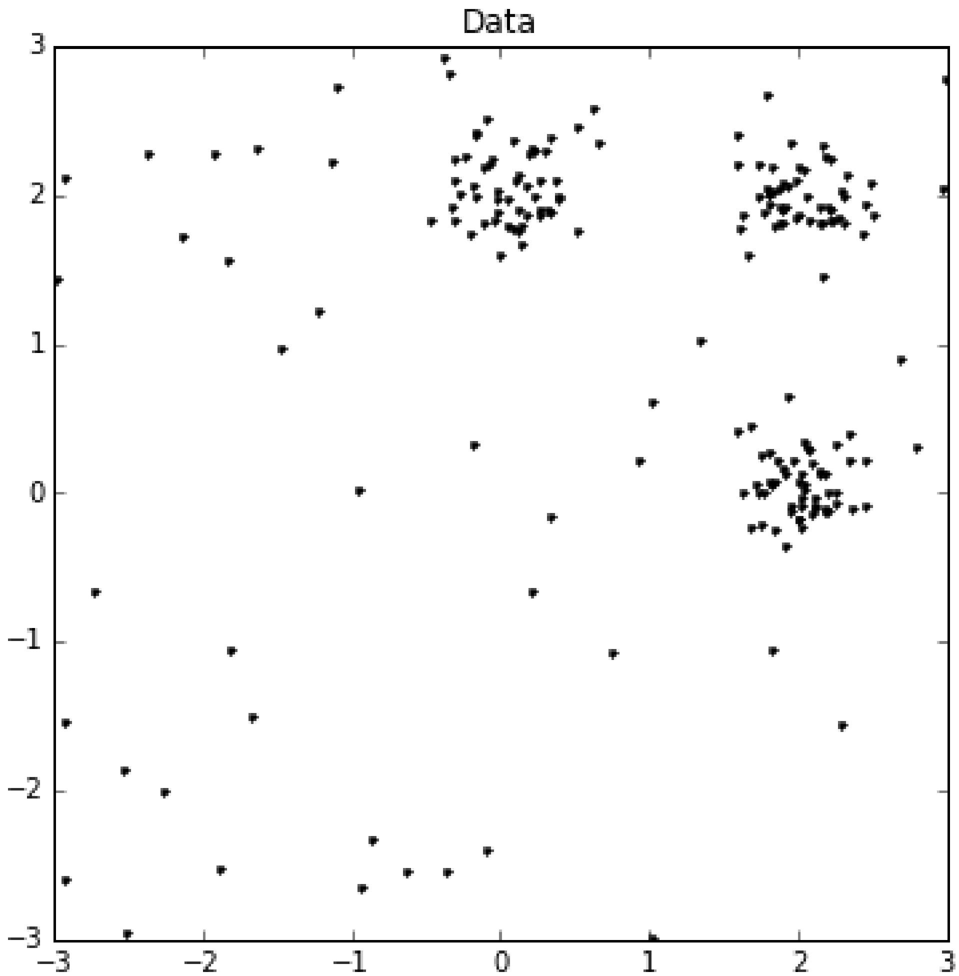
```
In [2]: def demo_1_data():
            data = np.genfromtxt("./data/data-clustering-1.csv", delimiter=',')
            print("{} samples of {} dimensional data".format(*(data.T).shape))

            fig = plt.figure(figsize=(6, 6))
            ax = fig.add_subplot(111)
```

```
        plt_rex.plot2d(data, colwise_data=True, show=False, hatch='k.',
                       title="Data", axs=ax)

        return data.T
```

1.2.2 The Data

```
In [3]: mydata = demo_1_data()
```

```
200 samples of 2 dimensional data
```




```
In [4]: def demo_1_init(data, k, seed=9000):
            nX, mX = data.shape
            np.random.seed(seed)

            # Random choices from data
            m1 = np.copy(data[np.random.choice(np.arange(nX), size=k)])
```

```
        np.random.seed(seed + seed)

        # Random choice of one
        m2 = np.copy(data[np.random.choice(np.arange(nX), size=k)])

        # explicit init
        m3 = np.array([
                [2, 2],
                [0, 2],
                [2, 0]
            ])

        return m1, m2, m3
```

```
In [5]: def demo_1_lloyd(data, k):
            inits = demo_1_init(data, k, seed=800)
            titles = [
                "Lloyd's - {} random choices to init 1".format(k),
                "Lloyd's - {} random choices to init 2".format(k),
                "Lloyd's - human init",
            ]
            fig = plt.figure(figsize=(15, 5))
            sp = [1, 3, 0]

            for i, t in zip(inits, titles):
                try:
                    m, l = km_rex.lloyd2(data, i, verbose=True)
                except UserWarning:
                    print("Did not converge for {}".format(t))

                # plotting
                sp[-1] += 1
                ax = fig.add_subplot(*sp)

                h_d = ['r.', 'g.', 'b.']
                h_m = ['rs', 'gs', 'bs']
                h_i = ['ko', 'ko', 'ko']
                for c, hd, hm, hi in zip(range(k), h_d , h_m, h_i):
                    plt_rex.plot2d(data[l == c], False, show=False, axs=ax,
                                   hatch=hd,
                                   title=t)
                    plt_rex.plot2d(m[c, :].reshape(1, m.shape[1]), False, show=False,
                                   axs=ax, hatch=hm)
                    plt_rex.plot2d(i[c, :].reshape(1, m.shape[1]), False, show=False,
                                   axs=ax, hatch=hi)

        def demo_1_hart(data, k, seeds):
            titles = ["Hartigan's - Random Seed {}".format(s) for s in seeds]
            fig = plt.figure(figsize=(15, 5))
            sp = [1, 3, 0]

            for s, t in zip(seeds, titles):
                try:
                    m, l = km_rex.hartigan2(data, k, seed=s)
```

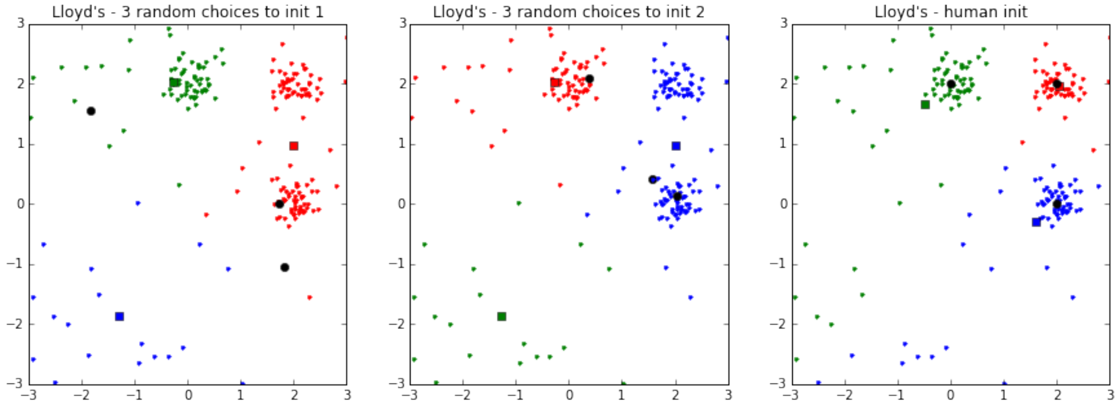
```
        except UserWarning:
            print("Did not converge for {}".format(t))

        # plotting
        sp[-1] += 1
        ax = fig.add_subplot(*sp)

        h_d = ['r.', 'g.', 'b.']
        h_m = ['rs', 'gs', 'bs']
#         h_i = ['ko', 'ko', 'ko']
        for c, hd, hm in zip(range(k), h_d , h_m):
            plt_rex.plot2d(data[l == c], False, show=False, axs=ax,
                           hatch=hd,
                           title=t)
            plt_rex.plot2d(m[c, :].reshape(1, m.shape[1]), False, show=False,
                           axs=ax, hatch=hm)
#             plt_rex.plot2d(i[c, :].reshape(1, m.shape[1]), False, show=False,
#                            axs=ax, hatch=hi)

def demo_1_macqueen(data, k, seeds):
    titles = ["MacQueen's"] + \
        ["MacQueen's - Random shuffle {}".format(s) for s in seeds]
    fig = plt.figure(figsize=(15, 5))
    sp = [1, 3, 0]

    datas = [np.copy(data)]
    for s in seeds:
        np.random.seed(s)
        np.random.shuffle(data)
        datas.append(np.copy(data))


    for d, t in zip(datas, titles):
        try:
            m, l = km_rex.mcqueen2(d, k)
        except UserWarning:
            print("Did not converge for {}".format(t))

        # plotting
        sp[-1] += 1
        ax = fig.add_subplot(*sp)

        h_d = ['r.', 'g.', 'b.']
        h_m = ['rs', 'gs', 'bs']
        h_i = ['ko', 'ko', 'ko']
        i = d[:k, :]
        for c, hd, hm, hi in zip(range(k), h_d , h_m, h_i):
            plt_rex.plot2d(d[l == c], False, show=False, axs=ax,
                           hatch=hd,
                           title=t)
            plt_rex.plot2d(m[c, :].reshape(1, m.shape[1]), False, show=False,
                           axs=ax, hatch=hm)
            plt_rex.plot2d(i[c, :].reshape(1, m.shape[1]), False, show=False,
                           axs=ax, hatch=hi)
```

1.2.3 Lloyd's Algorithm

- Very Sensitive to initialization values
- Converges, but no guarantees (esp in case of bad initializations)
- No Guarantee about the results either
- Really Fast (if no catastrophy)

```
In [6]: demo_1_lloyd(mydata, 3)
```

```
Converged after 4 iterations
Converged after 9 iterations
Converged after 3 iterations
```




```
In [7]: def demo_1_lloyd2(data, k, dist, seed):
            i = demo_1_init(data, k, seed=seed)[0]
            titles = [
                "Lloyd's - random choices to init - {}".format(d) for d in dist]
            fig = plt.figure(figsize=(15, 5))
            sp = [1, 3, 0]

            for d, t in zip(dist, titles):
                try:
                    m, l = km_rex.lloyd2(data, i, verbose=True, metric=d)
                except UserWarning:
                    print("Did not converge for {}".format(t))

                # plotting
                sp[-1] += 1
                ax = fig.add_subplot(*sp)

                h_d = ['r.', 'g.', 'b.']
                h_m = ['rs', 'gs', 'bs']
                h_i = ['ko', 'ko', 'ko']
                for c, hd, hm, hi in zip(range(k), h_d , h_m, h_i):
                    plt_rex.plot2d(data[l == c], False, show=False, axs=ax,
                                   hatch=hd,
```

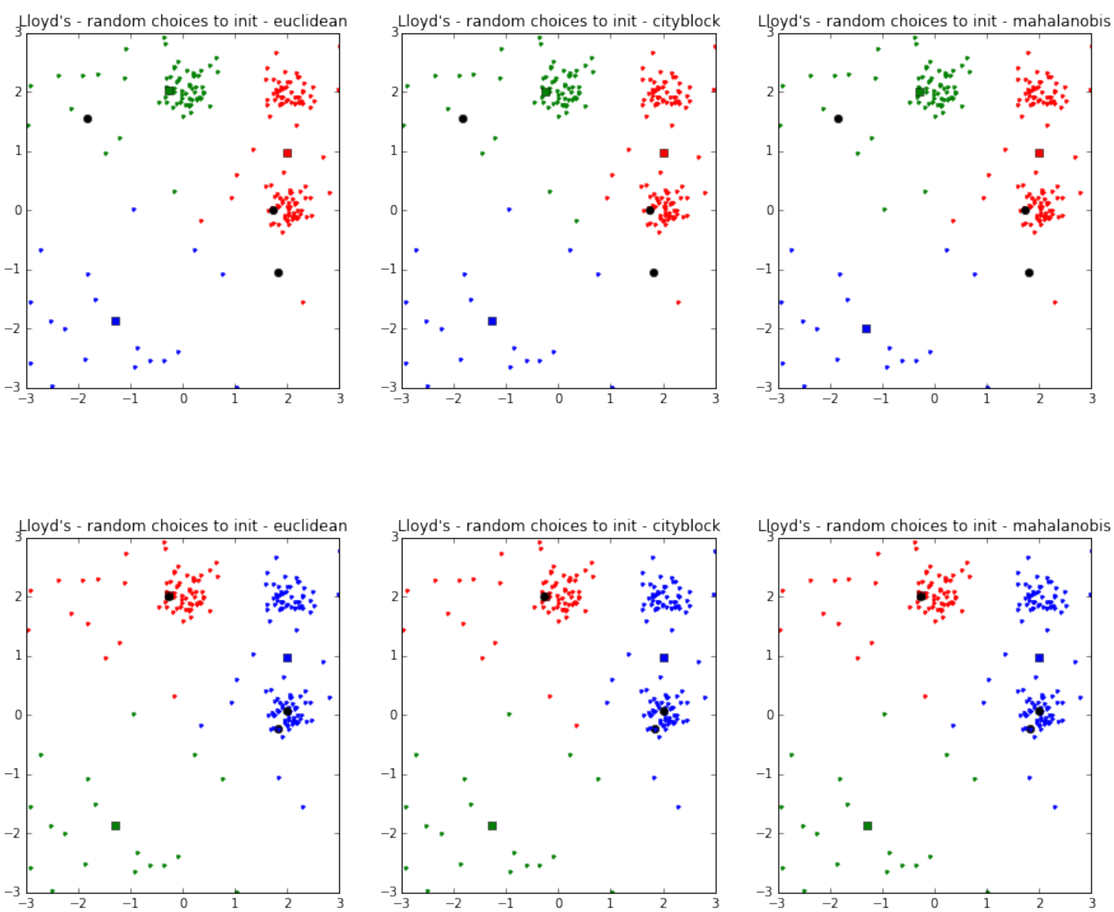
```
                         title=t)
plt_rex.plot2d(m[c, :].reshape(1, m.shape[1]), False, show=False,
                         axs=ax, hatch=hm)
plt_rex.plot2d(i[c, :].reshape(1, m.shape[1]), False, show=False,
                         axs=ax, hatch=hi)
```

1.2.4 Different Similarity Measures

- The data does seem to have **Gaussian Blobs**
  - The problem with the data is different
- Different similarity metric will probably not give different results
  - Except in case of relatively bad similarity metrics

```
In [8]: demo_1_lloyd2(mydata, 3, ['euclidean', 'cityblock', 'mahalanobis'], 800)
        demo_1_lloyd2(mydata, 3, ['euclidean', 'cityblock', 'mahalanobis'], 999)
```

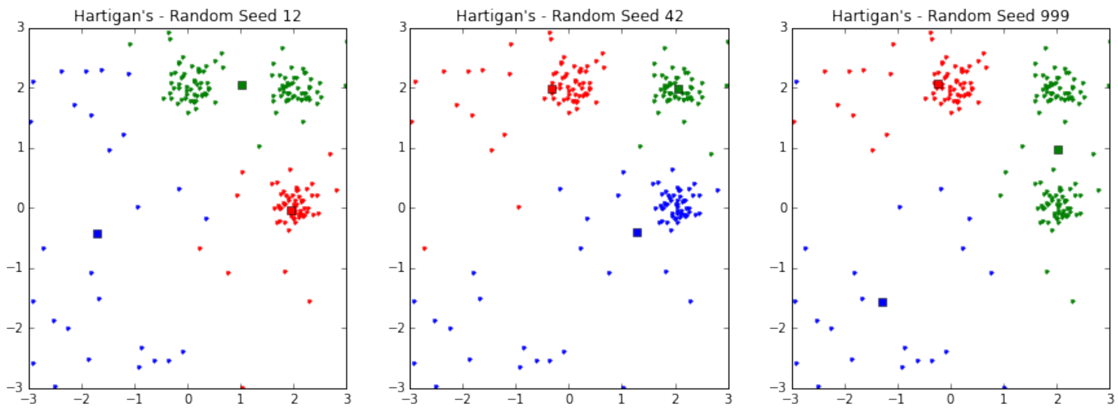
```
Converged after 4 iterations
Converged after 4 iterations
Converged after 4 iterations
Converged after 5 iterations
Converged after 5 iterations
Converged after 5 iterations
```



1.2.5 Hartigan's Algorithm

- Converges quickly
- Still sensitive to initialization of classes

```
In [9]: demo_1_hart(mydata, 3, [12, 42, 999])  # These took some time to choose
```



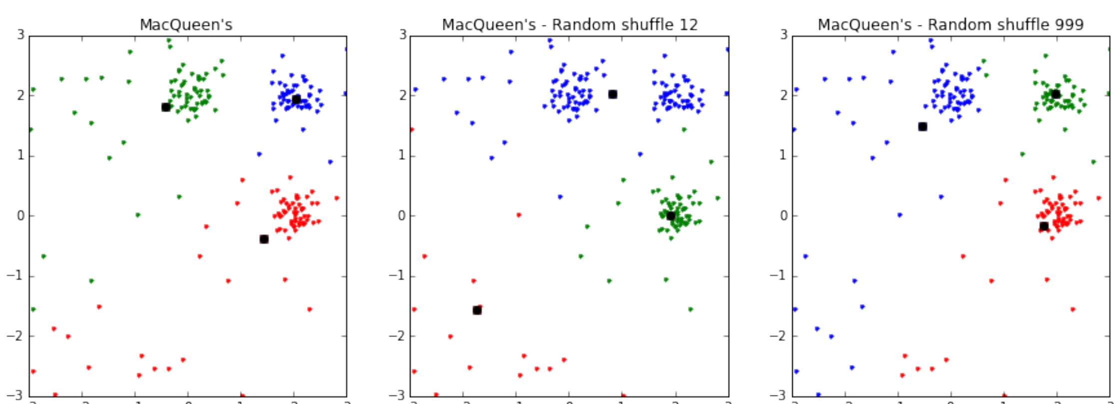
Smarter Way?

