

# Algorithms. Matching

Part II. Preference model.

B9 - Algorithms Matching

M-ALG-102

## Introduction

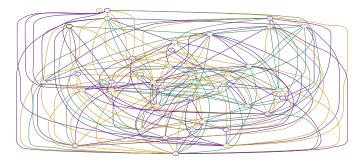


Figure: Graph

#### Introduction

 $https://github.com/nlehir/ALGO2\\ We will need (the installation of these packages should work with pip):$ 

- matplotlib
- pandas
- sklearn
- optionnally : ipdb

## Day 2

## Compatibility graphs

Simple geometrical data Complex data

#### Probability distributions

Reminders on probabilities Analyzing a distribution Optimization and Maximum Likelihood

Multivariate analysis and clustering

Correlation

Gradients

Kmeans clustering

Similarities and Spectral Clustering

Similarities

Spectral Clustering

Additional considerations and conclusions



- Yesterday we processed graphs describing relationship between data
- ▶ If two nodes were related, they were linked by an edge in the graph.

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- ▶ If two nodes were related, they were linked by an edge in the graph.
- ► Today we are interested in building such graphs directly from the data, we call them **compatibility graphs**.

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We are interested in building **compatibility graphs**. Given two nodes in a graph, should there be an edge between them ?

**Note:** it is not the same problem as the matching problem. In the matching problem, the edges are already defined. However, once the edges are built, we can apply a matching to it.

# Example applications

- Social networks management
- Recommendations

# Building compatibility graphs

- ▶ We will build graphs first from simple data
- ▶ Then from more complex data.

# Building a graph from simple data

▶ We will first build a graph from simple data in the 2D space.

## Euclidian distance and compatibility

#### Consider the following data:

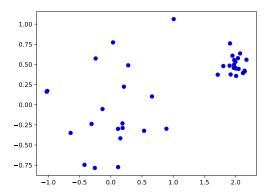


Figure: Data : we would like to define edge between some of them

# Is this set of edges a good solution?

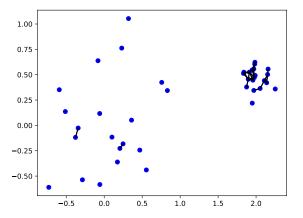


Figure: Some definition of edges

## Is this set of edges a good solution?

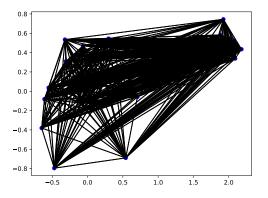
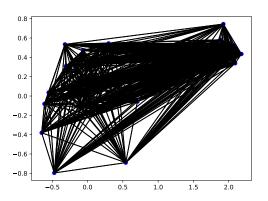


Figure: Some definition of edges

## Euclidian distance and compatibility

Here, all we know about the data is their euclidian distance :



## This one looks ok

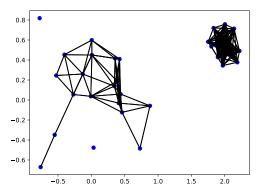
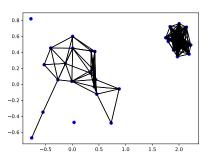


Figure: A proposition of edges

## Backboard

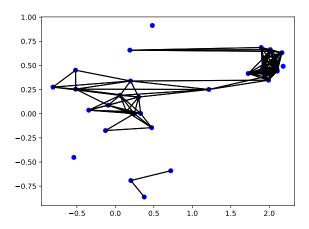
Euclidian distance and threshold.

Exercice 1 : Setting a threshold **cd compatibility\_simple** and set the threshold used in **build\_graph.py** to draw relevant edges between the nodes. Feel free to use another dataset!



#### Exercice 2: Changing the distance

- ► Assess the impact of changing the distance used. Possible choices :
  - ► L1 distance (Manhattan)
  - ▶  $||||_{\infty}$  distance (backboard)
  - custom distance
- use build\_graph\_other\_distance.py and edit the distances used at the end of the file.
- Try several values for the threshold.



