

# Spectral clustering techniques for biological data

17 septembre 2014

# Plan

- 1 Project presentation
- 2 Spectral clustering
- 3 Results on synthetic data / biological data

# Plan

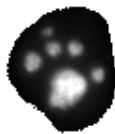
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# Project Presentation

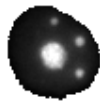
- strong correlation between structure of the nucleolus of a cell and potential diseases of this cell
- biologist have generated a database by annihilating some specific genes of the cells (silencers) and they have visually observed different conformations of the nucleolus



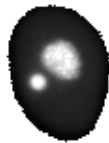
Well A12



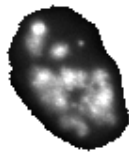
Well A12



Well F12



Well F12



Well E02

1 well of cells = 1 silencer

# Project Presentation

Objective :

- clustering the cells based on the conformation of their nucleolus
- maximize the number of cluster

Hypothesis :

- the cell of the same well should belong to the same cluster

# Project Presentation

After an image analysis processing, each cell is represented by a 15-dimensional characteristics' vector  $x_i \in \mathbb{R}^{15}$

Example : elliptic regularity, number of connected component, luminous intensity

Presence of the noise :

- some cells of a well could not have reacted to the silencer
- 2D representation of a 3D cell

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# Graph clustering

data points :  $x_1, \dots, x_n \in \mathbb{R}^P$

similarity matrix :  $W = (w_{ij})_{i,j=1..n} = w(x_i, x_j)$

similarity graph  $G = (V, E)$

$V$  : vertices (data points)

$E$  : edges with weight  $w_{ij}$

Problem of clustering  $\leftrightarrow$  Partition the graph so that edges within a group have large weights and edges across groups have small weights.

## Construction of the connectivity matrix

For each vertices, selection of the  $m$ -nearest neighbors  $\rightarrow$   
 $C(i, j) = 1$  if  $j$  is one of the  $m$ -nearest neighbors of  $i$  and 0 otherwise.

$C$  is not symmetric :

- $C_{norm} = \max(C, C') \rightarrow C(i, j) = 1$  if  $i$  is one of the  $m$ -nearest neighbors of  $j$  OR if  $j$  is one of the  $m$ -nearest neighbors of  $i$  : each vertice has at least  $m$  neighbors (normal graph)
- $C_{mut} = \min(C, C') \rightarrow C(i, j) = 1$  if  $i$  is one of the  $m$ -nearest neighbors of  $j$  AND if  $j$  is one of the  $m$ -nearest neighbors of  $i$  : each point has at most  $m$  neighbors (mutual graph)

$\rightarrow$  Connectivity matrix  $C_{norm}$  or  $C_{mut}$  : **sparse** matrix

## Construction of the similarity matrix

If  $i$  and  $j$  are connected  $w_{ij} = e^{-\frac{\|x_i - x_j\|^2}{2\sigma^2}}$   $\rightarrow \sigma$  controls the size of the neighborhood

How to choose  $\sigma$  :

- human-specified parameter
- local scaling ([1] Zelnik-Manor, 2005) : one value of  $\sigma$  for each point. Ex :  $\sigma_i = \max_j (\|x_i - x_j\|)$  for  $j$  in the neighborhood of  $i$

# Definitions

Degree of a vertex  $i$  :  $d_i = \sum_{j=1}^n w_{ij}$

Degree diagonal-matrix with coefficients  $d_i$  :  $D$

Laplacian matrix :

$$L = D - W$$

Normalized Laplacian matrix :

- $L_{rw} = D^{-1}L$
- $L_{sym} = D^{-1/2}LD^{-1/2}$

## Numbers of connected components and spectrum of $L_{rw}$

The multiplicity  $k$  of the eigenvalue 0 of  $L_{rw}$  equals the number of connected components  $A_1, \dots, A_k$  in the graph. The eigenspace of the eigenvalue 0 is spanned by the indicator vector  $\mathbb{1}_{A_1}, \dots, \mathbb{1}_{A_k}$