- We couldn't figure out any smarter way, than :
  - only recalculate objective function for the current class
    - Not reliable, esp when the data is disproportionate among classes
  - Halved the number of data points for which the distance is calculated, compared to Naive
    - Does not fully utilize the potential, eg vectorization

1.2.6 MacQueen's Algorithm

- Convenient for streams
- Sensitive to order of data
  - Essentially, still sensitive to initialization

```
In [10]: demo_1_macqueen(mydata, 3, [12, 999])
```

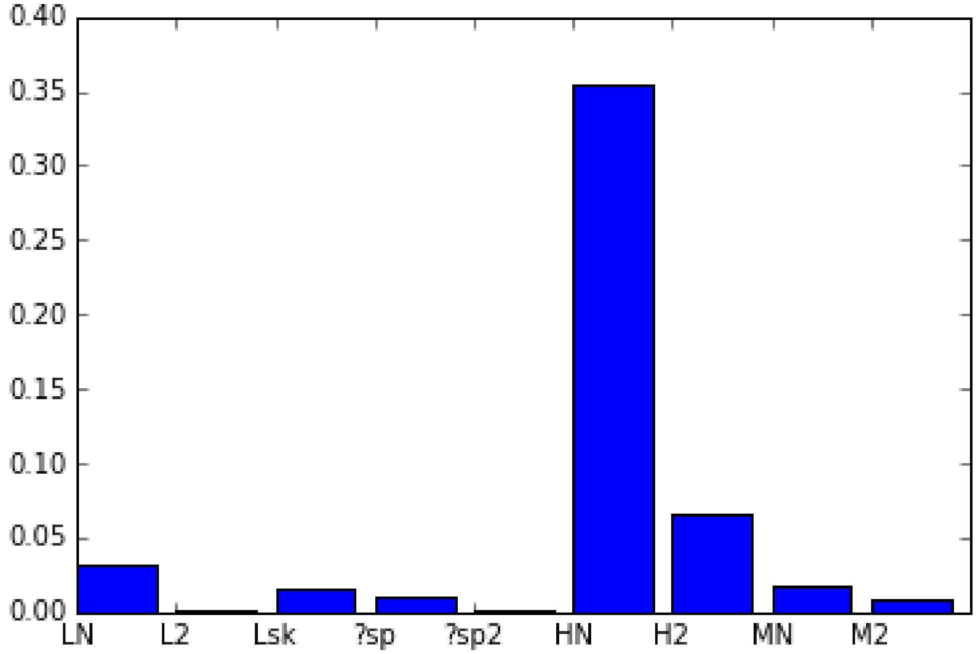


```
In [51]: def demo_1_t():
             print("Mac OSX - 10.11.3")
             print("2,9 GHz Intel Core i7")
             print("Python 3.4")
             print("\nLloyd - Naive")
             %timeit km_rex.kmeans_Lloyd(mydata, 3, init_c, save_plot=False)

             print("\nLloyd - 2")
             %timeit km_rex.lloyd2(mydata, init_c, verbose=False)

             print("\nLloyd - sklearn.cluster.KMeans")
             %timeit KMeans(n_clusters=3).fit(mydata)

             print("\n?? - scipy.cluster.vq.kmeans")
             %timeit kmeans(mydata, 3, check_finite=False)

             print("\n?? - scipy.cluster.vq.kmeans2")
             %timeit kmeans2(mydata, 3, minit='points', check_finite=False)

             print("\nHartigan - Naive")
             %timeit km_rex.kmeans_hartigans(mydata, 3, save_plot=False, show_plot=False)

             print("\nHartigan - 2")
             %timeit km_rex.hartigan2(mydata, 3, seed=9000)

             print("\nMacQueen - Naive")
             %timeit km_rex.kmeans_macqueen(mydata, 3, save_plot=False)

             print("\nMacQueen - 2 (numpy-ed)")
             %timeit km_rex.mcqueen2(mydata, 3)

             t = [
                 (32e-3, "LN"),
                 (833e-6, "L2"),
                 (15.1e-3, "Lsk"),
                 (10.8e-3, "?sp"),
                 (880e-6, "?sp2"),
                 (354e-3, "HN"),
                 (66.7e-3, "H2"),
                 (18.1e-3, "MN"),
                 (9.44e-3, "M2")
             ]

             tt = [t_[0] for t_ in t]
             tl = [t_[1] for t_ in t]

             fig, ax = plt.subplots()
             ax.bar(np.arange(len(tt)), tt)
             ax.set_xticklabels(tl)
```

1.2.7 Run times!

```
In [53]: np.random.seed(9000)
         init_c = np.copy(mydata[np.random.choice(np.arange(mydata.shape[0]), size=3)])
         demo_1_t()
```

```
Mac OSX - 10.11.3
2,9 GHz Intel Core i7
Python 3.4

Lloyd - Naive
10 loops, best of 3: 31.5 ms per loop

Lloyd - 2
1000 loops, best of 3: 864 µs per loop

Lloyd - sklearn.cluster.KMeans
100 loops, best of 3: 15.3 ms per loop

?? - scipy.cluster.vq.kmeans
100 loops, best of 3: 10.6 ms per loop

?? - scipy.cluster.vq.kmeans2
1000 loops, best of 3: 906 µs per loop

Hartigan - Naive
1 loops, best of 3: 488 ms per loop

Hartigan - 2
10 loops, best of 3: 67.1 ms per loop

MacQueen - Naive
100 loops, best of 3: 18.5 ms per loop

MacQueen - 2 (numpy-ed)
100 loops, best of 3: 9.41 ms per loop
```



1.3 Task 3.2

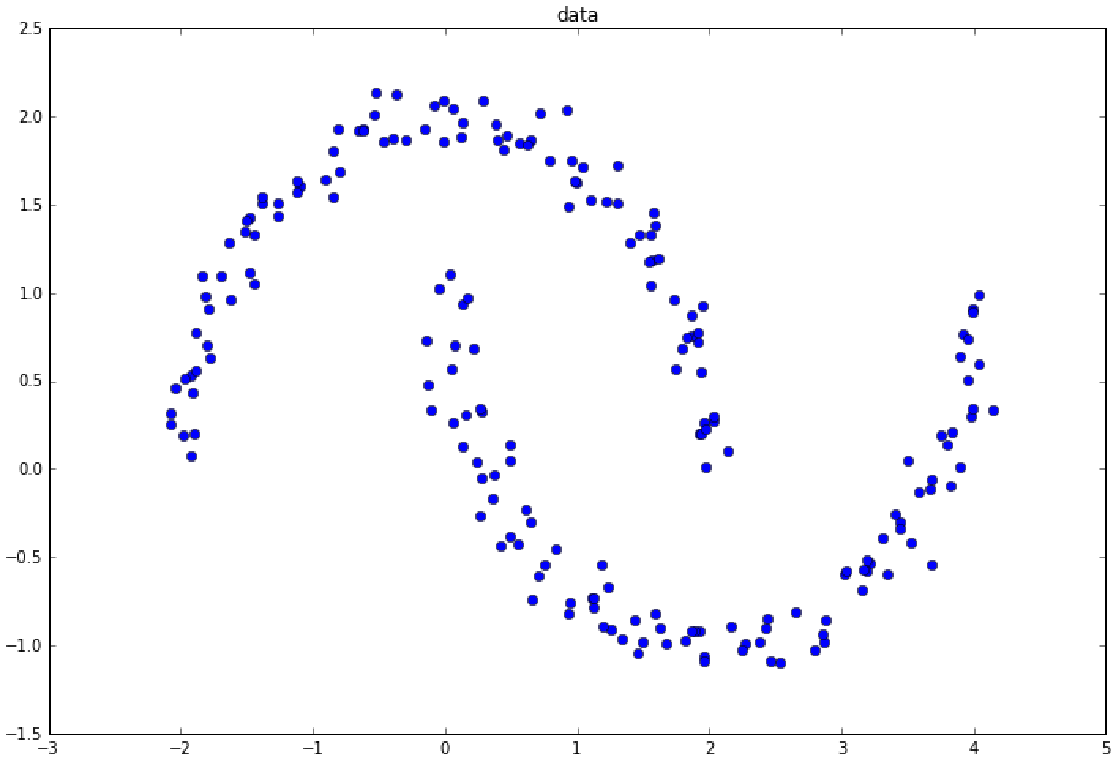
1.3.1 Spectral Clustering

1.3.2 Syllabus

- Apply K-means
- Apply Spectral Clustering
- Apply Spectral Clustering using Andrew Ng's Alorithm

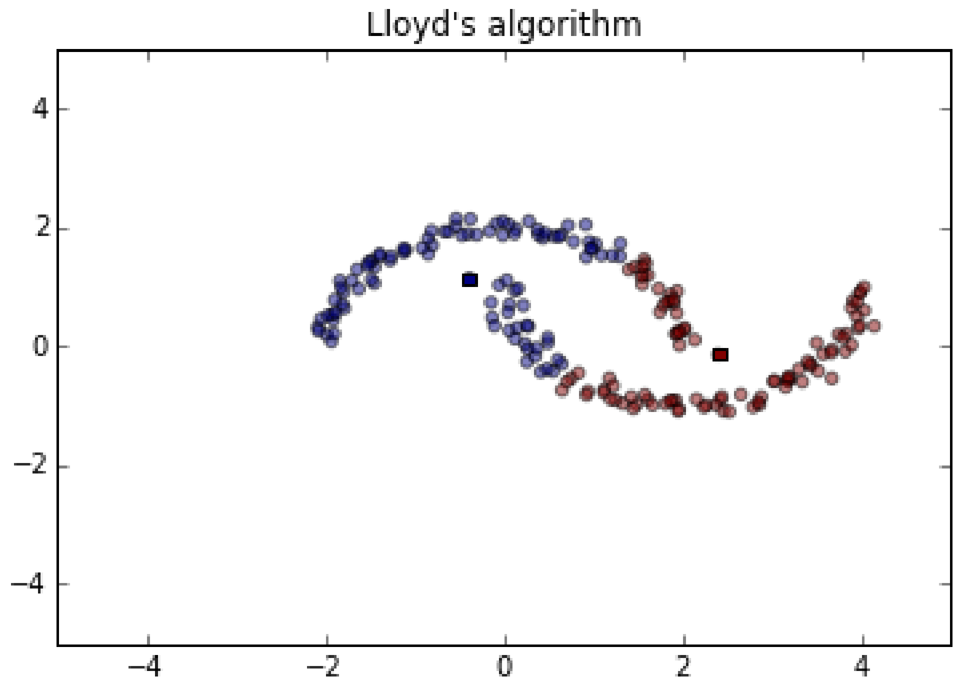
```
In [56]: def demo_2_1():
             my_data = np.genfromtxt('data/data-clustering-2.csv', delimiter=',')
             x = my_data[0,:]
             y = my_data[1,:]

             # plotting
             fig = plt.figure(figsize=(12, 8))
             axs = fig.add_subplot(111)

             plt_rex.plot2d(my_data, colwise_data=True, hatch='bo',
                            show=False, axs=axs, set_aspect_equal=False,
                             title="data")

             return my_data
```

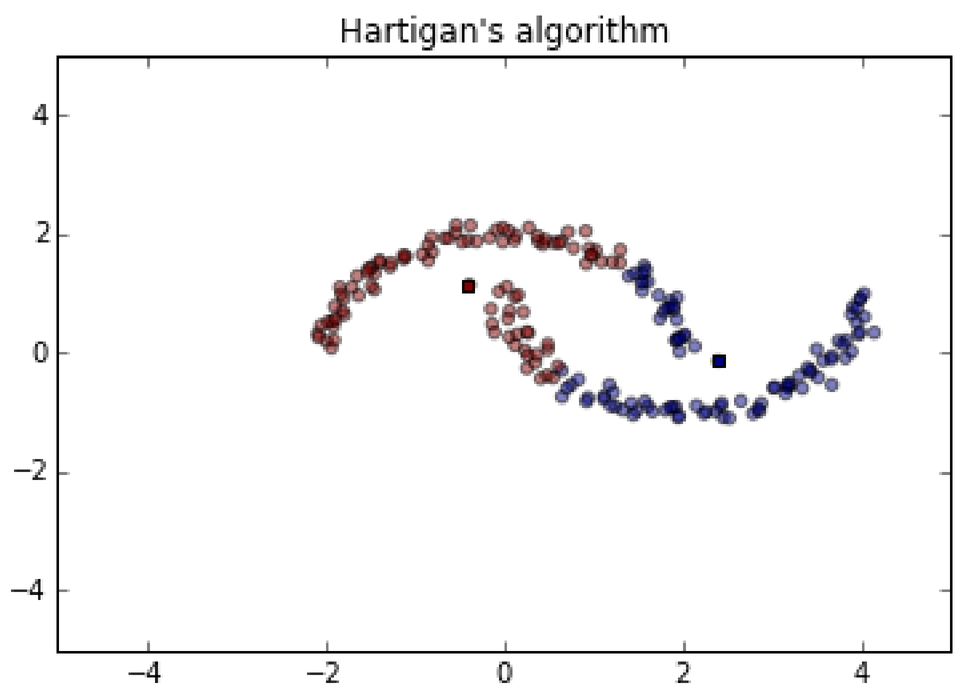
```
In [57]: my_data = demo_2_1()
```

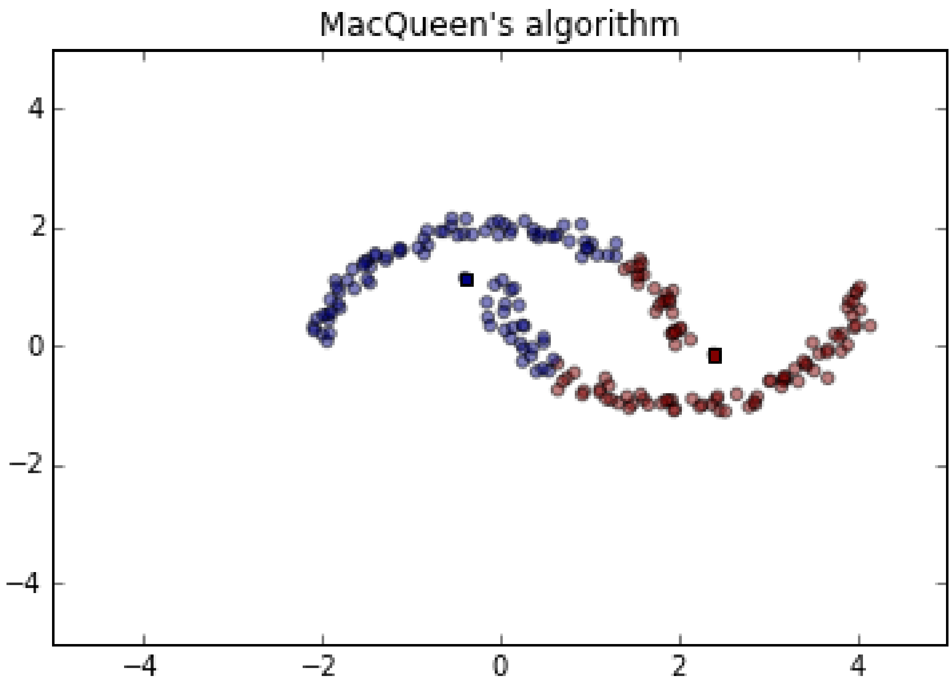


1.3.3 Apply K-means on Data

```
In [65]: def demo_2_2(my_data):
             k = 2
             data = my_data.T
             centroidsInit = np.array([[1, 2], [3, 4]])
             centroids, idx = km_rex.lloyd2(data, centroidsInit, verbose=False)
             # idx, _ = km_rex.vq(data, centroids)
             km_rex.show_plotted_cluster(data, idx, centroids, "Lloyd's algorithm",k)

             # Hartigan's algorithm
             centroids, idx = km_rex.hartigan2(data, k)
             km_rex.show_plotted_cluster(data, idx, centroids, "Hartigan's algorithm",k)

             # MacQueen's algorithm
             centroids, idx = km_rex.mcqueen2(data, k)
             km_rex.show_plotted_cluster(data, idx, centroids, "MacQueen's algorithm",k)

In [66]: demo_2_2(my_data)
```


Lloyd's algorithm
4
2
0
−2
−4
−4
−2
0
2
4


Hartigan's algorithm
4
2
0
−2
−4
−4
−2
0
2
4



1.4 Apply Spectral Clustering on Data

- Get a good result at beta = 11
- By observation, we see that some edges points would be mis-judged as beta grows from 1 to 15
- The Upper half contains 100 points, and so is the lower half.

1.4.1 Play around the number of halfs

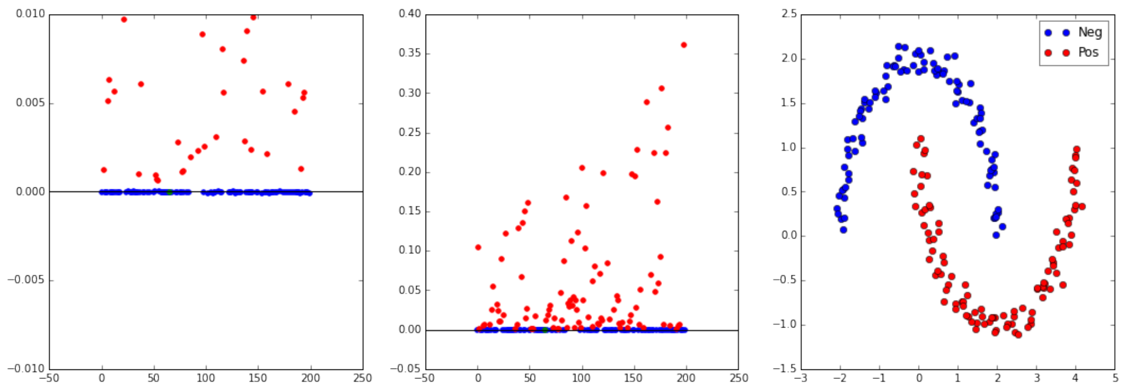
- See how the number of halfs changes

```
In [12]: def demo_2_4(my_data):
             for i in np.arange(1,20,1):
                 ur,index,u_idx_pos,u_idx_neg = sc_rex.SpectralClustering(my_data, i)
                 if(len(u_idx_pos[0])>=(len(u_idx_neg[0]))):
                     print(i,len(u_idx_pos[0]))
                 else:
                     print(i,len(u_idx_neg[0]))
                 if(len(u_idx_pos[0])==(len(u_idx_neg[0]))):
                     print("Got",i," with 100 each")
                     sc_rex.plot(my_data,ur,index,u_idx_pos,u_idx_neg)
```

```
In [13]: demo_2_4(my_data)
```

```
1 103
2 104
3 101
4 104
5 109
6 114
```

```
7 116
8 116
9 115
10 107
11 100
Got 11  with 100 each
12 114
13 105
14 112
15 113
16 113
17 114
18 121
19 107
```



1.5 Exam the Laplacian Matrix

- S = exp(-beta* |x_i-x_j|^2) which is independant on the data order
- D = Sum(j to n)(Sij) if i=j which is depandent on the data order
- L = D - S

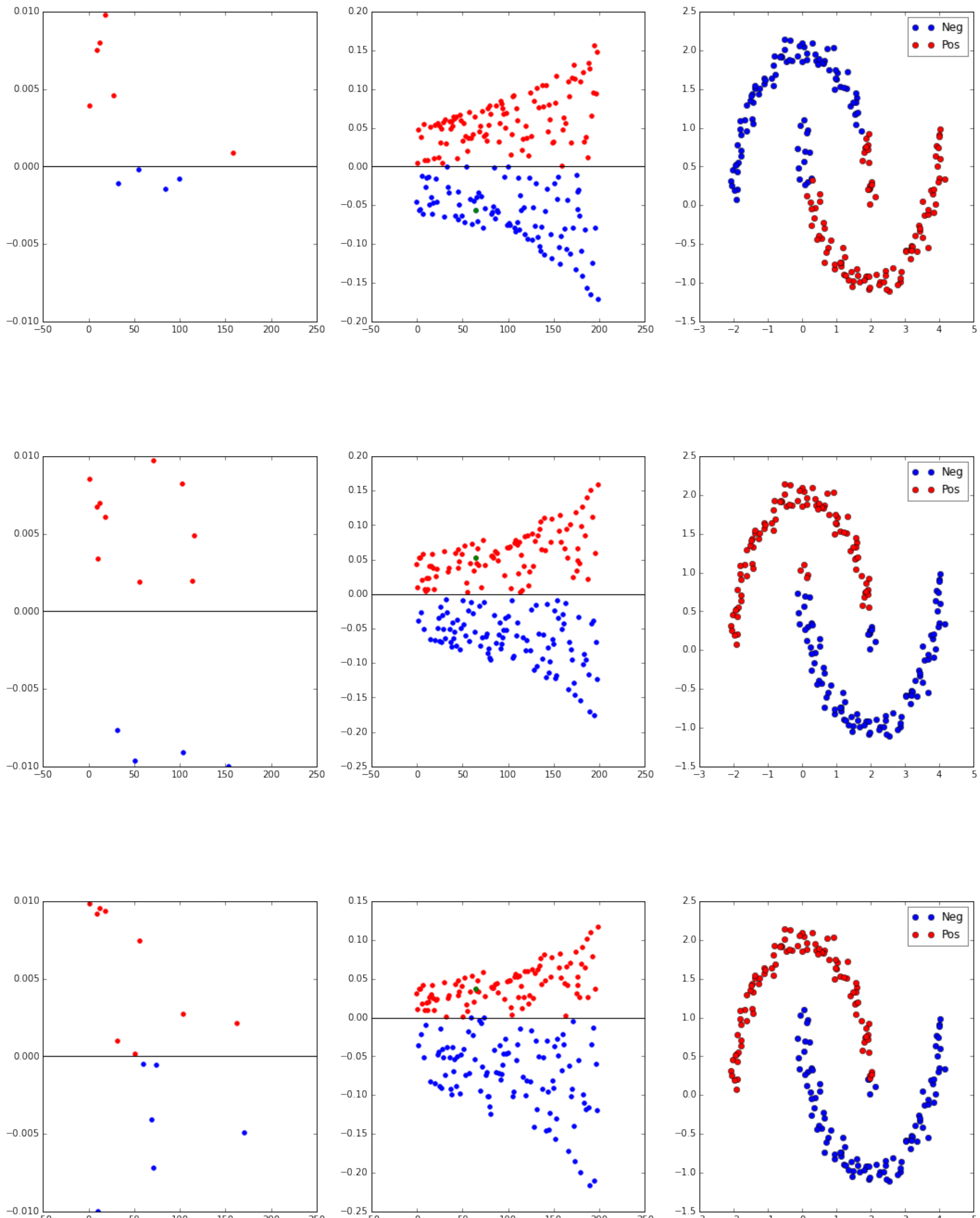
1.5.1 Shuffle the data order to see the result

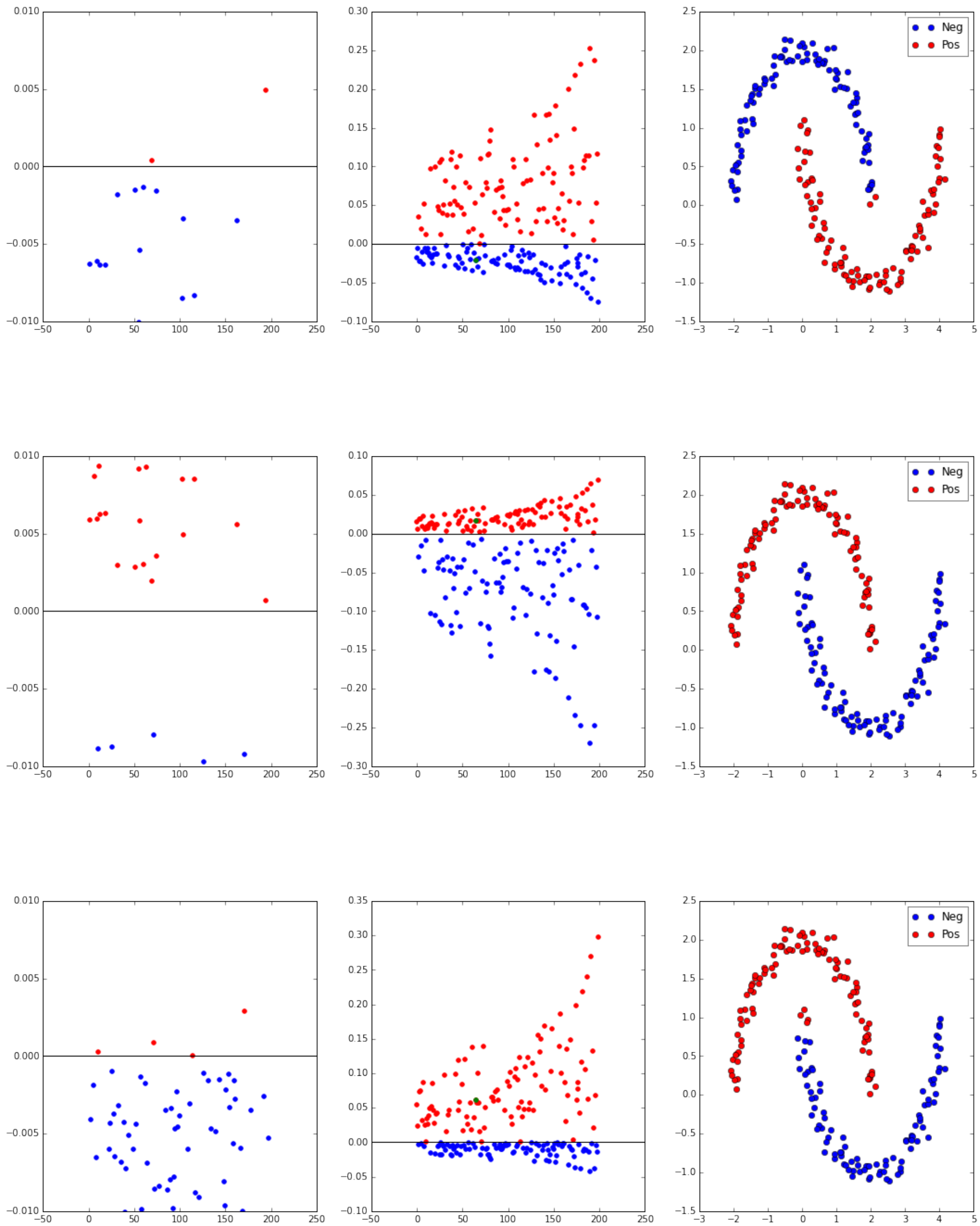
- we would have a differnet beta or even unable to get one sometime. Sometimes we got a lot
- But we see that the upper half gathered close to y=0 line, while the lower half spread around.