## General notion of a distance

Let us generalize what we experimentally studied.

$$x = (x_1, ..., x_p)$$
 and  $y = (y_1, ..., y_p)$  are p-dimensional **vectors**.

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• weighted L1 : 
$$\sum_{k=1}^{p} w_k |x_k - y_k|$$

# Hamming distance

•  $\#\{x_i \neq y_i\}$  (Hamming distance)

## Hamming distance and edit distance

- $\#\{x_i \neq y_i\}$  (Hamming distance)
- ▶ linked to **edit distance** : used to quantify how dissimilar two strings are by counting the number of operations needed to transform one into the other (several variants exist)

A **distance** on a set E is an application  $d: E \times E \to \mathbb{R}_+$  that must :

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- ▶ separate the values :  $\forall x, y, d(x, y) = 0 \Leftrightarrow x = y$
- respect the **triangular inequality**  $\forall x, y, z, d(x, y) \leq d(x, z) + d(y, z)$

## Building compatibility graphs for more complex data

- ▶ We will do the same with more complex data:
  - possibly more dimensions
  - possibility categorical variables

## Random variables

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- For instance :
  - ▶ the result of a dice throw



Figure: Dice

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  - waiting time with RATP



Figure: Some metro station

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  - waiting time with RATP
  - weather



Figure: Weather in November

- ▶ A random variable is a quantity that can take several values
- For instance :
  - the result of a dice throw
  - waiting time with RATP
  - weather
  - number of cars taking the periphrique at the same time

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- **continuous**: weather, RATP

What are the differences between these random variables?

- ► Some are continuous, others discrete
- continuous : weather, RATP
- ▶ discrete : dice (6 possibilities), number of cars (> 10000)

A random variable is linked to a **probability distribution**.

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- ▶ It quantifies the probability of observing one outcome.

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- ▶ It quantifies the probability of observing one outcome.
- ► For a discrete variable : each possible outcome is associated with a number between 0 and 1

- ▶ For a dice game, the possible outcomes are in the set  $\{1, 2, 3, 4, 5, 6\}$
- ► For a dice game : P(1) = P(2) = P(3) = P(4) = P(5) = P(6) =

- ► For a dice game, the possible outcomes are in the set  $\{1, 2, 3, 4, 5, 6\}$
- ► For a dice game :  $P(1) = \frac{1}{6}$ ,  $P(2) = \frac{1}{6}$ ,  $P(3) = \frac{1}{6}$ ,  $P(4) = \frac{1}{6}$ ,  $P(5) = \frac{1}{6}$ ,  $P(6) = \frac{1}{6}$
- This is called a uniform distribution

► Periphrique :

 Periphrique : probably a time-dependent very complicated distribution

#### Continuous variables

► How would you model a continuous variable ? Can you assign a number to a waiting time or a weather ?

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- ▶ One needs to use **probability densities**. Formally, the probably of being between x and x + dx is p(x)dx.

#### Continuous variables

- ► How would you model a continuous variable? Can you assign a number to a waiting time or a weather?
- ▶ One needs to use **probability densities**. Formally, the probably of being between x and x + dx is p(x)dx.
- ▶ Let's see some examples