## Partitioning a graph

For two subsets  $A, B$  of  $V$  :  $W(A, B) = \sum_{i \in A, j \in B} w_{ij}$

Two ways for measuring the "size" of a subset  $A$  :

- $|A|$  : number of vertices in  $A$
- $vol(A) = \sum_{i \in A} d_i$

Two criteria to partitioning a graph :

$$cut(A_1, \dots, A_k) = \frac{1}{2} \sum_{i=1}^k W(A_i, \bar{A}_i)$$

$$Ncut(A_1, \dots, A_k) = \frac{1}{2} \sum_{i=1}^k \frac{W(A_i, \bar{A}_i)}{vol(A_i)} = \sum_{i=1}^k \frac{cut(A_i, \bar{A}_i)}{vol(A_i)}$$

# Partitioning a graph

- Minimize cut leads to solution which separate one individual vertex from the rest of the graph.
- By dividing the cut by  $vol(A_i)$ , we explicitly request that the sets  $A_1, \dots, A_k$  are reasonably large.

Problem : minimizing Ncut is NP-Hard  $\rightarrow$  Spectral clustering is a way to solve relaxed version of this problem.

# Spectral clustering

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**Algorithm** Normalized spectral clustering (Shi and Malik 2000)

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L=D-W

Compute the  $k$  first eigenvector  $u_1, \dots, u_k$  of  $L_{rw} = D^{-1}L$  by solving  $Lu = \lambda Du$

$$U = \begin{pmatrix} u_1(1) & \dots & u_k(1) \\ \vdots & \dots & \vdots \\ u_1(i) & \dots & u_k(i) \\ \vdots & \dots & \vdots \\ u_1(n) & \dots & u_k(n) \end{pmatrix} = \begin{pmatrix} y_1 \\ \vdots \\ y_i \\ \vdots \\ y_n \end{pmatrix} \quad y_i \in \mathbb{R}^k$$

$[C_1, \dots, C_k] \leftarrow kmeans(\{y_i\}_{i=1..n}, k)$

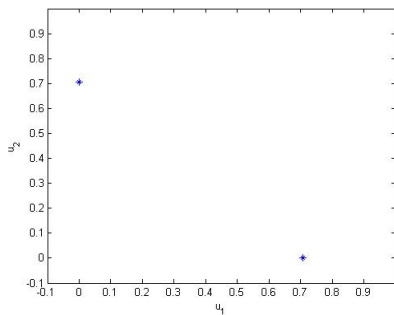
Output : Clusters  $A_1, \dots, A_k$  with  $A_i = \{x_j | y_j \in C_i\}$

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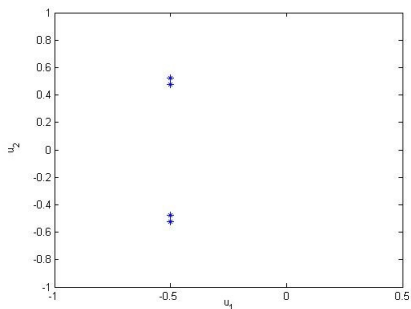
## Why does it work?

$$W = \begin{pmatrix} 1 & 1 & 0 & 0 \\ 1 & 1 & 0 & 0 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 1 & 1 \end{pmatrix} \quad U = \begin{pmatrix} 0.7 & 0 \\ 0.7 & 0 \\ 0 & 0.7 \\ 0 & 0.7 \end{pmatrix}$$



## Why does it work?

$$W = \begin{pmatrix} 1 & 1 & 0.2 & 0 \\ 1 & 1 & 0 & 0.1 \\ 0.2 & 0 & 1 & 1 \\ 0 & 0.1 & 1 & 1 \end{pmatrix} \quad U = \begin{pmatrix} -0.5 & -0.4745 \\ -0.5 & -0.5243 \\ -0.5 & 0.4745 \\ -0.5 & 0.5243 \end{pmatrix}$$



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## Information theoretic measures for clustering