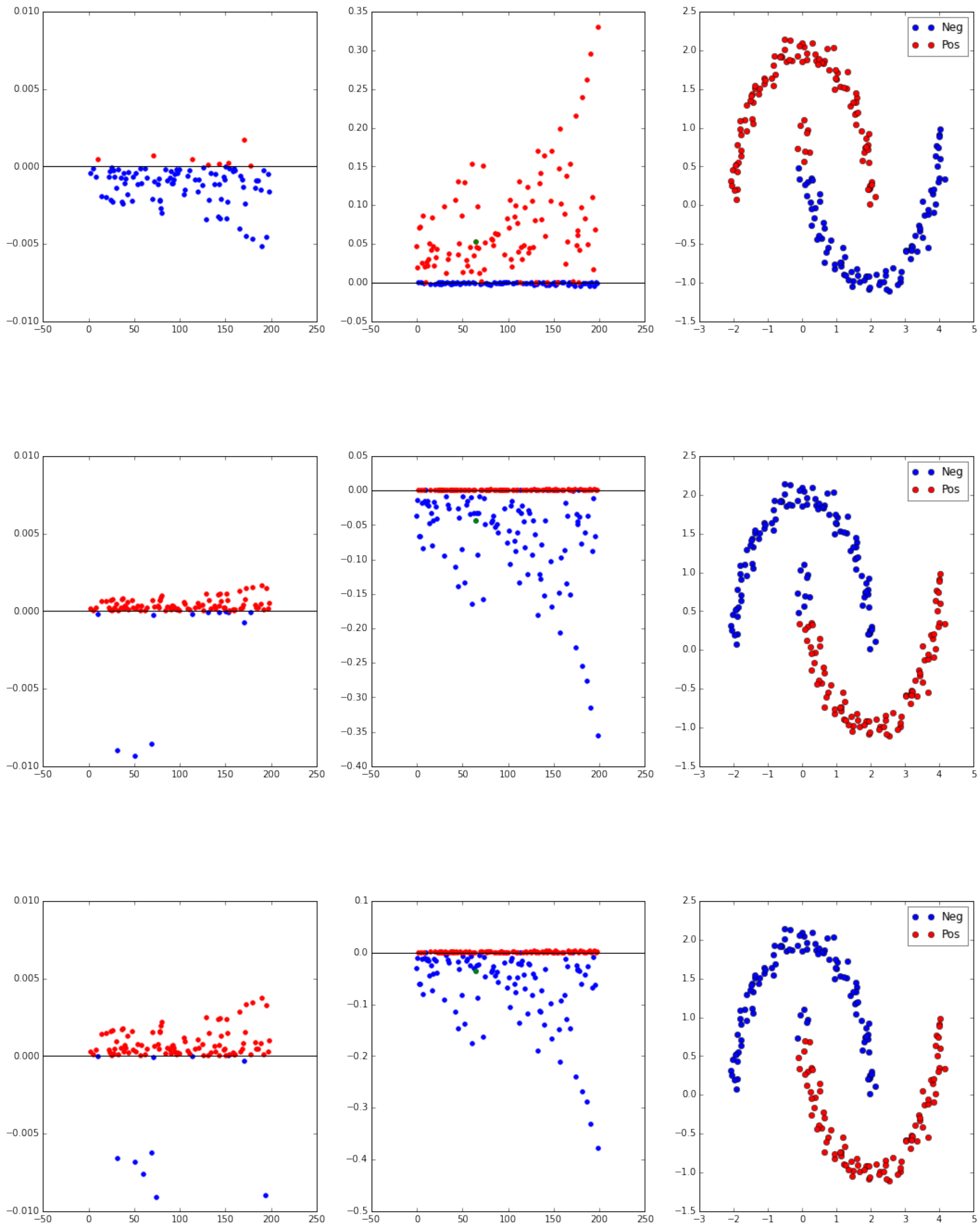
```
In [15]: def demo_2_5(my_data):
             idx = np.arange(0,200,1)
             np.random.shuffle(idx)

             for i in np.arange(1,20,1):
                 ur,index,u_idx_pos,u_idx_neg = sc_rex.SpectralClustering(my_data[:,idx], i)
                 if(len(u_idx_pos[0])==(len(u_idx_neg[0]))):
                     print("Got",i)
                 sc_rex.plot(my_data[:,idx],ur,index,u_idx_pos,u_idx_neg)
```