#### Uniform discrete

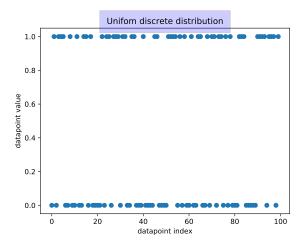


Figure: Uniform discrete distribution

### Bernoulli

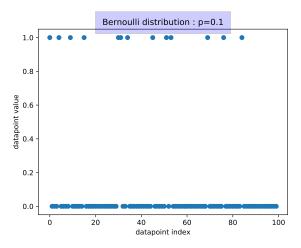


Figure: Bernoulli distribution

## Bernoulli p

- With probability p, X = 1
- With probability 1 p, X = 0

### Bernoulli

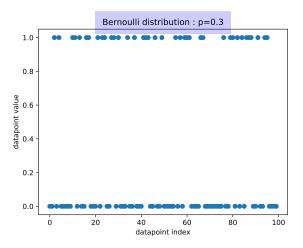


Figure: Bernoulli Distribution

### Bernoulli

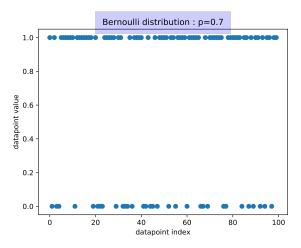


Figure: Bernoulli Distribution

## Uniform continuous

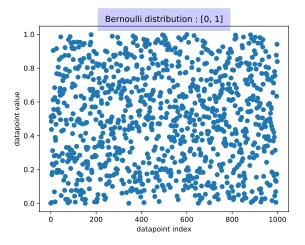


Figure: Uniform continuous distribution

## Uniform continuous

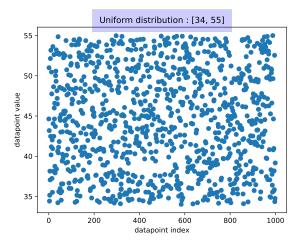


Figure: Uniform continuous distribution

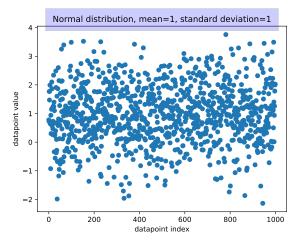


Figure: Normal distribution

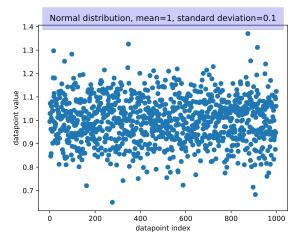


Figure: Normal distribution

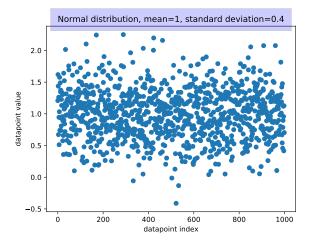


Figure: Normal distribution

### White noise

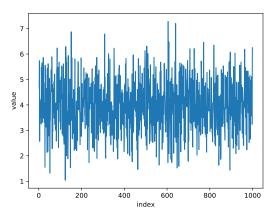


Figure: White noise

## Histograms

Is looking at the raw dataset really informative ?

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Is looking at the raw dataset really **informative?** It is informative, but often a **histogram** tells more.

#### Uniform discrete

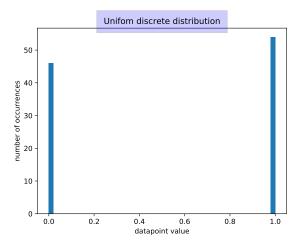


Figure: Historgram 1

### Bernoulli

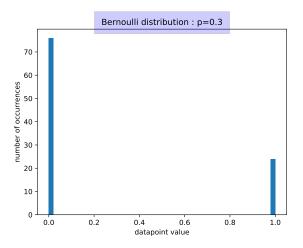


Figure: Historgram 2

### Uniform continuous

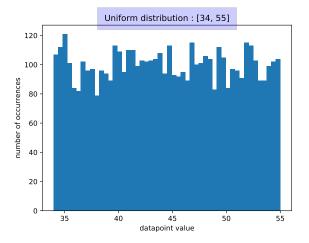


Figure: Historgram 3

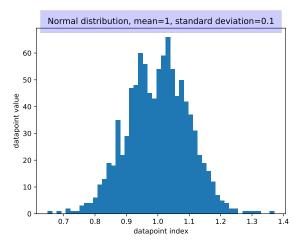


Figure: Historgram 4

Exercice 3 : Analyzing a distribution I put values in the file **mysterious\_distro\_1.csv** 

#### Exercise

Exercice 4: Analyzing a distribution I put values in the file mysterious\_distro\_1.csv
Can you analyze these values in terms of a distribution?
Use read\_myst\_1.py to analyze the distribution (suggestion: change the number of bins used)

#### Exercise

When you have guessed the kind of distribution it is, you need to finds its **parameters**.