Pb : How to evaluate the quality of a clustering? ([3] Vinh 2010)

Basing the following array, we can compare two clusterings

$K = (K_1, \dots, K_p)$  et  $C = (C_1, \dots, C_r)$

	$K_1$	...	$K_i$	...	$K_p$	Sum
$C_1$	$ C_1 \cap K_1 $	...	$ C_1 \cap K_i $	...	$ C_1 \cap K_p $	$a_1$
$\vdots$		...		...		
$C_{i'}$	$ C_{i'} \cap K_1 $	...	$ C_{i'} \cap K_i $	...	$ C_{i'} \cap K_p $	$a_{i'}$
$\vdots$		...		...		
$C_r$	$ C_r \cap K_1 $	...	$ C_r \cap K_i $	...	$ C_r \cap K_p $	$a_r$
Sum	$b_1$	...	$b_i$	...	$b_p$	$\sum_{ij} n_{ij} = n$

with  $n_{ij} = |C_i \cap K_j|$

## Information theoretic measures for clustering

$$H(C) = - \sum_{i=1}^r \frac{a_i}{n} \log \left( \frac{a_i}{n} \right) \quad \text{Entropy}$$

$$H(C|K) = - \sum_{i=1}^r \sum_{j=1}^p \frac{n_{ij}}{n} \log \left( \frac{\frac{n_{ij}}{n}}{\frac{b_j}{n}} \right) \quad \text{Conditional entropy}$$

$$I(C, K) = \sum_{i=1}^r \sum_{j=1}^p \frac{n_{ij}}{n} \log \left( \frac{\frac{n_{ij}}{N}}{\frac{a_i b_j}{N^2}} \right) \quad \text{Mutual Information}$$

$$I(C, K) = H(C) - H(C|K) = H(K) - H(K|C)$$

## Information theoretic measures for clustering

$$NMI(K, C) = \frac{I(K, C)}{\sqrt{H(C)H(K)}}$$

Normalized Mutual Information

$$0 \leq NMI(K, C) \leq 1$$

if  $K = C$  then  $NMI(K, C) = 1$

# Spectral Clustering vs Kmeans

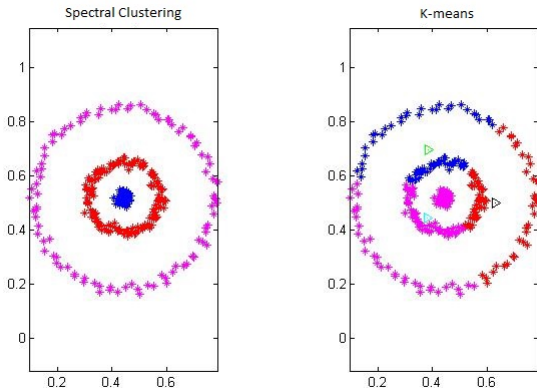
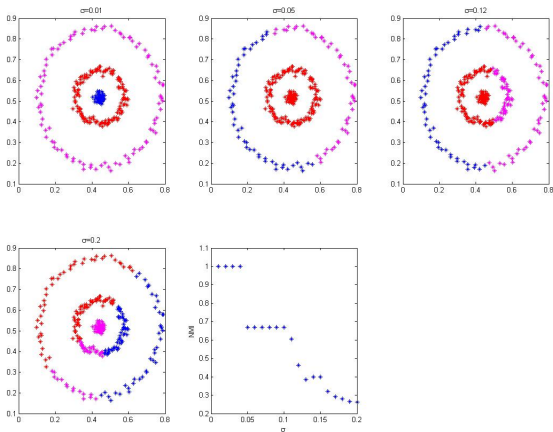