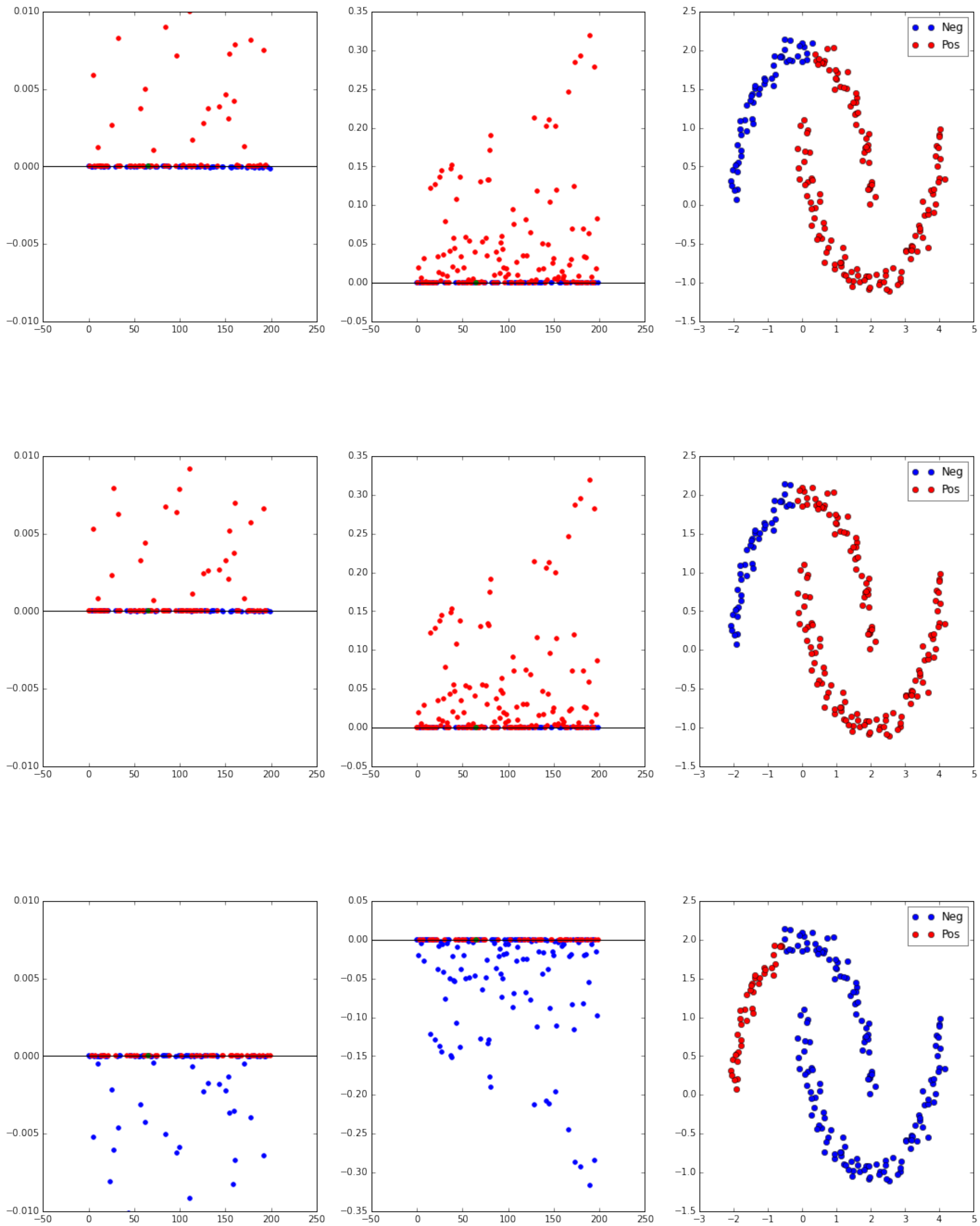
```
In [16]: demo_2_5(my_data)
```

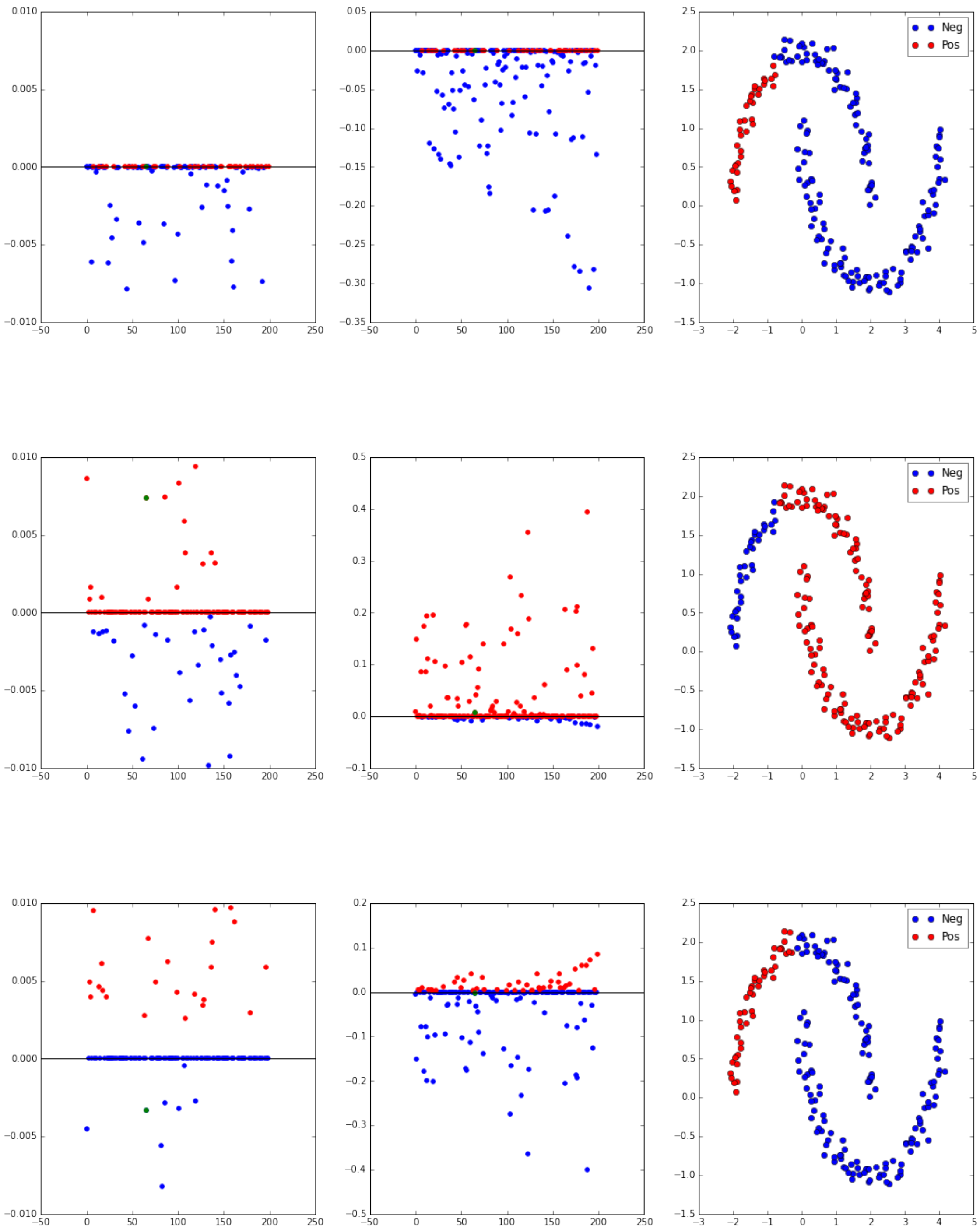
```
Got 5
Got 16
```

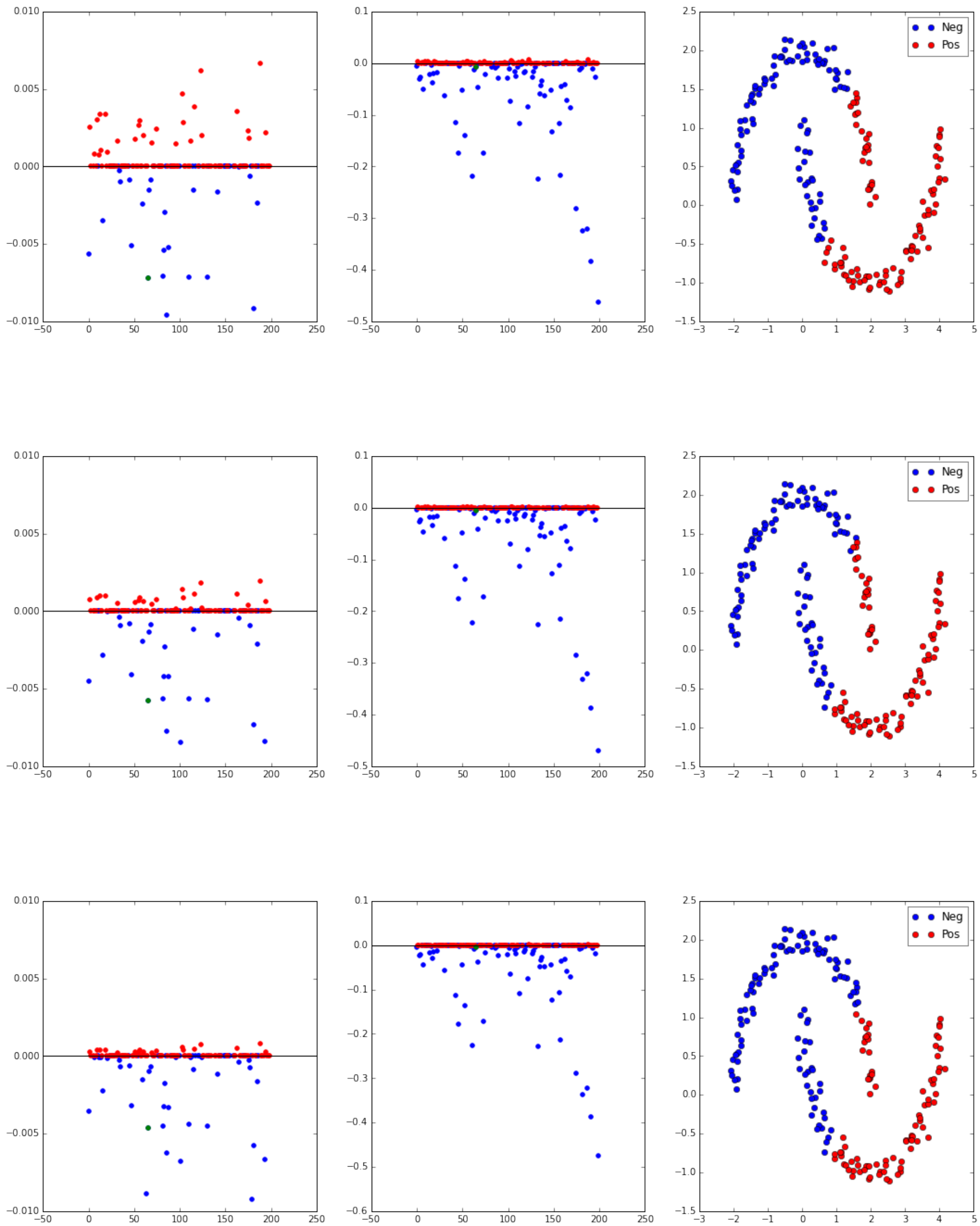

Neg
Pos

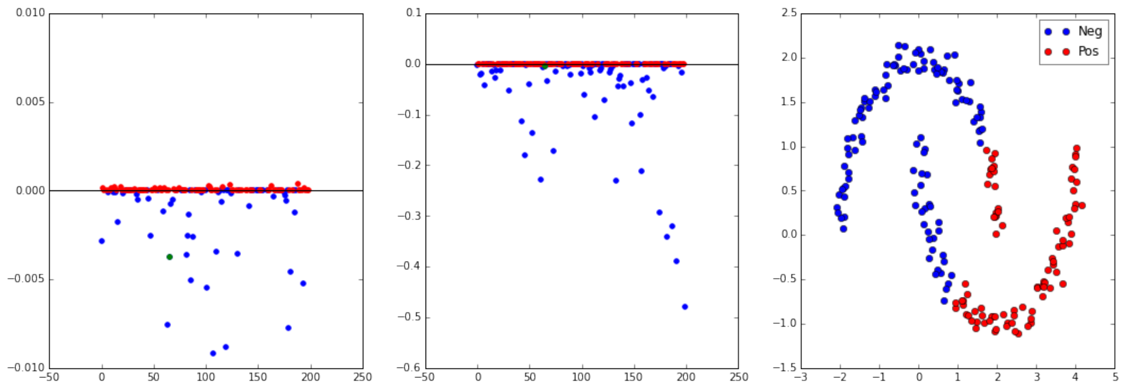

Neg
Pos
Neg
Pos
Neg
Pos


Neg
Pos
Neg
Pos
Neg
Pos


Neg
Pos


Neg
Pos
Neg
Pos
Neg
Pos

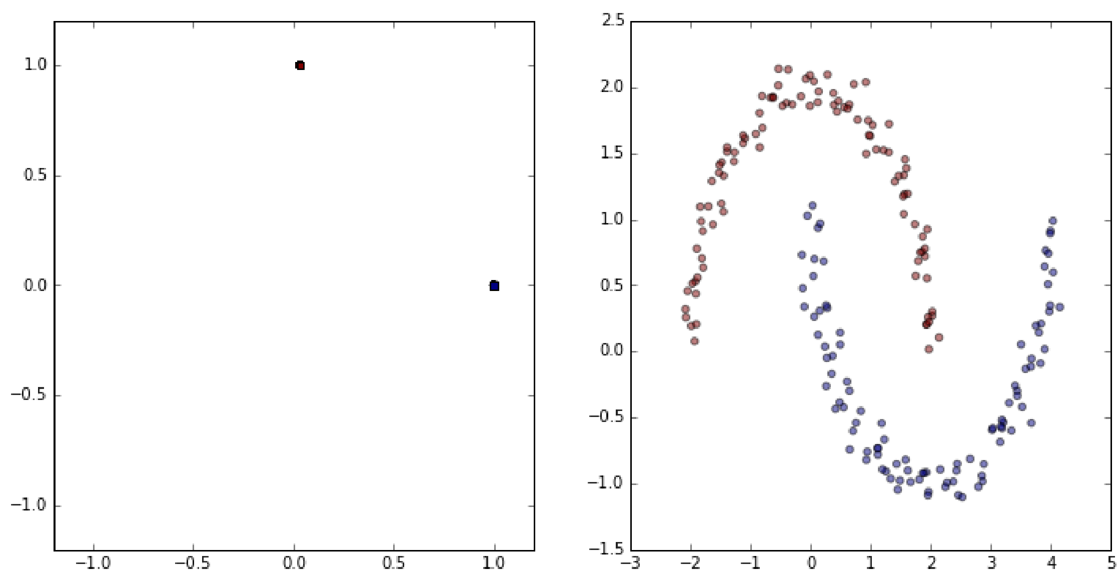

Neg
Pos

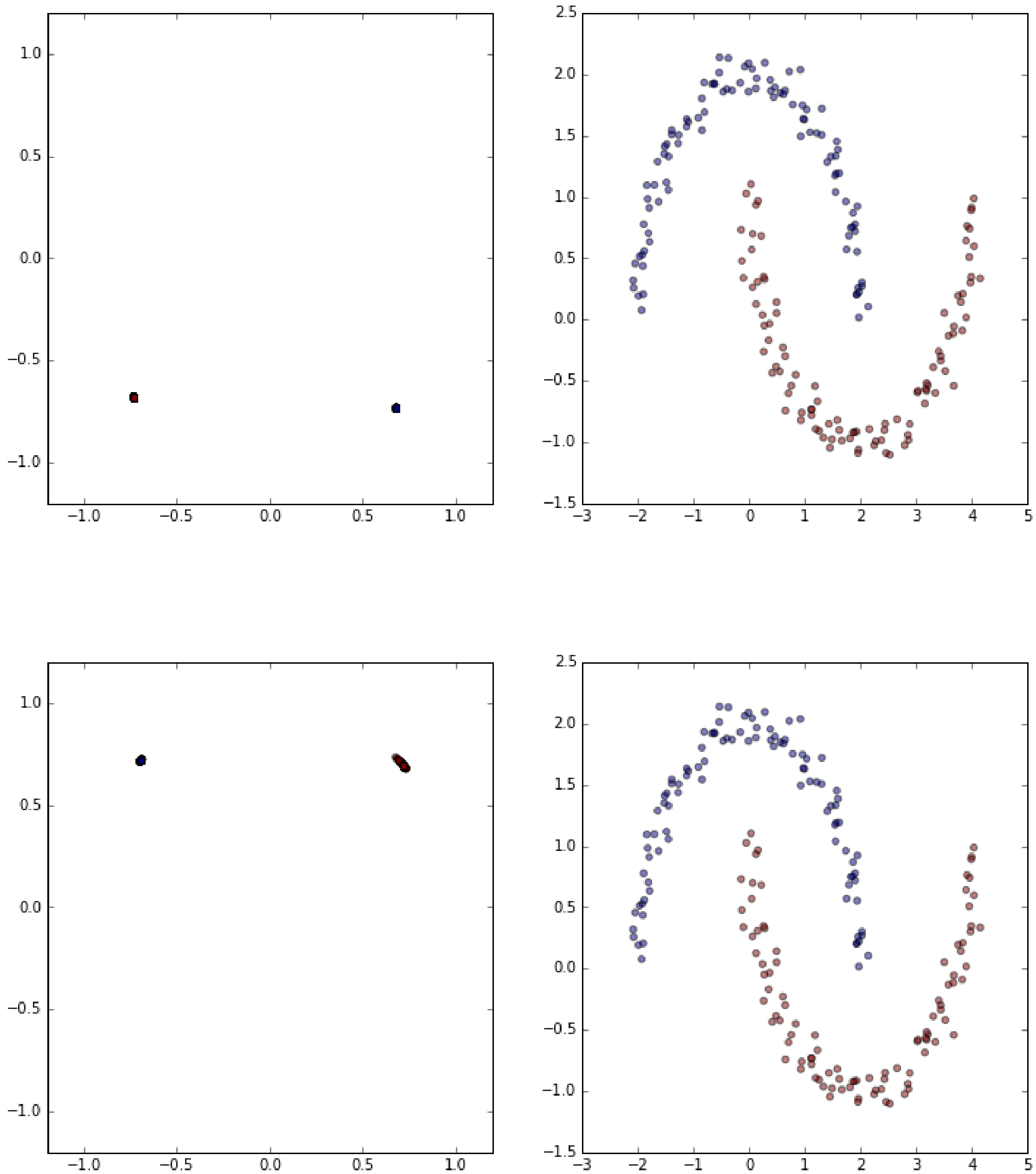


1.6 Spectral Clustering using Andrew Ng's Algorithm

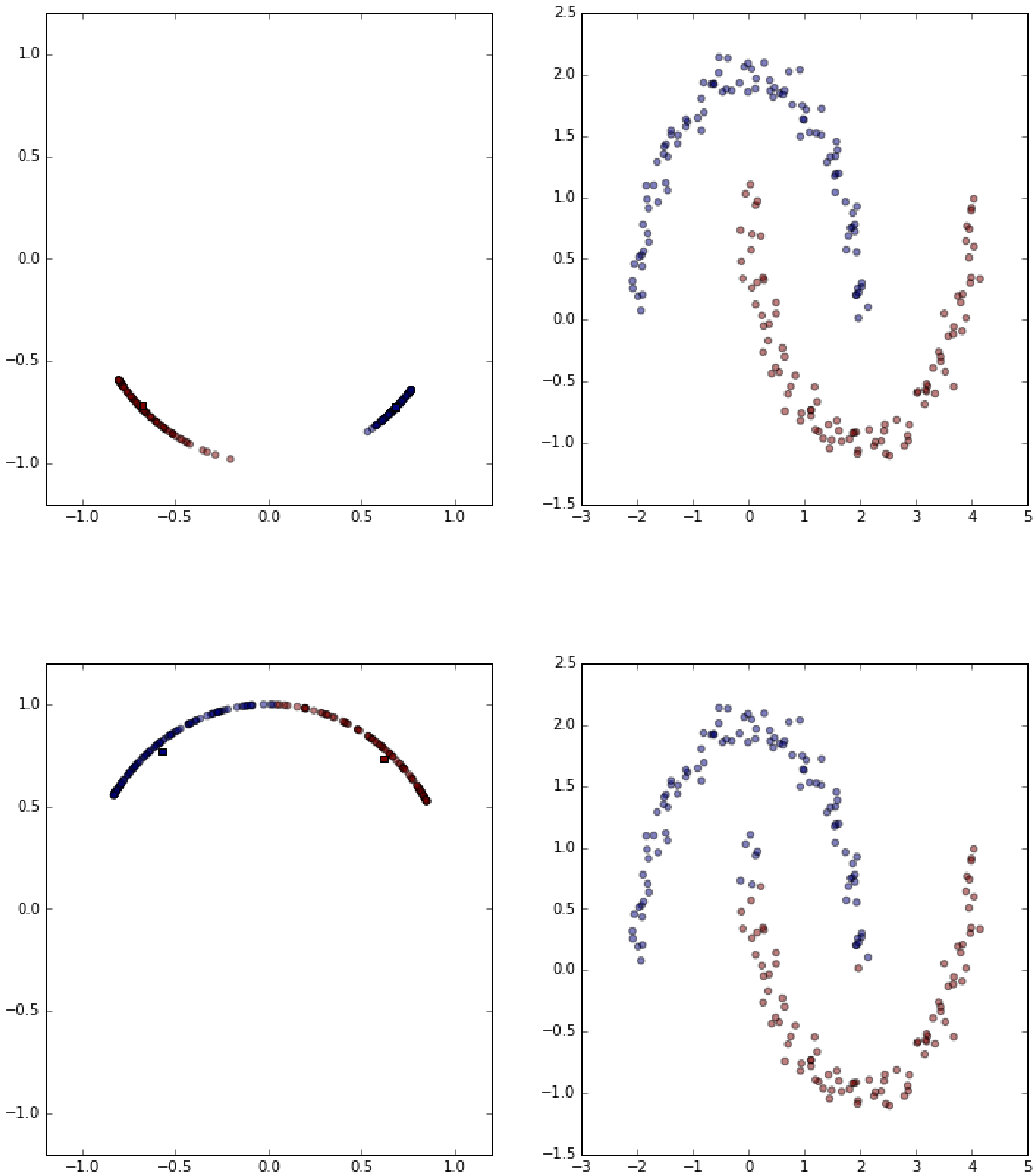
- On Spectral Clustering: Analysis and an algorithm by Andre Ng, etal.
- S = exp(-|x_i-x_j|ˆ2 / 2*(sigmaˆ2))
- D = diagonal matrix whose (i, i)-element is the sum of A's i-th row
- L = $D^{(-1/2)AD}$(-1/2)
- FInd the k largest eigenvectors of L and normalized them into matrix X
- Treating X as new set of data, apply k-means clustering
- Based on the clustering result to cluster the original data

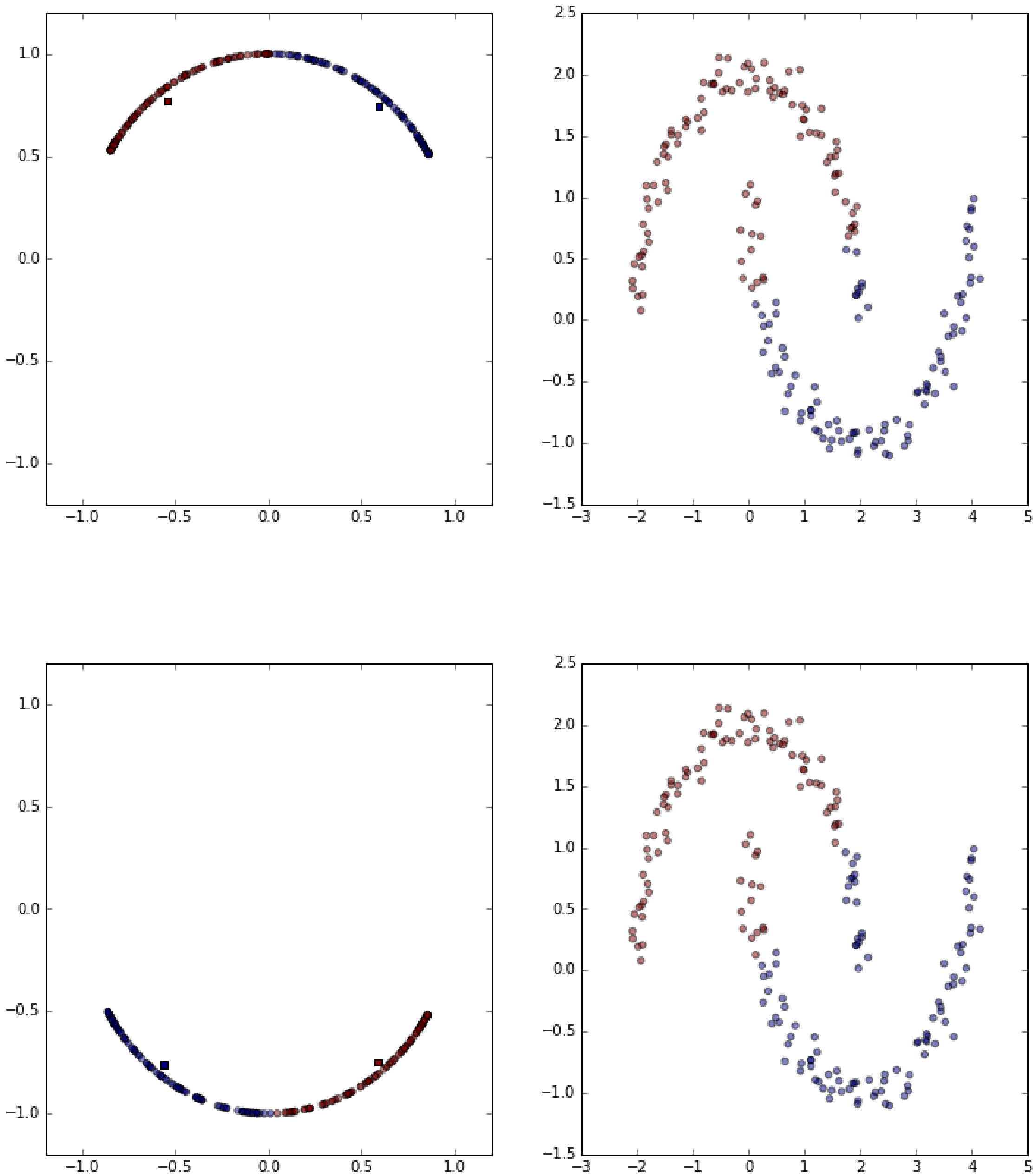
```
In [19]: scan_rex.demo1(my_data,2, 0.05, 1, 0.1)  #(my_data,k, sigma, start, end, step):
```

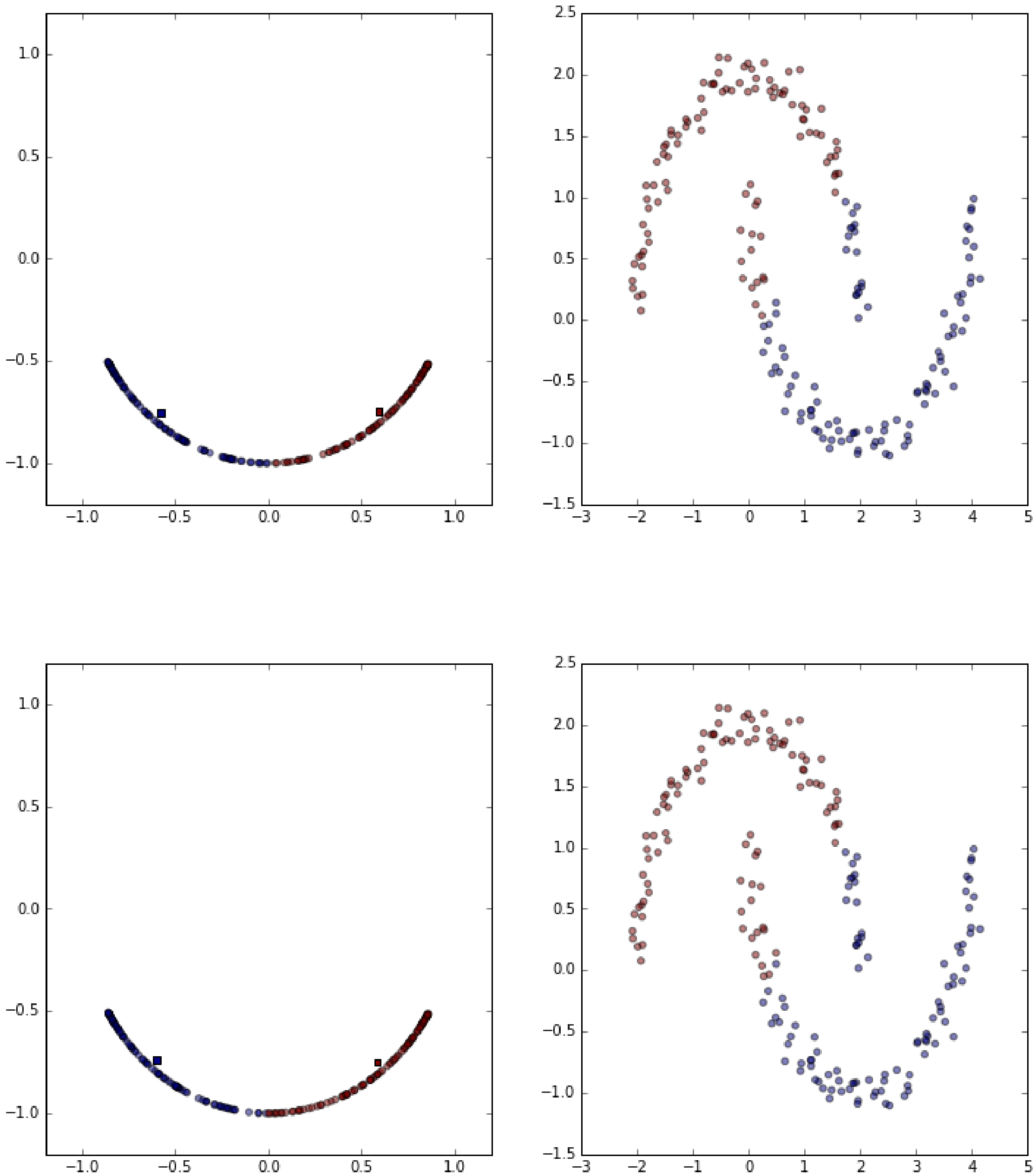




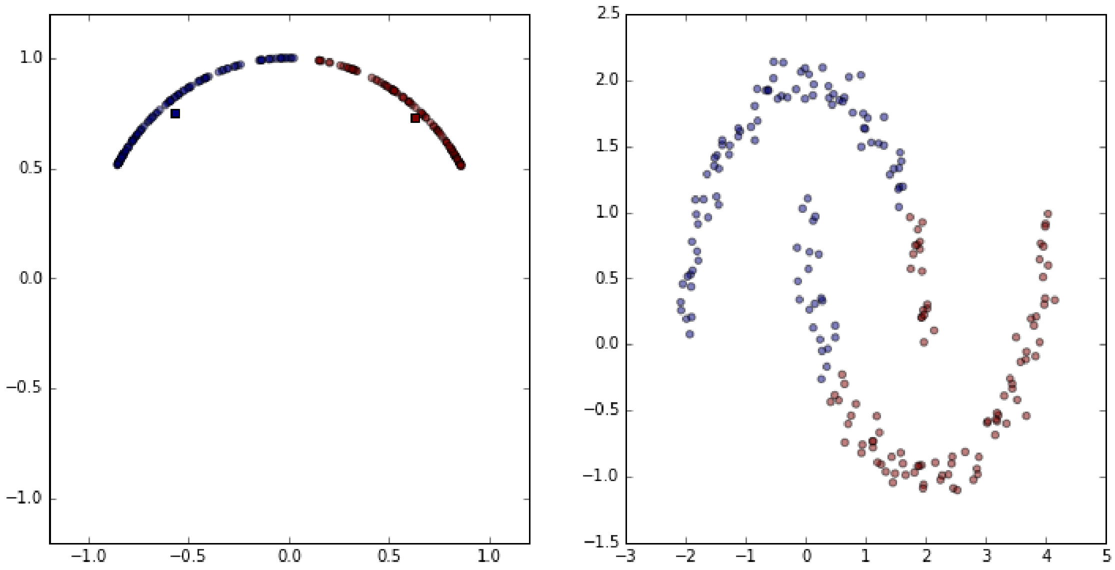
1.0
0.5
0.0
−0.5
−1.0
−1.0 −0.5 0.0 0.5 1.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−3 −2 −1 0 1 2 3 4 5


1.0
0.5
0.0
−0.5
−1.0
−1.0 −0.5 0.0 0.5 1.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−3 −2 −1 0 1 2 3 4 5
1.0
0.5
0.0
−0.5
−1.0
−1.0 −0.5 0.0 0.5 1.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−3 −2 −1 0 1 2 3 4 5


1.0
0.5
0.0
−0.5
−1.0
−1.0 −0.5 0.0 0.5 1.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−3 −2 −1 0 1 2 3 4 5