- its mean
- its standard deviation

This is called **fitting** a distribution to a dataset : it's a classical machine learning problem.

To do so, uncomment the last section of the script read\_myst\_1

## Distribution 1

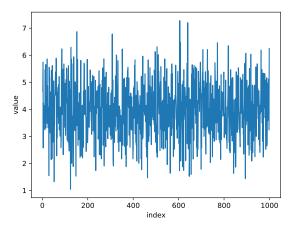


Figure: The data we analyze

# histograms

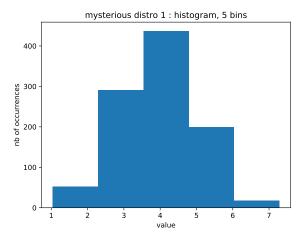


Figure: 5 bins

# histograms

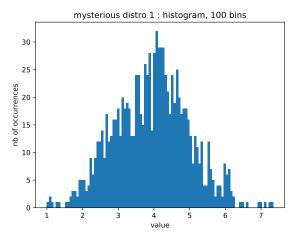


Figure: 100 bins

# histograms

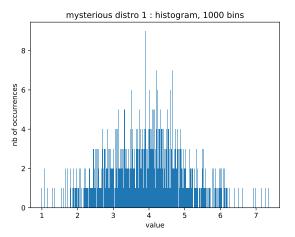


Figure: 1000 bins (too many)

#### Normal distribution

```
import csv
import numpy as np

file_name = 'mysterious_distro_1.csv'

mean = 4

std_dev = 1
nb_point = 1000

with open('csv_files/' + file_name, 'w') as csvfile:
    filewriter = csv.writer(csvfile, delimiter=',')
    for point in range(1, nb_point):
        random_variable = np.random.normal(loc=mean, scale=std_dev)
        filewriter.writerow([str(point), str(random_variable)])
```

Figure: create\_normal.py : Creation of the distribution

# Second example

Let's try to perform the same analysis on the file **mysterious\_distro\_2.csv** using **read\_myst\_1**.

# Second example

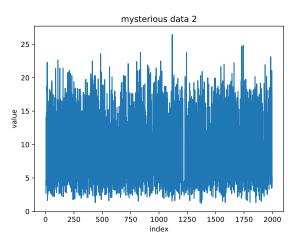


Figure: Second distribution

### Multimodal distribution

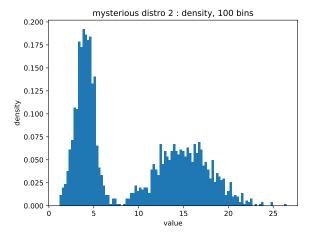


Figure: This distribution has several modes

#### Multimodal distribution

```
mean_1 = 4
std_dev_1 = 1
nb_point_1 = 1000

mean_2 = 15
std_dev_2 = 3
nb_point_2 = 1000

nb_point = nb_point_1 + nb_point_2

with open('csv_files/' + file_name, 'w') as csvfile:
    filewriter = csv.writer(csvfile, delimiter=',')
    for point in range(1, nb_point):
        if random.randint(1, 2) == 1:
            random_variable = np.random.normal(loc=mean_1, scale=std_dev_1)
            filewriter.writerow([str(point), str(random_variable]])
        else:
            random_variable = np.random.normal(loc=mean_2, scale=std_dev_2)
            filewriter.writerow([str(point), str(random_variable]])
```

Figure: create\_bimodal.py : Generation of multimodal distribution

# **Fitting**

In most cases, it won't be that straightforward to fit a distribution :

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In most cases, it won't be that straightforward to fit a distribution .