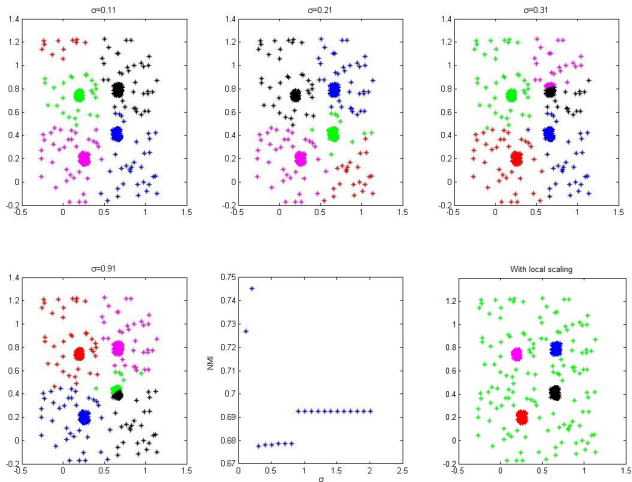
Figure: Spectral Clustering vs Kmeans

# Influence of $\sigma$ (normal graph - 20 neighbors)





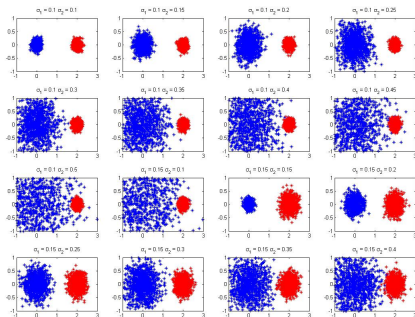
# Local scaling (normal graph - 20 neighbors)



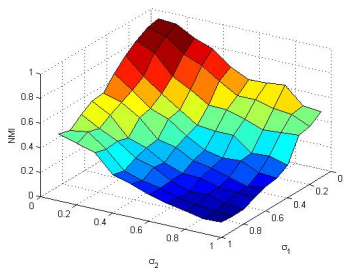
# Influence of the noise

Experimental protocol :

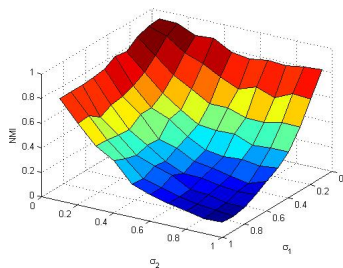
- given two gaussian distributions (1000 points in each)  $(\mu_1, \sigma_1)$  and  $(\mu_2, \sigma_2)$  where  $\mu_1$  and  $\mu_2$  are fixed so that  $\|\mu_1 - \mu_2\| = 1$ . We test our algorithm by varying  $\sigma_1$  and  $\sigma_2$  from 0.1 to 1