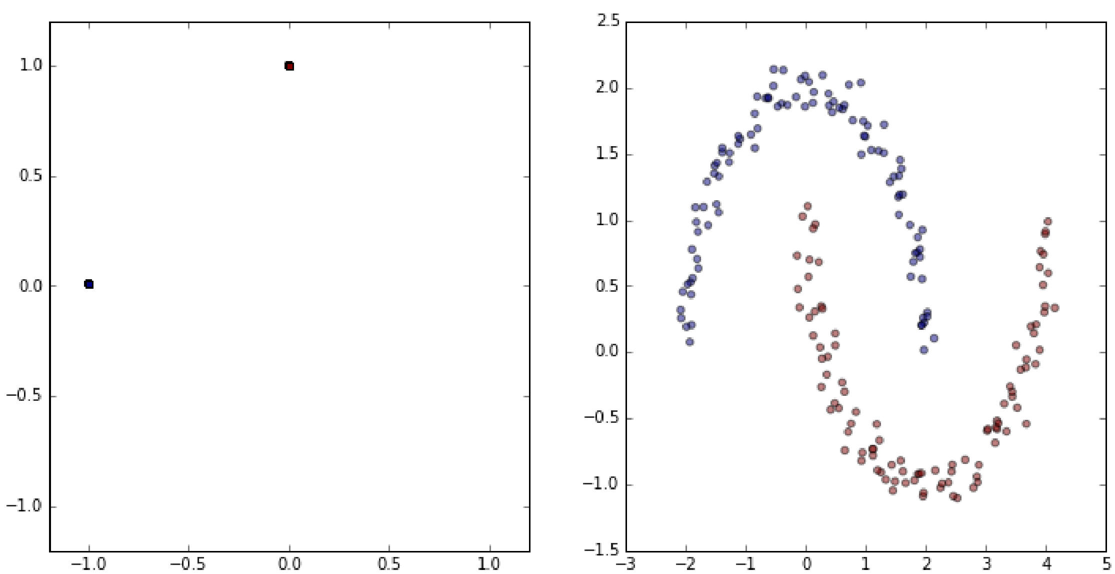
1.0
0.5
0.0
−0.5
−1.0
−1.0 −0.5 0.0 0.5 1.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−3 −2 −1 0 1 2 3 4 5

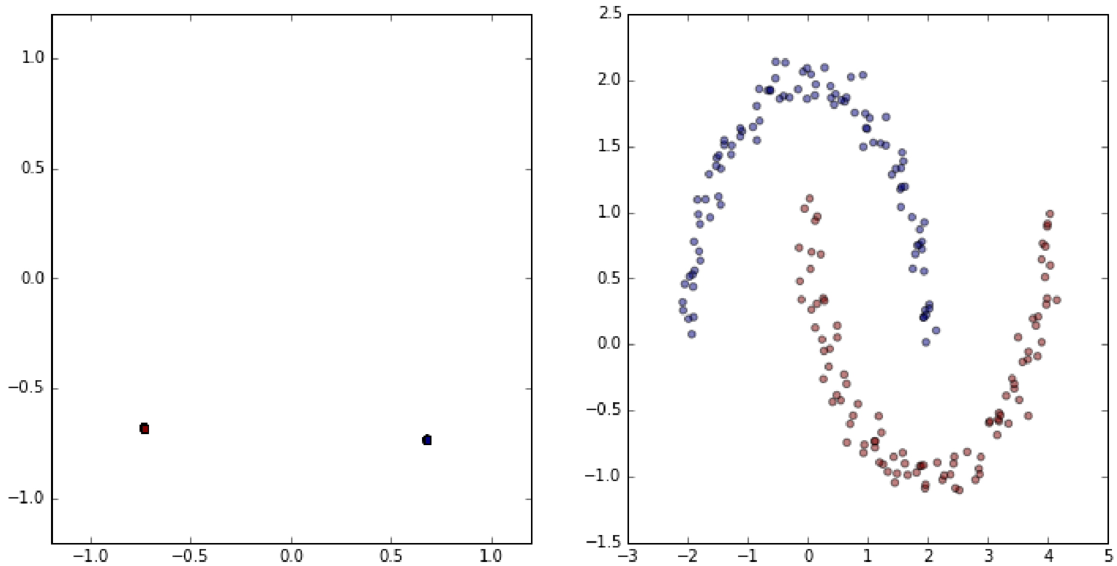


1.6.1 Shuffle the data order to see the result

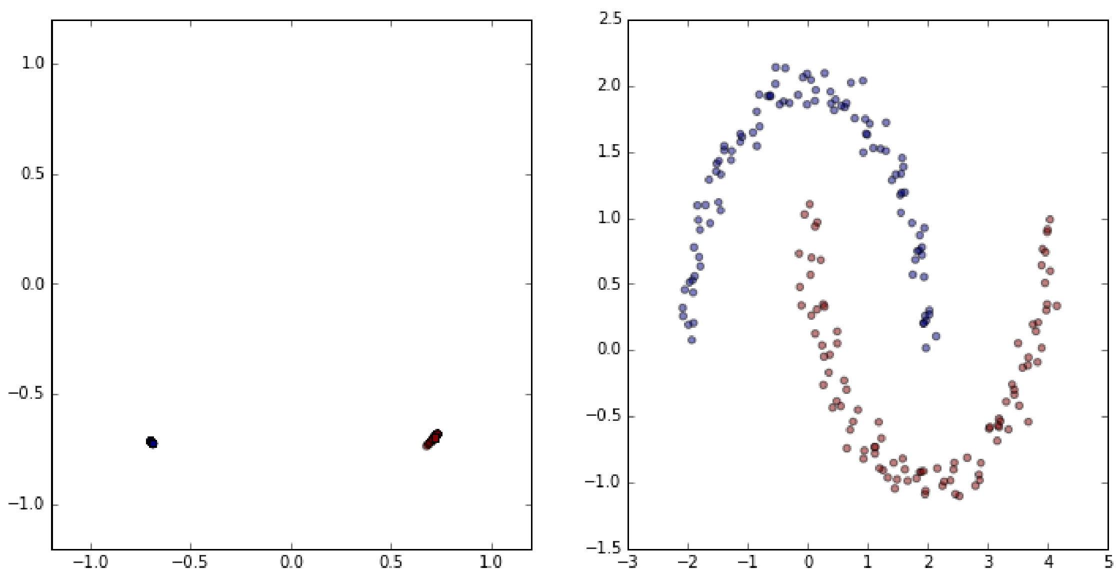
- We would have same L on differnet odering of data
- As prediction, the resulting sigma would not change

In [20]:
```
idx = np.arange(0,200,1)
np.random.shuffle(idx)
scan_rex.demo1(my_data[:,idx],2, 0.05, 1, 0.1)  #(my_data,k, sigma, start, end, step):
```

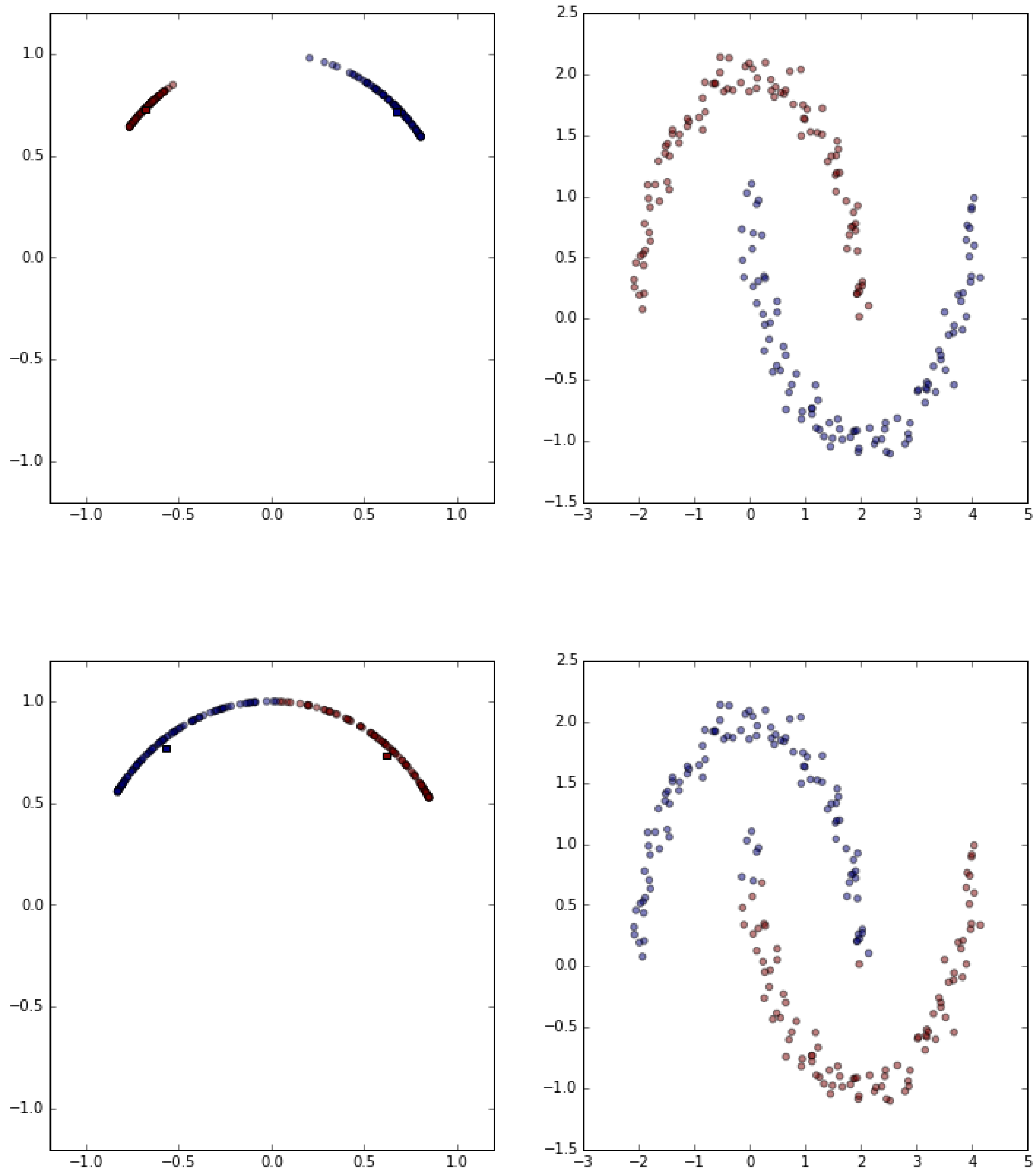


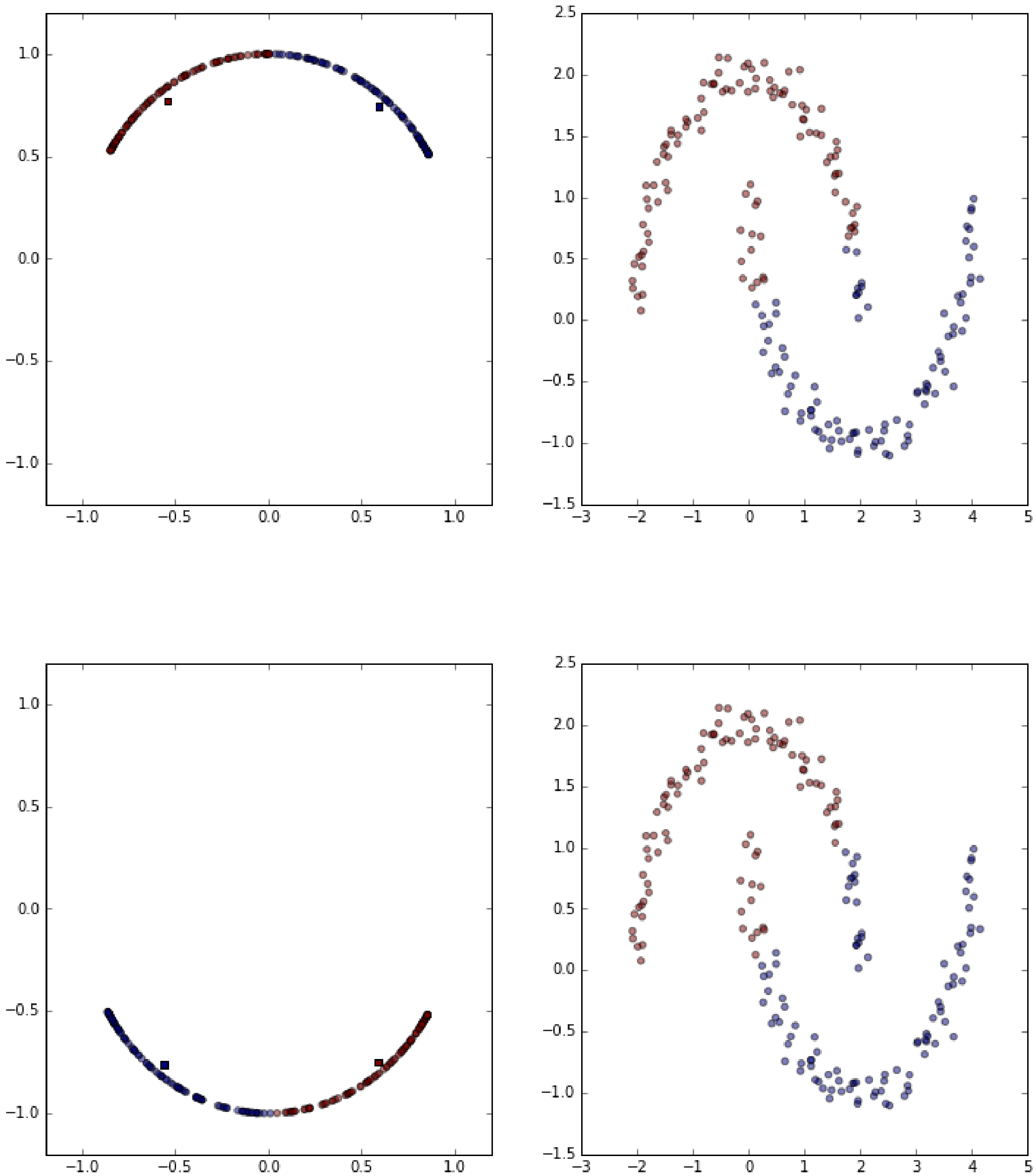


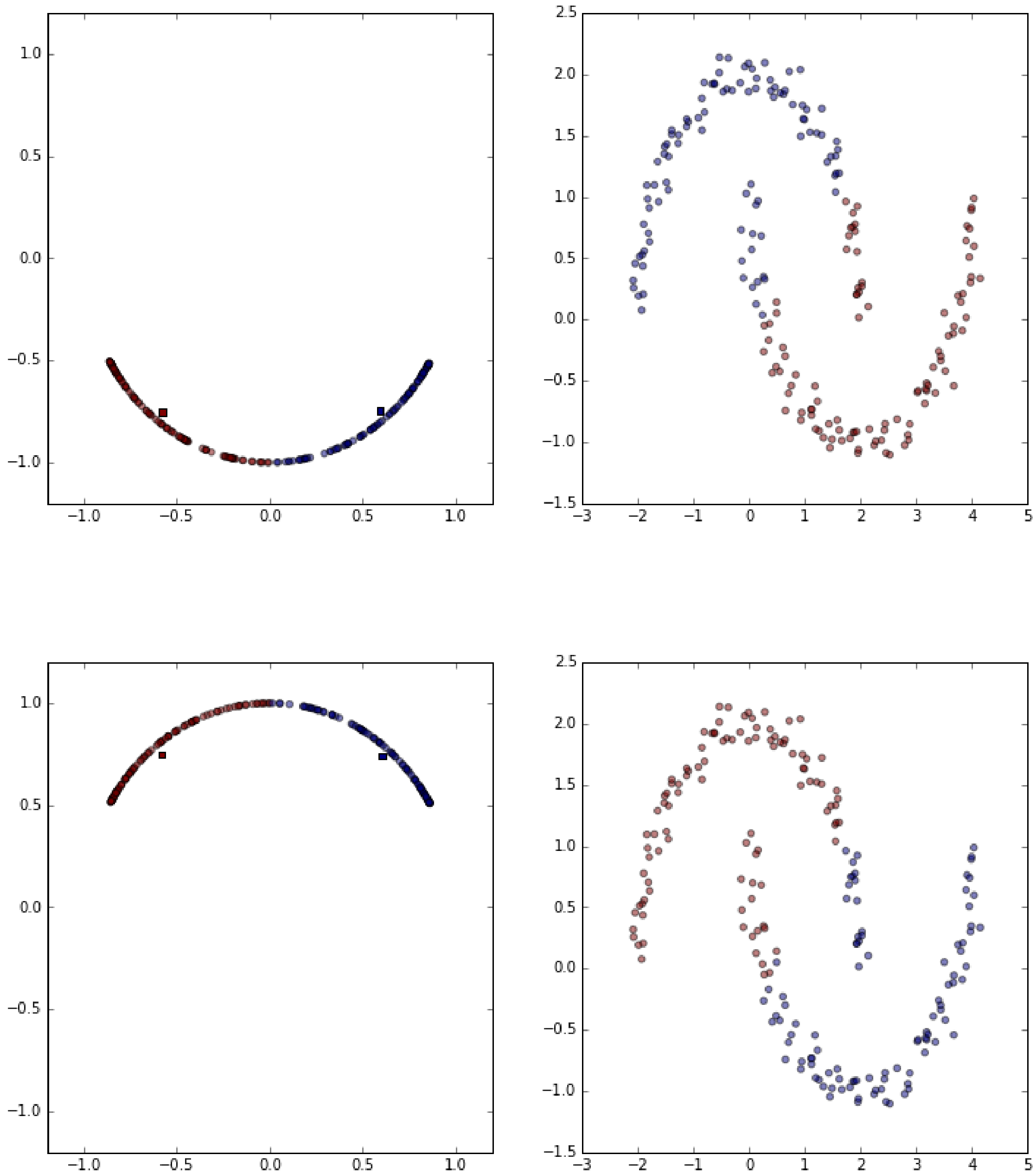
1.0
0.5
0.0
−0.5
−1.0
−1.0 −0.5 0.0 0.5 1.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−3 −2 −1 0 1 2 3 4 5



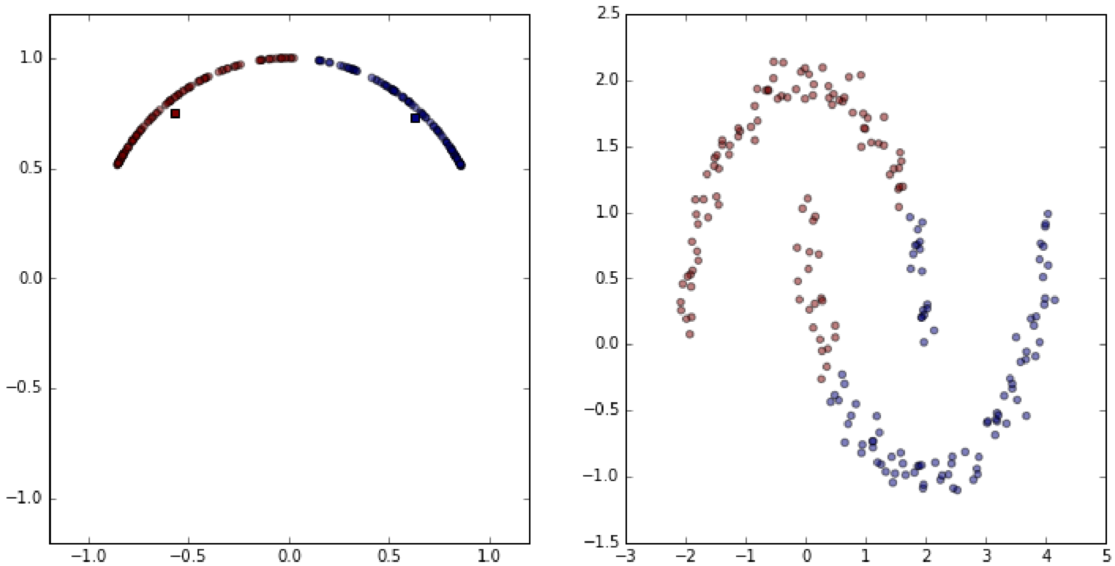
1.0
0.5
0.0
−0.5
−1.0
−1.0 −0.5 0.0 0.5 1.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−3 −2 −1 0 1 2 3 4 5


1.0
0.5
0.0
−0.5
−1.0
−1.0 −0.5 0.0 0.5 1.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−3 −2 −1 0 1 2 3 4 5
1.0
0.5
0.0
−0.5
−1.0
−1.0 −0.5 0.0 0.5 1.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−3 −2 −1 0 1 2 3 4 5


1.0
0.5
0.0
−0.5
−1.0
−1.0
−0.5
0.0
0.5
1.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−3
−2
−1
0
1
2
3
4
5



1.0
0.5
0.0
−0.5
−1.0
−1.0 −0.5 0.0 0.5 1.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−3 −2 −1 0 1 2 3 4 5



1.7 Discussion

- Even if the data is shuffled, the sigma to generate good clustering is stable.
- We could evaluate the result based on how tight the processed group is.
- It is easier to determine whether this Y is valid or not.