- what distribution do we want to use ?
- even if we know the right shape of the distribution, how to choose the parameters ?

The **Maximum Likelihood** method is one example method used in Machine Learning.

Say you have a dataset  $(x_1, ..., x_n)$ .

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You first need to choose a **model** (which is the distribution) of your dataset, p.

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Say you have a dataset  $(x_1, ..., x_n)$ .

You first need to choose a **model** (which is the distribution) of your dataset, p.

Then, you must optimize the **parameters of this model**, noted  $\theta$ .

The Likelihood of your model is

$$L(\theta) = \prod_{i=1}^{n} p(x_i | \theta)$$
 (1)

The Likelihood of your model is

$$L(\theta) = \prod_{i=1}^{n} p(x_i | \theta)$$
 (2)

This is the function that you want to **maximise**.

Most of the time it's written this way : "minimise  $-logL(\theta)$ " Why ?

Most of the time it's written this way : "minimise  $-logL(\theta)$ " Because the log **transforms the product into a sum**, which is easier to **derivate**.

$$-logL(\theta) = -\sum_{i=1}^{n} \log(p(x_i|\theta))$$
 (3)

#### Max Likelihood

So how can we minimise  $-logL(\theta)$ ? In the case of very large datasets, and large numbers of parameters (tens, hundredths, more), most of the time an **analytic solution** is not available. So people use **gradient descent**.

## The gradient descent

We want x to **minimise** f. We perform, until some criteria is satisfied :

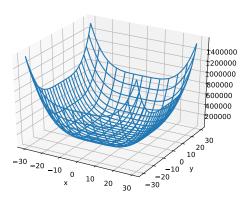
$$x \leftarrow x - \alpha \nabla_f(x) \tag{4}$$

Use the file "gradient\_algo.py" and implement the gradient algorithm on a simple example.

I inserted two errors in the code.

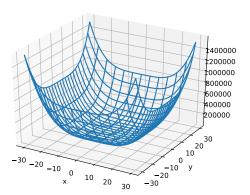
# The gradient descent

$$x \leftarrow x - \alpha \nabla_f(x) \tag{5}$$



## The gradient descent

Experiment with it, try to change all the parameters and to break it again. Is it stable ?



#### Multidimensional vectors

We can consider data that live in higher dimensional spaces than 2.

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We can consider data that live in higher dimensional spaces than

- 2. Examples ?
  - images
  - sensor that receives multimodal information

#### Correlation

Sometimes the components of a multidimensonial vector  $(x_1,...,x_n)$  are not independent.

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To study this, we can use the **covariance** of the two components, or the **correlation** which is actually clearer.

## Example

Look at the data contained in **mysterious\_distro\_3.csv**They contain a random variable with 5 dimensions. Some of these dimensions are correlated.

Think for instance to physics: temperature and pressure, etc. If you have measurements of temperature and pressure, the two would probably be **correlated**.

### Correlation matrix

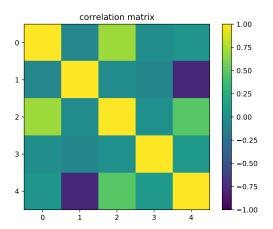


Figure: Correlation matrix for the distribution

#### Generation of the data

```
mean 1 = 4
std \overline{\text{dev }} 1 = 1
mean 2 = 15
std \overline{\text{dev }} 2 = 3
mean 3 = -5
std dev 3 = 2
mean noise = 0
noise std dev = 1
nb point = 1000
with open('csv_files/' + file_name, 'w') as csvfile:
    filewriter = csv.writer(csvfile, delimiter=',')
    for point in range(1, nb_point):
        noise = np.random.normal(loc=mean noise. scale=noise std dev)
        random variable 1 = np.random.normal(loc=mean 1, scale=std dev 1)
        random variable 2 = np.random.normal(loc=mean 2, scale=std dev 2)
        random variable 3 = random variable 1 + noise
        random_variable_4 = np.random.normal(loc=mean_3, scale=std_dev_3)
        random_variable_5 = -0.4 * random_variable_2 + noise
        filewriter.writerow([str(point),
                              str(random variable 1).
                              str(random variable 2),
                              str(random variable 3).
                              str(random variable 4),
                              str(random variable 5)1)
```