# Comparison Normal Graph - Mutual Graph 2D

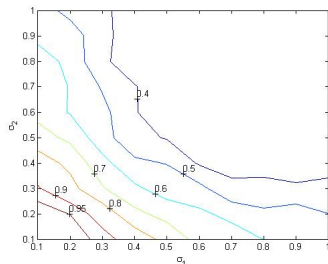


Normal graph

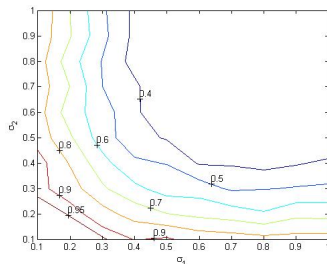


Mutual graph

# Contour line Normal Graph - Mutual Graph 2D

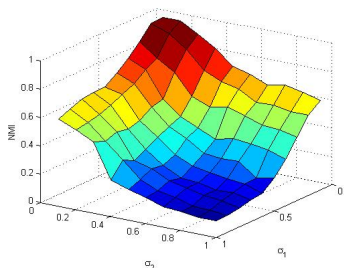


Normal graph

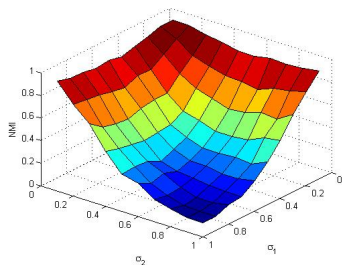


Mutual graph

# Comparison Normal Graph - Mutual Graph 3D

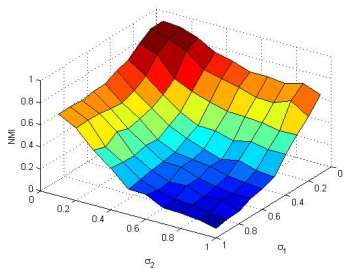


Normal graph

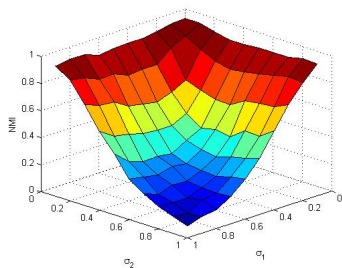


Mutual graph

# Comparison Normal Graph - Mutual Graph 4D



Normal graph



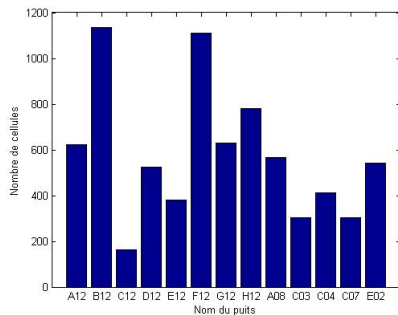
Mutual graph

# Results on biological data

Pb : the number of cluster  $k$  is unknown.

→ We test our algorithm for different values of  $k$  and we keep which has the largest value of NMI

Database :



# Results on biological data

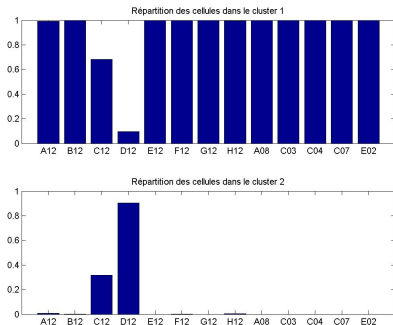
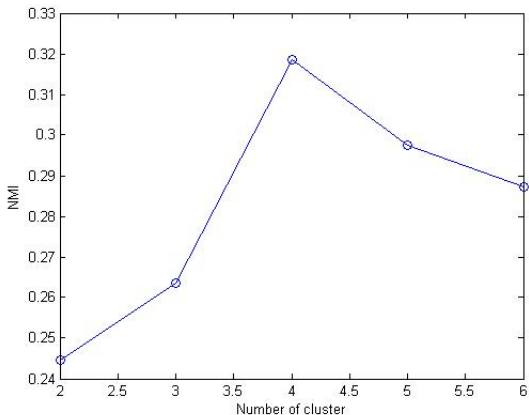


Figure: 2 Clusters (normal graph - 100 neighbors)



## Results on biological data



# Results on biological data

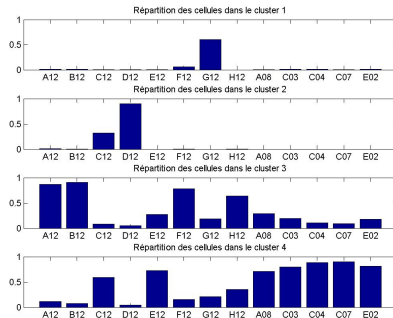


Figure: 4 Clusters

# Conclusion

Advantages of spectral clustering :

- quite simple to implement
- good results on our dataset

Future work :

- use other algorithm than kmeans to separate eigenvector
- clustering on one well of cells to identify the noise

Thanks for your attention  
Any questions?

## Bibliography

- [1] Zelnik-Manor L. Perona P. 'Self-tuning on Spectral Clustering' (2005)
- [2] Von Luxburg U. 'A Tutorial on Spectral Clustering' *Statistics and Computing*, 17 (4) (2007)
- [3] Vinh N. Epps J. 'Information Theoretic Measures for Clusterings Comparison : Variants, Properties, Normalization and Correction for Chance' *Journal of Machine Learning Research* 11 2837-2854(2010)
- [4] Shi J. Jambo J. 'Normalized Cut and Image Segmentation' (2000)