1.8 Evaluate the tightness of Data

- Variance
- Support Vector Machine

1.9 Task 3.3

1.9.1 Dimensionality Reduction

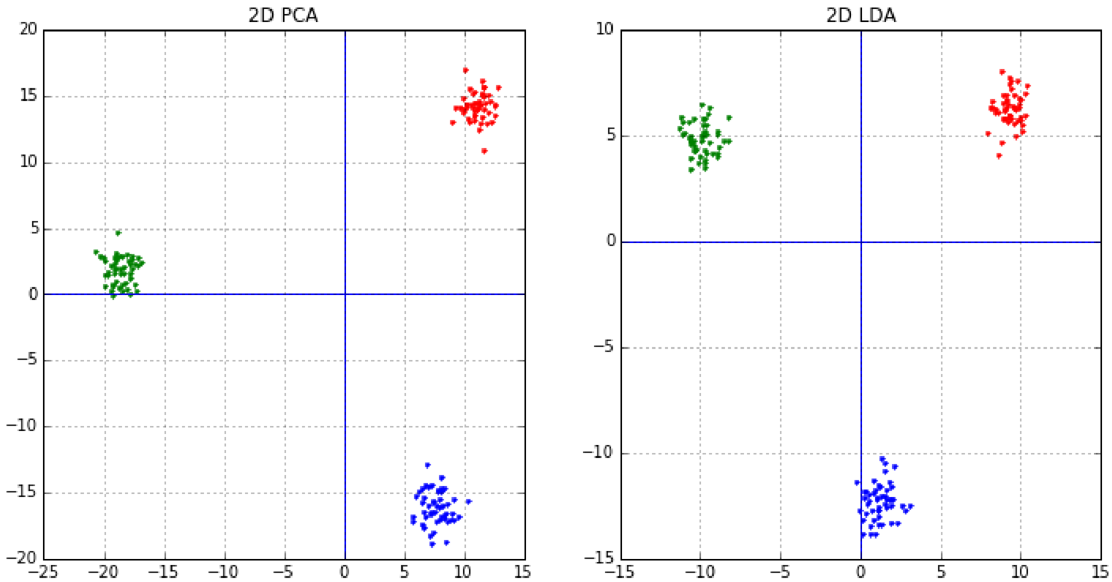
In [2]:
```
data_X = np.genfromtxt("./data/data-dimred-X.csv", delimiter=',')
data_y = np.genfromtxt("./data/data-dimred-y.csv", delimiter=',')
```

In [52]:
```
def demo_3(X, y, k, err=0.0, ddof=0, use_eigh=True, use_abs_evals=False):
    print("\n# PCA ########################################")
    res_pca = dim_rex.pca(X, k=k, err=err,
                          use_eigh=use_eigh, use_abs_evals=use_abs_evals)

    print("\n# LDA ########################################")
    res_lda = dim_rex.lda(X, y, k=k, err=err, use_eigh=use_eigh, ddof=ddof,
                          use_abs_evals=use_abs_evals)

    projections = [res_pca[0], res_lda[0]]
    classes = np.unique(y)
```

```python
        # Plotting
        if k == 2:
            fig = plt.figure(figsize=(12, 6))
            sbp = [1, 2, 0]

            for p, t in zip(projections, ["{}D PCA".format(k), "{}D LDA".format(k)]):
                sbp[-1] += 1

                ax = fig.add_subplot(*sbp)
                for c, h in zip(classes, ['r.', 'g.', 'b.']):
                    plt_rex.plot2d(p[y == c], False,
                                   axs=ax, hatch=h, show=False,
                                   title=t)

                ax.grid()
                ax.axhline(y=0)
                ax.axvline(x=0)
        elif k == 3:
            for p, t in zip(projections, ["{}D PCA".format(k), "{}D LDA".format(k)]):
                fig = plt.figure()
                axs = plt.axes(projection='3d')
                for l, c in zip([1., 2., 3.], ['r', 'g', 'b']):
                    d2 = p[y == l]
                    axs.scatter3D(d2[:, 0], d2[:, 1], d2[:, 2], c=c)

                axs.set_title(t)

        return res_pca, res_lda
```

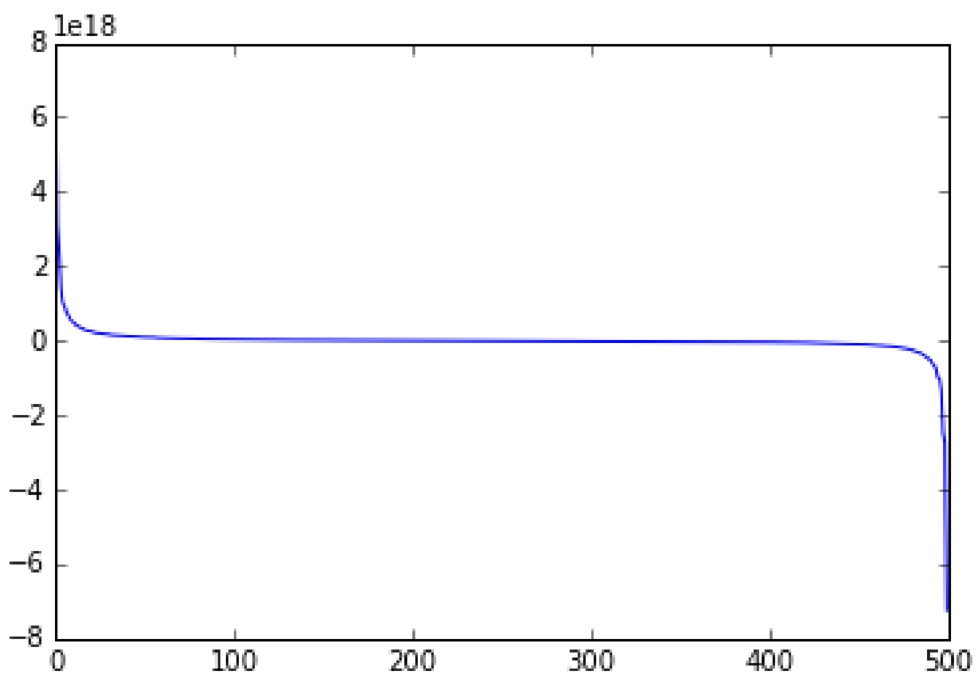
In [41]:
```python
res_pca, res_lda = demo_3(data_X, data_y, 2)
```

```
# PCA ########################################
Found that choosing k as 2 will lead to at most error 59.310584579881876%

# LDA ########################################
Found 3 classes of 500 dimensional data
Class 1.0: 50 samples
Class 2.0: 50 samples
Class 3.0: 50 samples
Found that choosing k as 2 will lead to at most error -8019.271384515379%
```




```
In [16]: evals = res_lda[-1][0]
         plt.plot(evals)
```

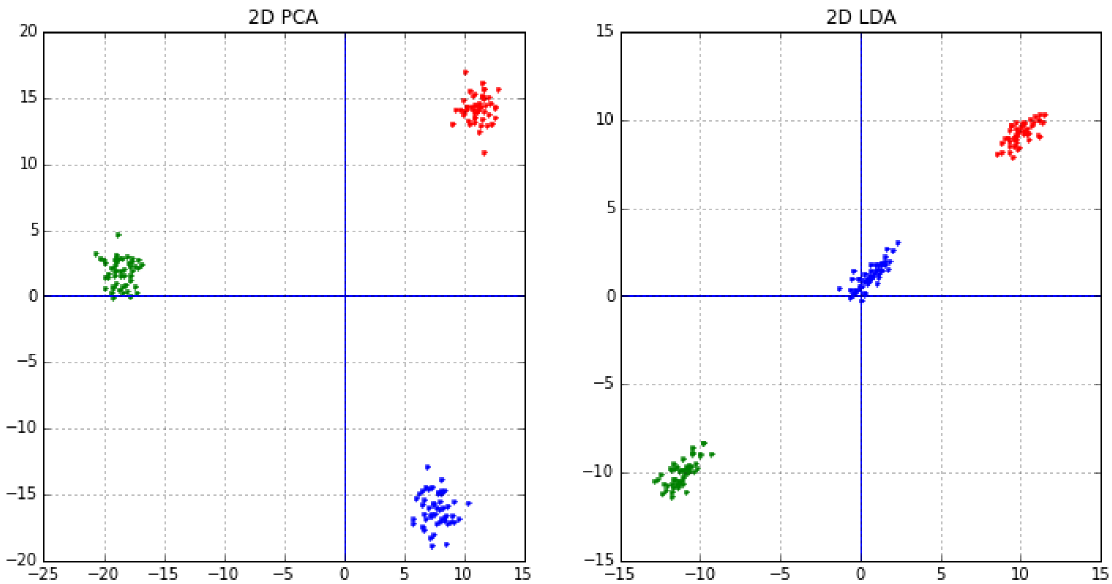
```
Out[16]: [<matplotlib.lines.Line2D at 0x1092220b8>]
```

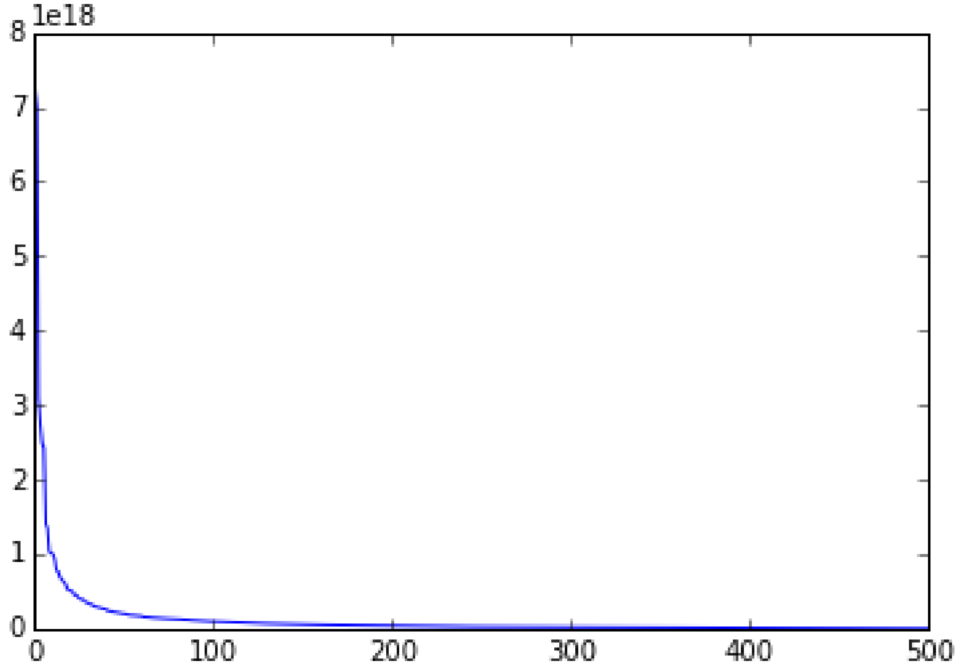



```
In [42]: res_pca, res_lda = demo_3(data_X, data_y, 2, use_abs_evals=True)
         plt.figure()
         plt.plot(res_lda[-1][0])
```

```
# PCA ######################################
Found that choosing k as 2 will lead to at most error 59.310584579881876%

# LDA ######################################
Found 3 classes of 500 dimensional data
Class 1.0: 50 samples
Class 2.0: 50 samples
Class 3.0: 50 samples
Found that choosing k as 2 will lead to at most error 77.29489861745998%
```

Out[42]: [<matplotlib.lines.Line2D at 0x10ade35c0>]

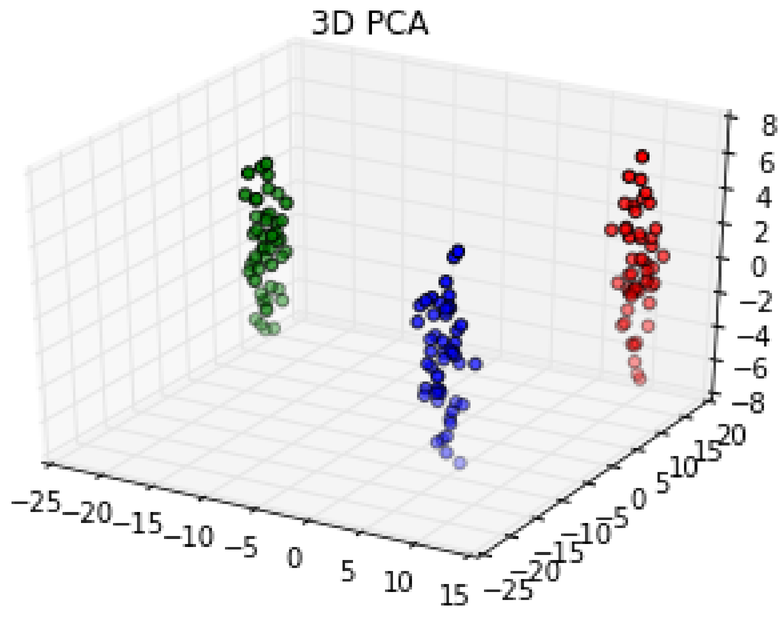


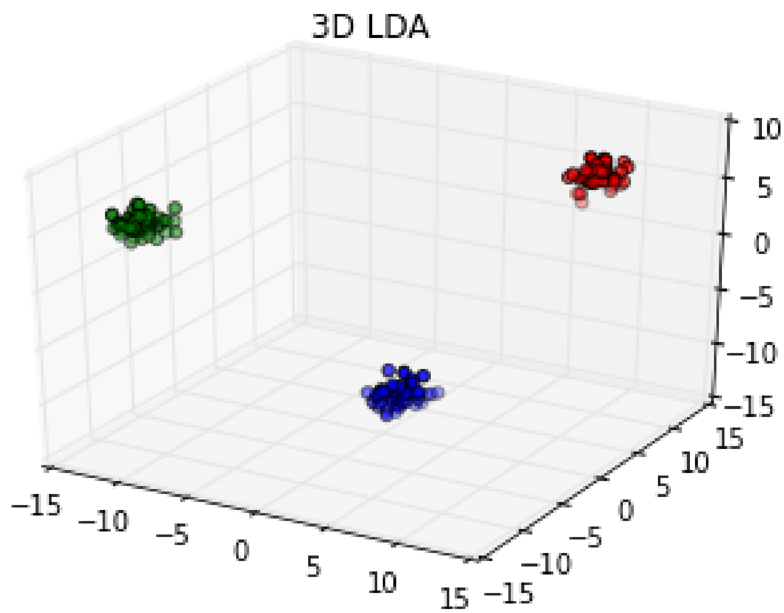


1.9.2 Let's see for 3D

```
In [57]: res_pca, res_lda = demo_3(data_X, data_y, 3, use_abs_evals=True)
```

```
# PCA ######################################
Found that choosing k as 3 will lead to at most error 58.37033070345618%

# LDA ######################################
Found 3 classes of 500 dimensional data
Class 1.0: 50 samples
Class 2.0: 50 samples
Class 3.0: 50 samples
Found that choosing k as 3 will lead to at most error 72.36080941543305%
```





1.9.3 Observations

- **PCA** finds the axes with maximum variance for the *whole* data
  - *unsupervised* algorithm
  - performs better for fewer samples per class
- **LDA** finds the axes for best separation *between* classes

    - *supervised* algorithm

- **Both** still have the underlying assumption of data having Gaussian Distribution

1.10 Task 3.4

1.10.1 Exploring Numerical Instabilities

1.10.2 We all read the paper

In general, we expected:

- `method_1`
    - to give the best 10th degree polygon,
    - be fast,
    - not face issues
- `method_2`
    - to give okay result (conditionally)
    - be slow,
    - to face numerical issues
- `method_3`
    - to give a good 10th degree polygon,
    - be fast,
    - not face issues
- `method_4`
    - to give results a bit better than `method_2`
    - be the slowest (added transform step)
    - not face issues in this particular case (may be)

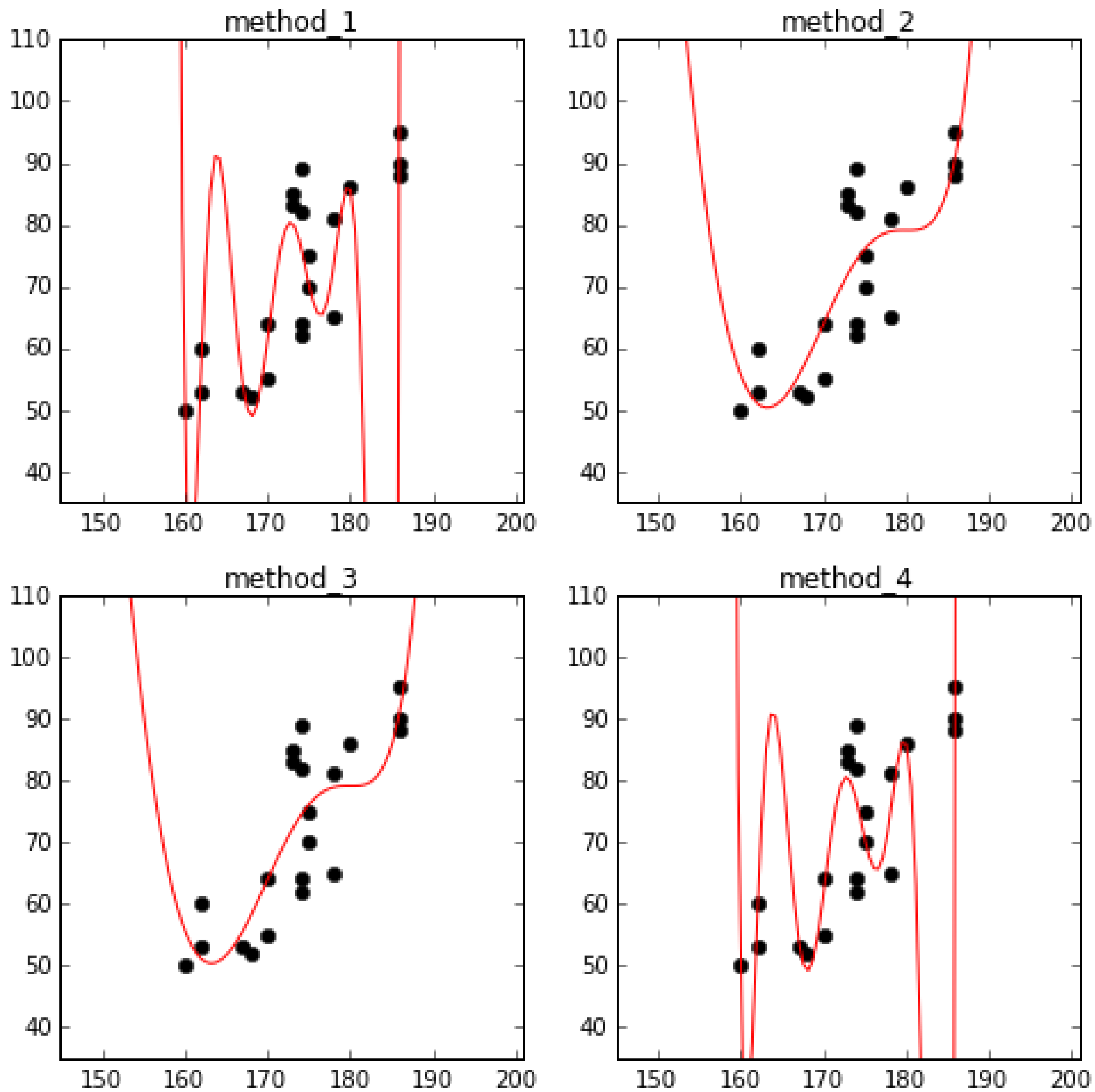
1.10.3 Let's test the expectations!