Figure: Multidimensional random variable

# Kmeans clustering

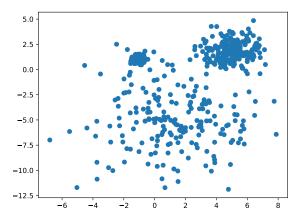


Figure: Data we want to cluster

# Kmeans clustering

Modify the **kmeans.py** file so that it performs the kmeans algorithm.

I inserted two errors in the code.

You should obtain something like this:

#### **Kmeans**

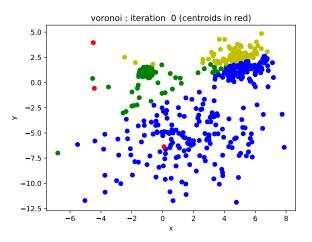


Figure: Voronoi 0th iteration

#### **Kmeans**

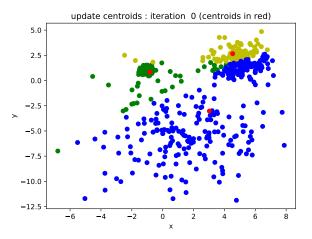


Figure: Centroids 0th iteration

### **Kmeans**

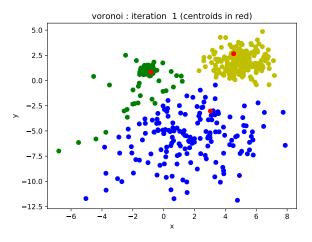


Figure: Voronoi 1st iteration

### **Kmeans**

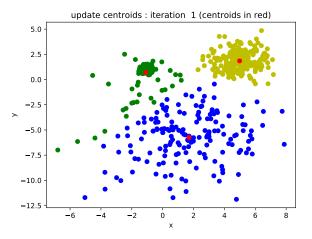


Figure: Centroids 1st iteration

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- But sometimes you do not have access to a distance between the points.

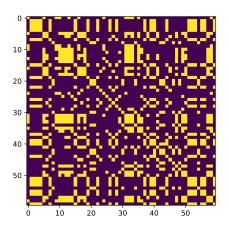
- ► The kmeans were based on a notion of **distance between points**
- But sometimes you do not have access to a distance between the points.
- You might need to work with something that is more general, for instance a similarity.

- ▶ When working with distances, two points that "look the same" should be separated by a **small distance** .
- ► When working with a similarity, two points that "look the same" should have a **high similarity**.

# Example of similarity: adjacency

- ► An example of similarity is the relationship of **adjacency**.
- ▶ If *i* and *j* are related by an edge,  $S_{ij} = 1$ .
- ▶ Otherwise  $S_{ij} = 0$ .

# Adjacency matrix



Differences between similarities and distances:

▶ A similarity *S* is not always symmetrical.

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- ▶ A similarity *S* is not always symmetrical.
- ▶ Indeed, in a **directed graph**, having a directed edge between *i* and *j* does not mean that we have an edge between *j* and *i*.

Differences between similarities and distances:

- ▶ A similarity *S* is not always symmetrical.
- ▶ Indeed, in a **directed graph**, having a directed edge between *i* and *j* does not mean that we have an edge between *j* and *i*.
- ▶  $S_{ij} = 0$  does not mean that i = j, it is rather the contrary.

► A similarity is a more general notion than a distance. Given a similarity between two points, we can deduce a similarity.

- ▶ A similarity is a more general notion than a distance. Given a similarity between two points, we can deduce a similarity.
- ▶ For instance this way, if  $d_{ij}$  is the distance between i and j:

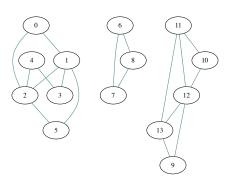
$$S_{ij} = \exp(-d_{ij}) \tag{6}$$

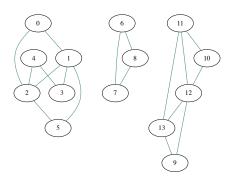
# Spectral Clustering

- ► A clustering method that works with similarities
- ► It performs a low dimensional embedding of the similarity matrix, followed by a Kmeans

### Exercise

We will perform Spectral Clustering on this graph :





Please **cd spectral\_clustering** and use **vanilla\_spectral\_clustering** in order to apply spectral clustering. You first need to input to right **affinity matrix** or **similarity matrix** and then use the **sklearn** library. You also need to **tune the number of clusters.** 

doc: check the sklean page for Spectral Clustering,

# Spectral clustering

Can you guess some drawbacks of the method?

# Spectral clustering

Can you guess some drawbacks of the method?

- Need to provide the number of clusters.
- Not adapted to a large number of clusters.
- kmeans step : so depends on a random initialization.

### Heuristic

► We would like a critetion in order to justify the number of clusters used.

# Normalized cut: a measurement of the quality of a clustering

- ► The cut of a cluster is the number of outside connections (connections with other clusters).
- ▶ The **degree** of a node is its number of adjacent edges
- ► The degree of a cluster is the sum of the degrees of its nodes.
- ▶ The **normalized cut** of a clustering is:

$$NCut(C) = \sum_{k=1}^{K} \frac{Cut(C_k, V \setminus C_k)}{d_{C_k}}$$
 (7)

### Normalization

► The normalization is useful in order to take the **weight** (degree) of a cluster into account.

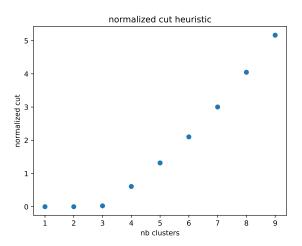
# Normalized cut and clustering

Let's see how the normalized cut can help us choose the right number of clusters (backboard).

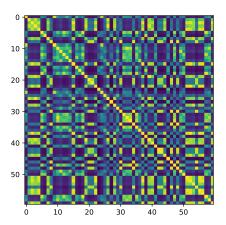
### Exercise: normalized cut elbow

Please use the criterion in the file  $normalized\_cut$  in order to guess the relevant number of clusters in order to process the data contained in data/

### Normalized cuts



# Similarity



### Example

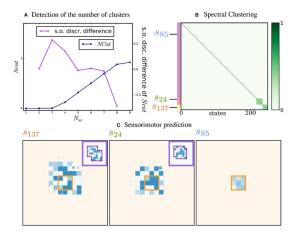


Figure: In a), the elbow method is used to choose the number of clusters. [Le Hir et al., 2018]

# Other methods to evaluate the quality of a clustering

- ▶ Stability of the result when lauching the algorithm many times
- Separation of the clusters (the mean distance between pairs of centroids is large)
- ▶ Ratio inter / intra
- Silhouette coefficient.

## Other interesting notions

- Agglomerative clustering (CHA : classification Hirarchique Ascendante)
- Xmeans : improvement of k means
- ▶ If you know more about probabilities or are curious :
  - Latent variables and variational learning
  - Auto Encoders
  - Boltzmann Machines

### Conclusion

#### Different kinds of problems exist:

- P problems where exact polynomial solutions exist (max matching)
- For other problems :
  - exhaustive search works but is too slow
  - to solve the problem a balance between rapidity and quality must be found.
- Evaluating the quality of a result is not an easy task.

# **Project**

Desciption of the project

# Questions?

### References



Le Hir, N., Sigaud, O., and Laflaquière, A. (2018). Identification of Invariant Sensorimotor Structures as a Prerequisite for the Discovery of Objects. *Frontiers in Robotics and AI*, 5(June):1–14.