In [28]:
```
import numpy.linalg as la
import numpy.polynomial.polynomial as poly

# Read data
ws, hs, gs = read_whdata()
HW = np.vstack((hs, ws)).astype(np.float)

# removing outliers
HW_new, neg_idx = pre_rex.only_all_positive(HW, True, return_neg_idx=True)

# unknown
hu = np.array([h for i, h in enumerate(hs) if i in neg_idx])

hgt = HW_new[0, :]
wgt = HW_new[1, :]
xmin = hgt.min()-15
xmax = hgt.max()+15
ymin = wgt.min()-15
ymax = wgt.max()+15
```

```
x = np.linspace(xmin, xmax, 100)

def demo_4_plot(y, titles):
    fig = plt.figure(figsize=(8, 8))
    sp = [2, 2, 0]
    for i, t in enumerate(titles):
        sp[-1] += 1
        ax = fig.add_subplot(*sp)
        ax.plot(hgt, wgt, 'ko', x, y[i], 'r-')
        ax.set_xlim(xmin, xmax)
        ax.set_ylim(ymin, ymax)
        ax.set_title(t)
```

```
In [84]: def trsf(x, div=100):
               return x / div

         n = 10

         def method_1(hgt=hgt, wgt=wgt, n=n, x=x):
             # regression using ployfit
             c = poly.polyfit(hgt, wgt, n)
             y = poly.polyval(x, c)
             return c, y

         def method_2(hgt=hgt, wgt=wgt, n=n, x=x):
             # regression using the Vandermonde matrix and pinv
             X = poly.polyvander(hgt, n)
             c = np.dot(la.pinv(X), wgt)
             y = np.dot(poly.polyvander(x,n), c)
             return c, y

         def method_3(hgt=hgt, wgt=wgt, n=n, x=x):
             # regression using the Vandermonde matrix and lstsq
             X = poly.polyvander(hgt, n)
             c = la.lstsq(X, wgt)[0]
             y = np.dot(poly.polyvander(x,n), c)
             return c, y

         def method_4(hgt=hgt, wgt=wgt, n=n, x=x, div=100):
             # regression on transformed data using the Vandermonde
             #    matrix and pinv
             X = poly.polyvander(trsf(hgt, div=div), n)
             c = np.dot(la.pinv(X), wgt)
             y = np.dot(poly.polyvander(trsf(x, div=div),n), c)
             return c, y

         demo_4_plot([m()[1] for m in [method_1, method_2, method_3, method_4]],
                     [m for m in ["method_1", "method_2", "method_3", "method_4"]])
```

```
/Users/myrmidon/.conda/envs/pattrex/lib/python3.4/site-packages/numpy/polynomial/polynomial.py:1383: Ra
  warnings.warn(msg, pu.RankWarning)
```



1.10.4 What happend?

- Warning raised by polyfit
  - **abdullah:** it is actually helpful
- `method_4` gives almost as 'good' a result as `method_1`
  - **can:** the `trsf` function is scaling the values by 1/100
  - **cifong:** problems with raising 10^2 values to powers of 10 might be getting resolved
  - **abdullah:** actually, no. Look at the coefficients. All are of order 10^{10}

In [60]:
```
coeffs = np.array([m()[0] for m in [method_1, method_2, method_3, method_4]])
print(coeffs.T)
```

```
[[  9.94143754e+11   3.39741629e-19   3.39741629e-19   5.01564415e+11]
 [ -3.61297680e+10   1.17900058e-11   1.17900058e-11  -1.40808912e+12]
 [  5.01765490e+08  -9.63490518e-15  -9.63490518e-15   9.77502398e+11]
 [ -2.82817017e+06   2.89518900e-13   2.89518900e-13   7.51115288e+11]
 [ -1.94892561e+03   2.13966507e-11   2.13966507e-11  -1.10264539e+12]
 [  9.06665686e+01   1.23047796e-09   1.23047796e-09  -3.67718543e+11]
 [ -1.48086662e-01   4.24710787e-08   4.24710787e-08   1.39301069e+12]
 [ -2.67679787e-03  -9.78013259e-10  -9.78013259e-10  -1.08608618e+12]
 [  1.75196332e-05   8.43625378e-12   8.43625378e-12   4.20281052e+11]
 [ -4.38544409e-08  -3.23109114e-14  -3.23109114e-14  -8.41040291e+10]
 [  4.13603892e-11   4.63624155e-17   4.63624155e-17   6.97330421e+09]]
```

```
/Users/myrmidon/.conda/envs/pattrex/lib/python3.4/site-packages/numpy/polynomial/polynomial.py:1383: Ran
  warnings.warn(msg, pu.RankWarning)
```

- **umut:** Let's Time them

```
In [78]: %timeit method_1()
         %timeit method_2()
         %timeit method_3()
         %timeit method_4()
```

```
1000 loops, best of 3: 263 µs per loop
10000 loops, best of 3: 182 µs per loop
10000 loops, best of 3: 181 µs per loop
10000 loops, best of 3: 180 µs per loop
```

```
/Users/myrmidon/.conda/envs/pattrex/lib/python3.4/site-packages/numpy/polynomial/polynomial.py:1383: Ran
  warnings.warn(msg, pu.RankWarning)
```

- **abdullah:** the dataset is too small. Run again with 1000 copies
  - it is still in milliseconds
  - **can:** don't go above 100,000

```
In [81]: hgt_11 = np.tile(hgt, (1000))
         wgt_11 = np.tile(wgt, (1000))
         print(hgt_11.shape[0])

         %timeit method_1(hgt_11, wgt_11)
         %timeit method_2(hgt_11, wgt_11)
         %timeit method_3(hgt_11, wgt_11)
         %timeit method_4(hgt_11, wgt_11)
```

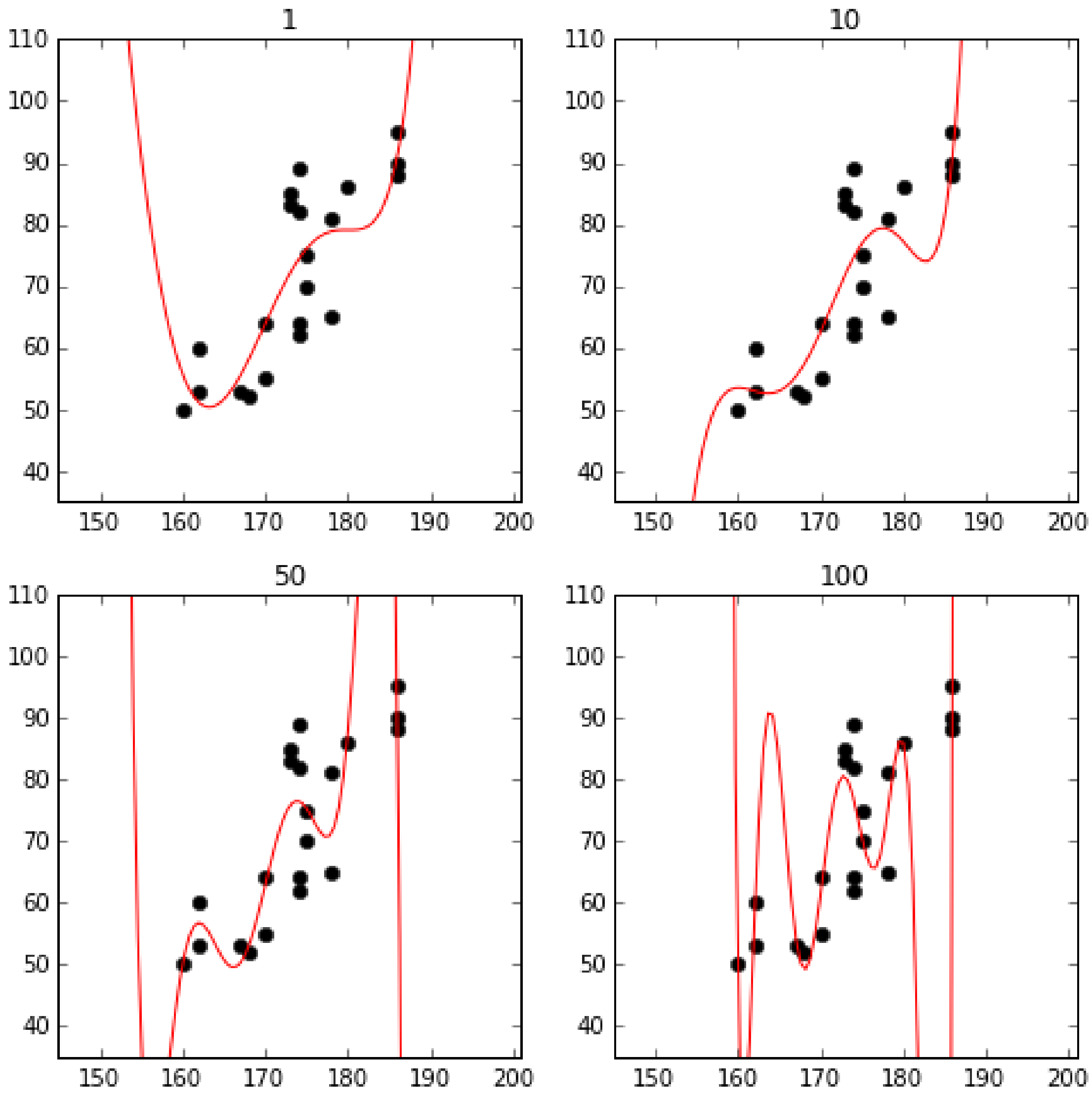
```
21000
100 loops, best of 3: 5.55 ms per loop
100 loops, best of 3: 8.41 ms per loop
100 loops, best of 3: 3.81 ms per loop
100 loops, best of 3: 8.69 ms per loop
```

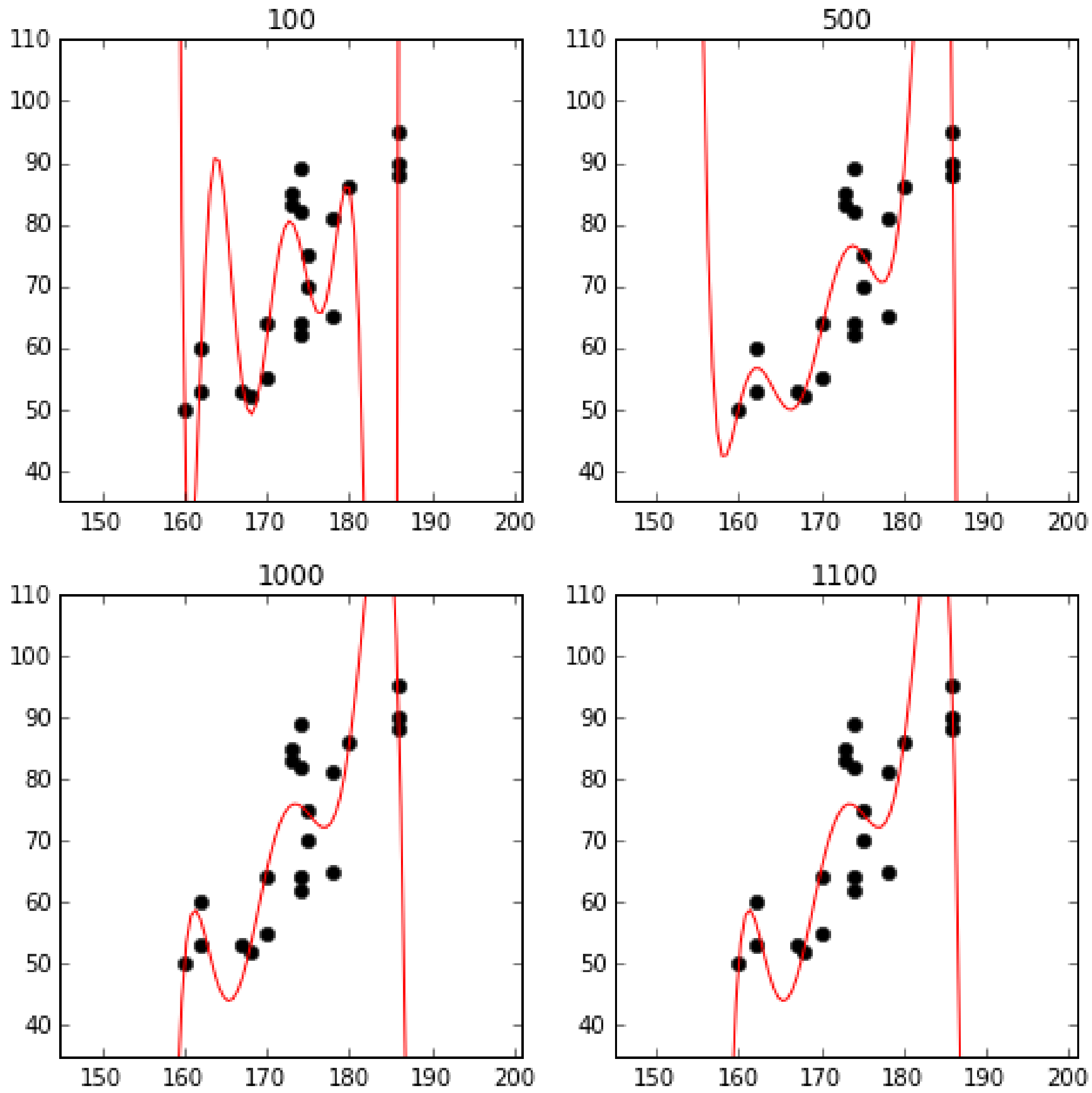
```
/Users/myrmidon/.conda/envs/pattrex/lib/python3.4/site-packages/numpy/polynomial/polynomial.py:1383: Ran
  warnings.warn(msg, pu.RankWarning)
```

- **cifong:** Let me dive into the transformation

1.10.5 How do results change for `method_4` for different divisors

```
In [96]: ys = []
         for d in [1, 10, 50, 100]:
             ys.append(method_4(div=d)[1])

         demo_4_plot(ys, [1, 10, 50, 100])
         ys = []
         for d in [100, 500, 1000, 1100]:
             ys.append(method_4(div=d)[1])

         demo_4_plot(ys, [100, 500, 1000, 1100])
```





1.11 The fitting dimention went up as the divisor goes up,

- The value in given data is 3 digit decimal,
- divisor = 100 make the value to 1 digit

1.12 Floating point issue in Python

- By Python Documentation
- 0.1(decimal) is presented as
- 0.00011001100110011001100110011001100110011001100110011010(Binary)
- Print (0.1)
- 0.1000000000000000055511151231257827021181583404541015625
- https://docs.python.org/2/tutorial/floatingpoint.html

```
In [89]: print(np.finfo(np.float32))
         print(np.finfo(np.float64))
```

```
Machine parameters for float32
---------------------------------------------------------------------
precision=   6   resolution= 1.0000000e-06
machep=    -23   eps=        1.1920929e-07
negep =    -24   epsneg=     5.9604645e-08
minexp=   -126   tiny=       1.1754944e-38
maxexp=    128   max=        3.4028235e+38
nexp  =      8   min=        -max
---------------------------------------------------------------------

Machine parameters for float64
---------------------------------------------------------------------
precision=  15   resolution= 1.0000000000000001e-15
machep=    -52   eps=        2.2204460492503131e-16
negep =    -53   epsneg=     1.1102230246251565e-16
minexp=  -1022   tiny=       2.2250738585072014e-308
maxexp=   1024   max=        1.7976931348623157e+308
nexp  =     11   min=        -max
---------------------------------------------------------------------
```

1.13 Looking in to `numpy.linalg.pinv`

- `numpy.linalg.pinv(a, rcond=1e-15)`
- `rcond` is the precision of float 64, which `linalg` supports
- we found this code inside

In [ ]:
```
a, wrap = _makearray(a)
_assertNoEmpty2d(a)
a = a.conjugate()
u, s, vt = svd(a, 0)
m = u.shape[0]
n = vt.shape[1]
cutoff = rcond*maximum.reduce(s)
for i in range(min(n, m)):
    if s[i] > cutoff:           #Suspicious part, set value to zero
        s[i] = 1./s[i]
    else:
        s[i] = 0.;
res = dot(transpose(vt), multiply(s[:, newaxis], transpose(u)))
return wrap(res)
```

1.14 Test this part

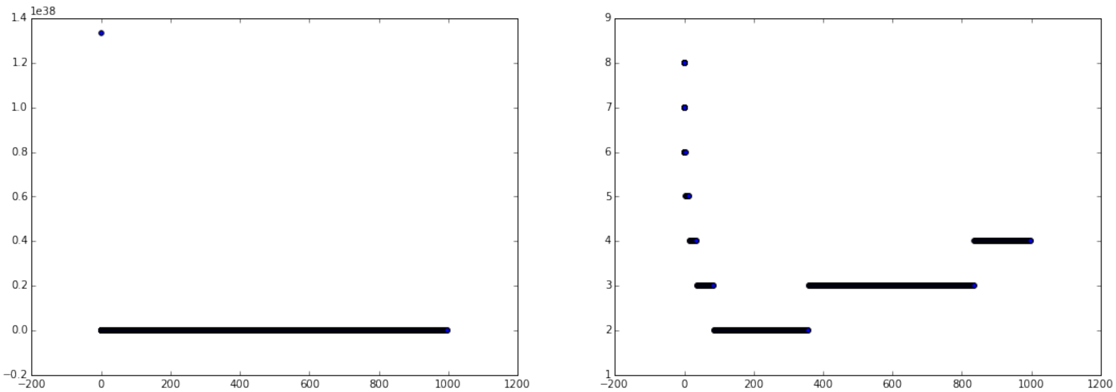
- See how many cutsin different divisor

In [90]:
```
from numpy.core import umath as um

 def countPinvCutoff(a):

     rcond=1e-15
     a = um.conjugate(a)
     u,s,vt = la.svd(a,0)
     sNoCut = np.copy(s)
     m = u.shape[0]
     n = vt.shape[1]
```

```
    cutoff = rcond*um.maximum.reduce(s)
    cutCount=0

    for i in range(min(n, m)):
        if s[i] < cutoff:
            cutCount+=1

    return cutCount, cutoff
```

In [91]:
```
count = []
cutoffValue = []
inteNI = np.arange(0.001,1,0.001)
intePI = np.arange(1,1000,1)
divisor = np.append(inteNI, intePI)
for i in divisor:
    X = poly.polyvander(trsf(hgt,i), n)
    cutCount, cutoff = countPinvCutoff(X)
    list.append(count, cutCount)
    list.append(cutoffValue, cutoff)

fig = plt.figure(figsize=(18, 6))
plt.subplot(121)
plt.scatter(divisor, cutoffValue)
plt.subplot(122)
plt.scatter(divisor, count)
```

Out[91]: <matplotlib.collections.PathCollection at 0x109015b70>

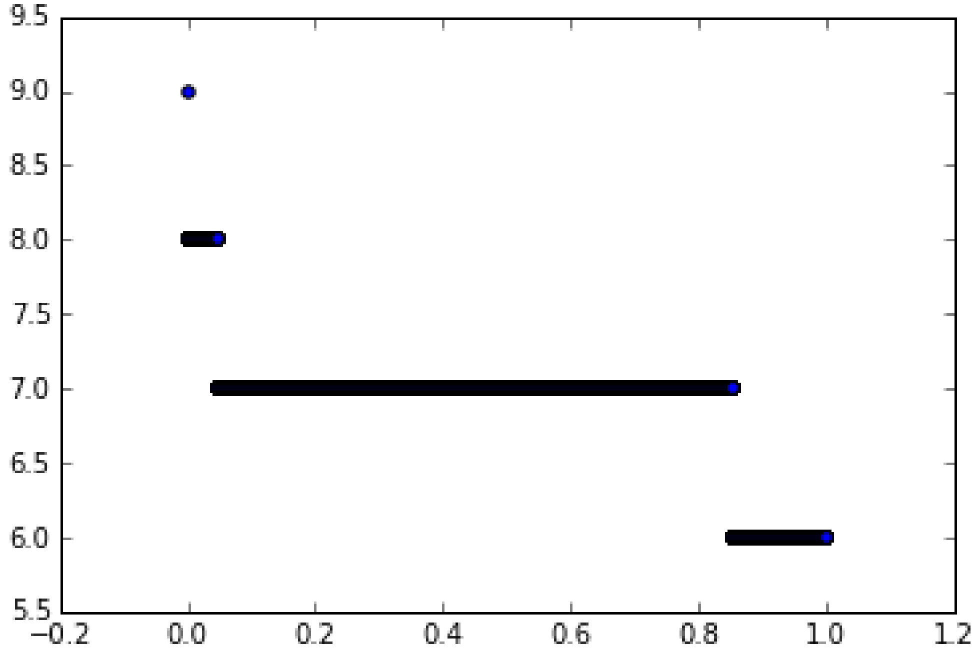


1.15 Discussion

- 1.Ther trend mathes the degeneration of fitting function that
- the lower the cut off, the higher remaining dimension we have
- 2.We would have at least 2 cutoffs in all divisor

In [99]:
```
count = []
for i in np.arange(0.0001,1,0.0001):
    X = poly.polyvander(trsf(hgt,i), n)
    count.append(countPinvCutoff(X)[0])

plt.scatter(np.arange(0.0001,1,0.0001), count)
```

Out[99]: <matplotlib.collections.PathCollection at 0x10b6e1c18>



In [102]:
```
def pinv(a):

    cntCO=0
    cntTol=0
    rcond=1e-15
    a = um.conjugate(a)
    u,s,vt = la.svd(a,0)
    sNoCut = np.copy(s)
    m = u.shape[0]
    n = vt.shape[1]
    cutoff = rcond*um.maximum.reduce(s)
    tolerence = max(m,n)*um.maximum.reduce(s)*rcond
#     print("calculated cutoff",cutoff)
#     print("calculated tolerence",tolerence)
    for i in range(min(n, m)):
        if s[i] < cutoff:
            cntCO+=1
        if s[i] > tolerence:
            s[i] = 1./s[i]
            sNoCut[i]=1./sNoCut[i]
        else:
            cntTol+=1
            s[i] = 0.
            sNoCut[i]=1./sNoCut[i]


    res = np.dot(vt.T,um.multiply(s[:,np.newaxis], u.T))
```

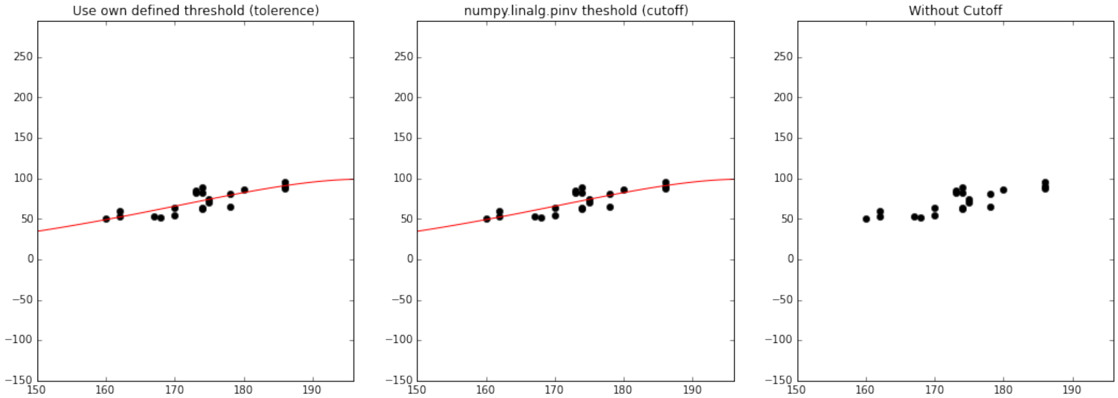
```
    resNoCut = np.dot(vt.T,um.multiply(sNoCut[:,np.newaxis], u.T))

    return res, resNoCut, tolerence, cutoff, cntTol, cntCO
#     resNoCut = np.dot(vt.T,um.multiply(sNoCut[:,np.newaxis], u.T))

def demoPic(divisor):
    xmin = hgt.min() - 10
    xmax = hgt.max() + 10
    ymin = wgt.min() - 200
    ymax = wgt.max() + 200
    X = poly.polyvander(trsf(hgt,divisor), n)
    inv, invN, tol, co, cntTol, cntCO = pinv(X)

    print("divisor: %4.4f, tolerence: %4.16f, tolCount:%2d, cutoff:%4.16f, CoCount:%2d" %
          (divisor, tol, cntTol, co, cntCO))

    cL = np.dot(la.pinv(X), wgt)
    yL = np.dot(poly.polyvander(trsf(x,divisor),n), cL)

    c = np.dot(inv, wgt)
    y = np.dot(poly.polyvander(trsf(x,divisor),n), c)

    fig = plt.figure(figsize=(18, 6))
    plt.subplot(131)
    plt.title("Use own defined threshold (tolerence)")
    plt.plot(hgt, wgt, 'ko',x, y, 'r-')
    plt.xlim(xmin, xmax)
    plt.ylim(ymin, ymax)

    plt.subplot(132)
    plt.title("numpy.linalg.pinv theshold (cutoff)")
    plt.plot(hgt, wgt, 'ko',x, yL, 'r-')
    plt.xlim(xmin, xmax)
    plt.ylim(ymin, ymax)

    cN = np.dot(invN, wgt)
    yN = np.dot(poly.polyvander(trsf(x,divisor),n), cN)
    plt.subplot(133)
    plt.title("Without Cutoff")
    plt.plot(hgt, wgt, 'ko',x, yN, 'r-')
    plt.xlim(xmin, xmax)
    plt.ylim(ymin, ymax)
    plt.show()
```

1.16 Plot some divisors on 3 variants

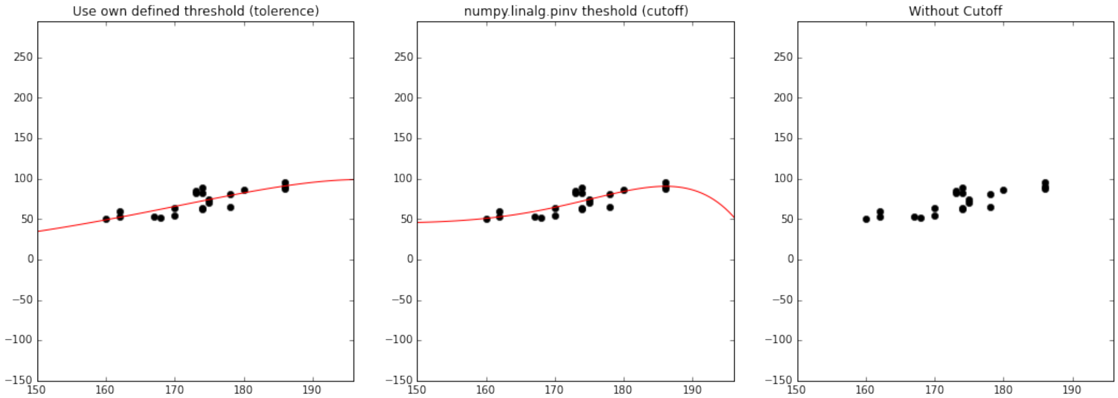
- Compare with the tolerence = epslon * max(m,n) * maximum(s)
- linalg.inv cutoff = epslon * maximum(s)
- No cut off

In [103]:
```
index = [0.01,0.05,0.1,0.5, 1,5, 10, 50, 100, 500, 1000]
for i in index:
    demoPic(i)
```

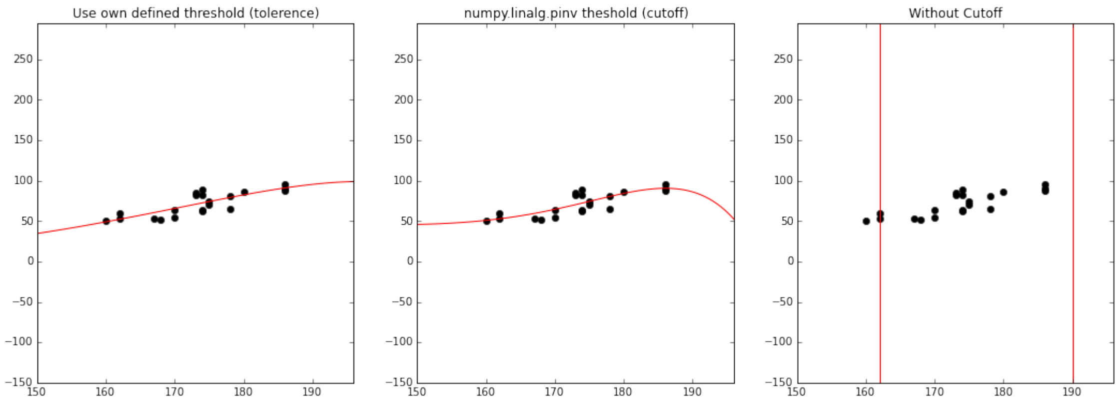
```
divisor: 0.0100, tolerence: 27958220282725386062070703718 4.0000000000000000, tolCount: 8, cutoff:133134
```



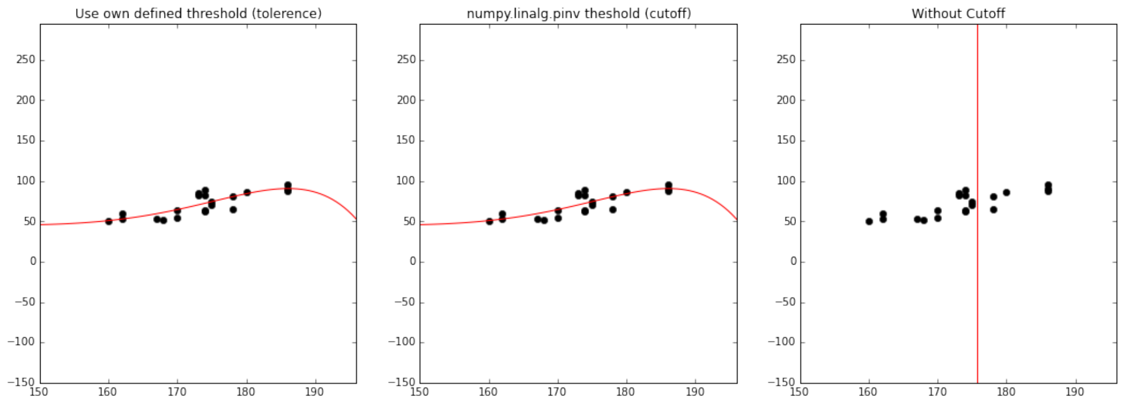

```
divisor: 0.0500, tolerence: 28629218642458107183104.0000000000000000, tolCount: 8, cutoff:13632961258831
```



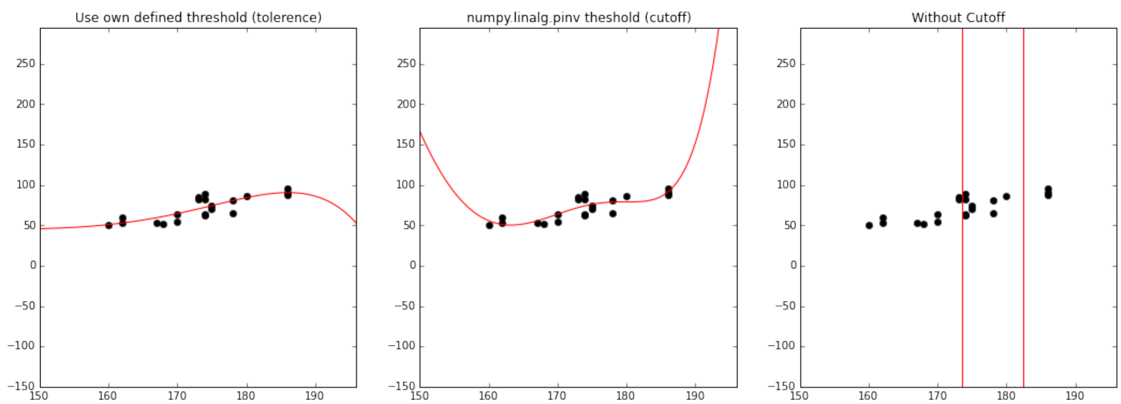

```
divisor: 0.1000, tolerence: 27958224604901580800.0000000000000000, tolCount: 8, cutoff:1331344028804837
```



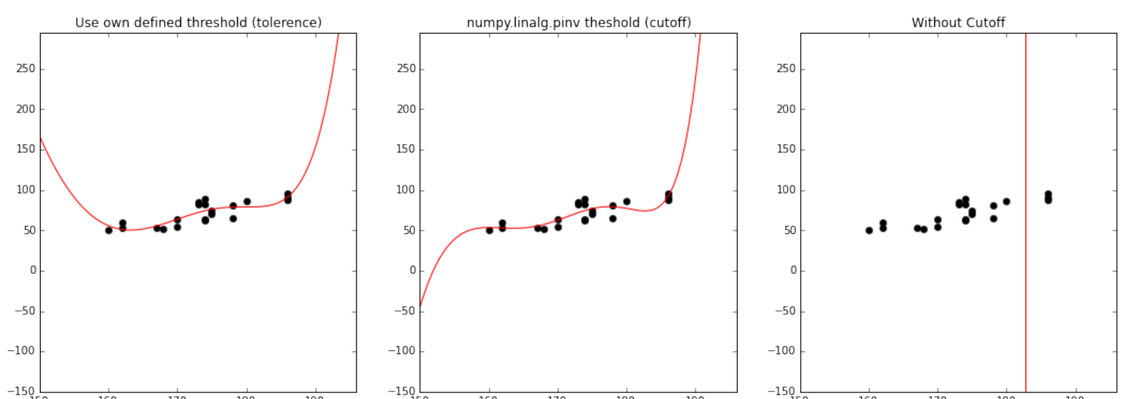

```
divisor: 0.5000, tolerence: 2862932929080.0292968750000000, tolCount: 7, cutoff:136330139480.0014038085
```



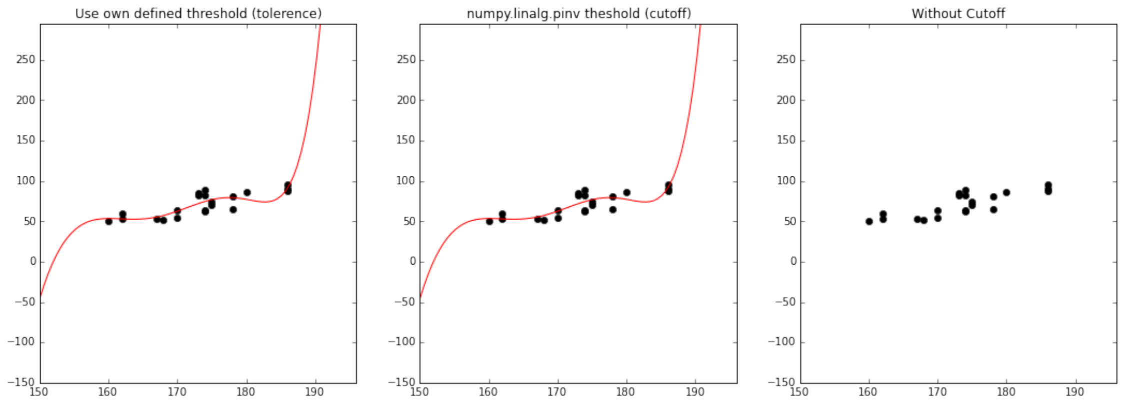
divisor: 1.0000, tolerence: 2795865683.2700839042663574, tolCount: 7, cutoff:133136461.1080992370843887



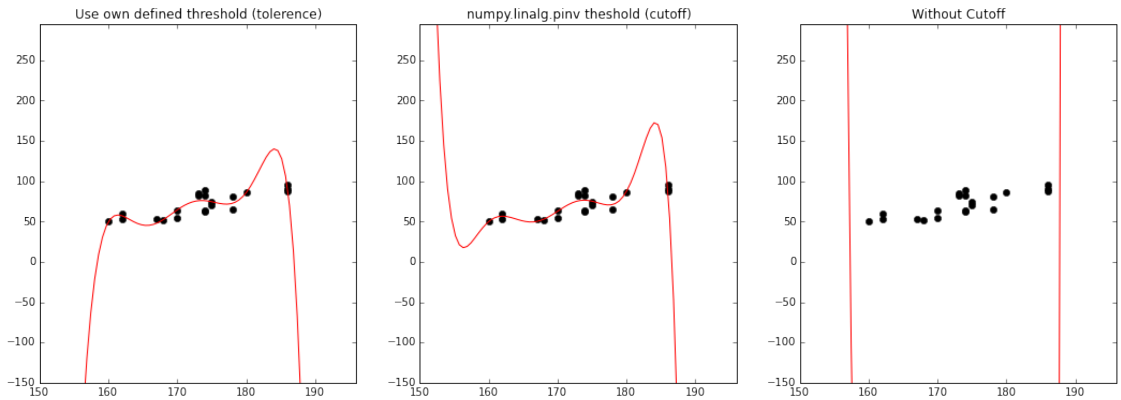
divisor: 5.0000, tolerence: 286.4040064468964601, tolCount: 6, cutoff:13.6382860212807824, CoCount: 5



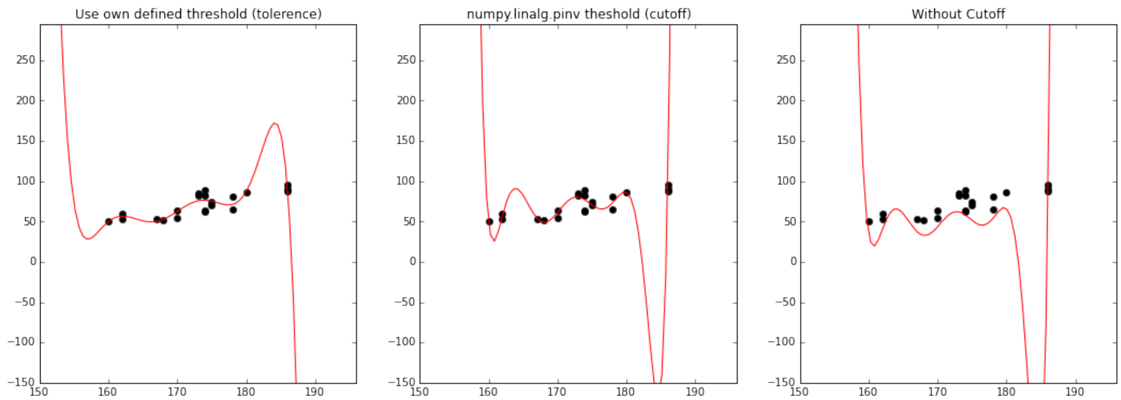
divisor: 10.0000, tolerence: 0.2800198168618731, tolCount: 5, cutoff:0.0133342769934225, CoCount: 5



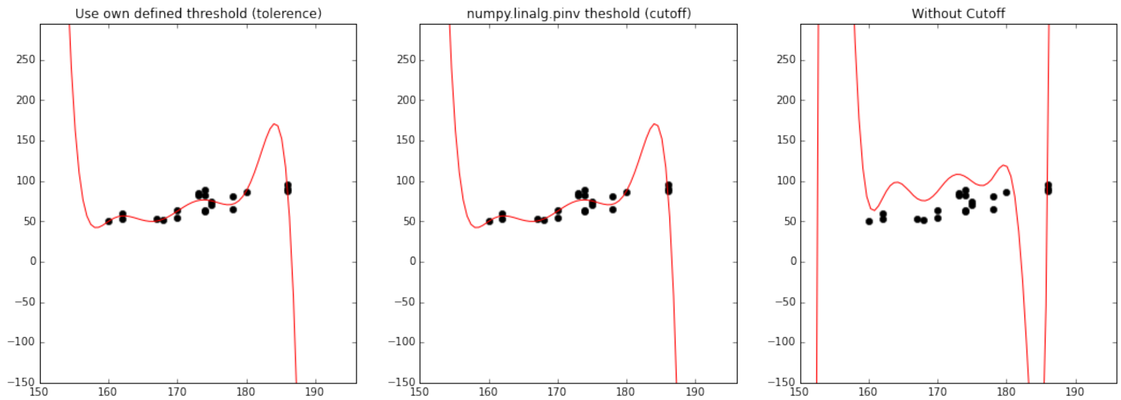
divisor: 50.0000, tolerence: 0.0000000298173451, tolCount: 4, cutoff:0.0000000014198736, CoCount: 3



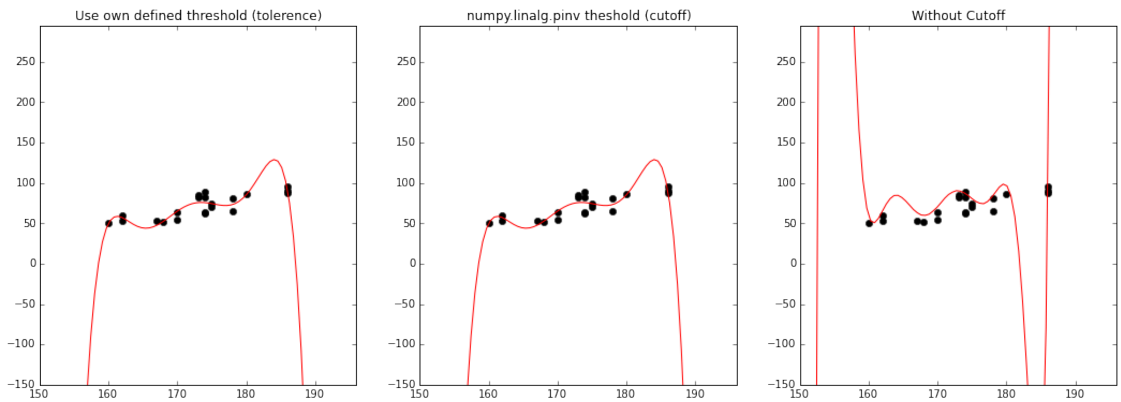
divisor: 100.0000, tolerence: 0.0000000000337292, tolCount: 3, cutoff:0.0000000000016062, CoCount: 2



divisor: 500.0000, tolerence: 0.0000000000001026, tolCount: 3, cutoff:0.0000000000000049, CoCount: 3




```
divisor: 1000.0000, tolerence: 0.0000000000000977, tolCount: 4, cutoff:0.0000000000000047, CoCount: 4
```



1.17 References

- Slides
- C. Bauckhage. Lecture Notes on Data Science: k-Means Clustering
- C. Bauckhage. Lecture Notes on Data Science: Online k-Means Clustering
- Andre Ng, etal On Spectral Clustering: Analysis and an algorithm
- A.M. Martinez et al. PCA vs. LDA

1.18 Questions?