

Algorithms

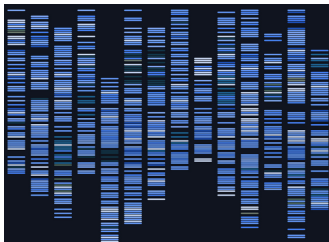
Clustering

Emanuele Rodolà
rodola@di.uniroma1.it



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Example: Discover groups of genes with similar functions, regardless of their particular role.



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What is a “good cluster”?
What does it mean to be “similar”?

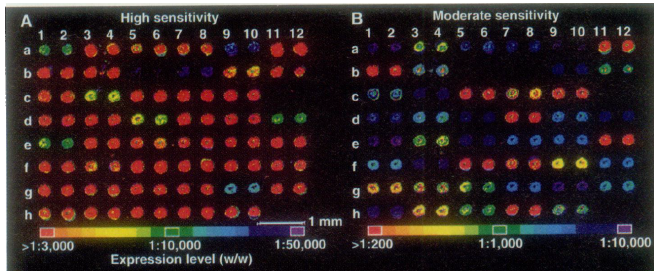
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expression matrix: each number is some measured **intensity**

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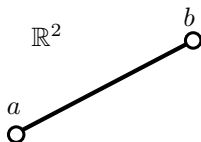
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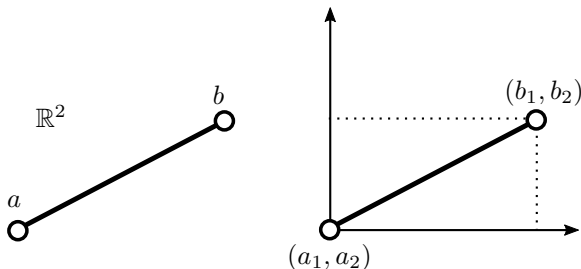


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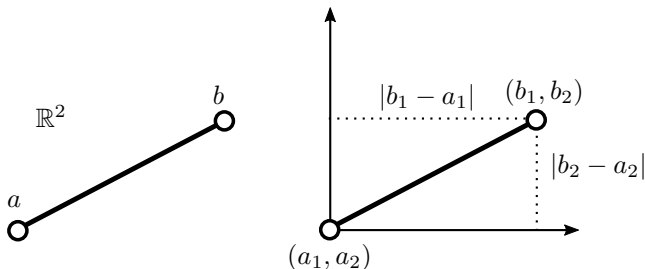


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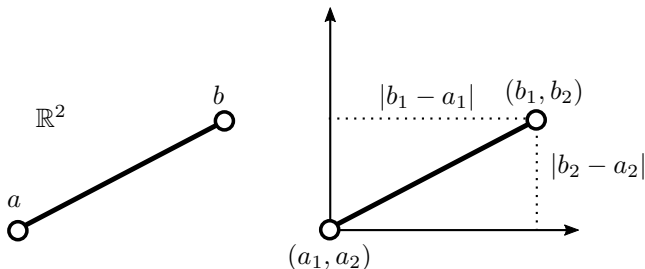


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Pythagoras' theorem: $d(a, b) = (|b_1 - a_1|^2 + |b_2 - a_2|^2)^{\frac{1}{2}}$

L_p distance

One can generalize to different power coefficients $p \geq 1$:

$$\begin{aligned} & (|a_1 - b_1|^2 + |a_2 - b_2|^2)^{\frac{1}{2}} \\ & \quad \Downarrow \\ & (|a_1 - b_1|^{\textcolor{red}{p}} + |a_2 - b_2|^{\textcolor{red}{p}})^{\frac{1}{\textcolor{red}{p}}} \end{aligned}$$

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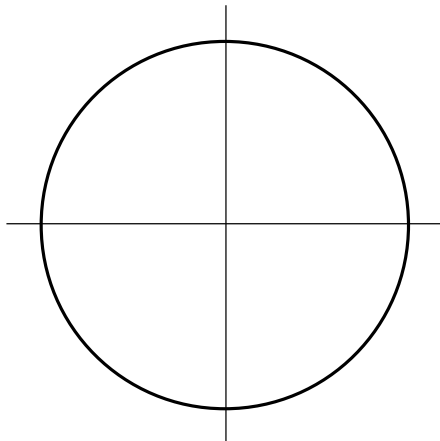
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This definition gives us the L_p distance between points in \mathbb{R}^k .

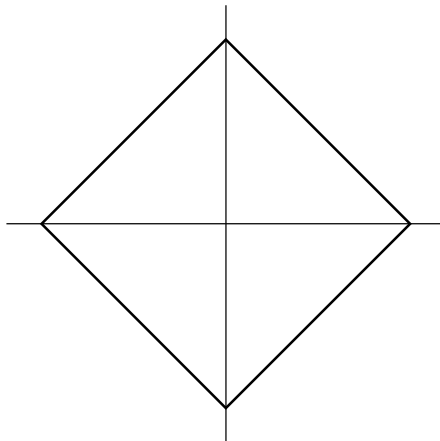
L_p unit balls in \mathbb{R}^2

For $p = 2$, we get the usual intuitive idea of a circle:



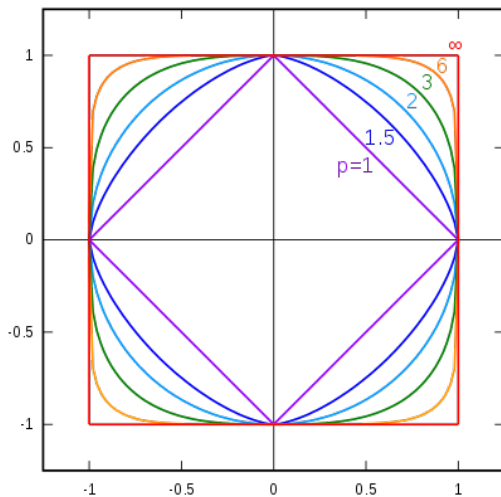
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For $p = 1$, we get a diamond-shaped boundary:



L_p unit balls in \mathbb{R}^2

For general $p \geq 1$, we get a general notion of “ball”:



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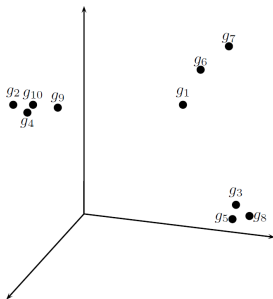
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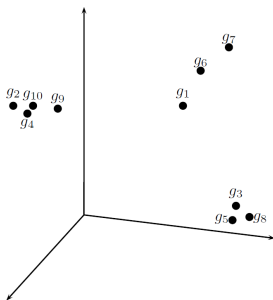
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Let us look at the L_2 distances between each pair of genes:

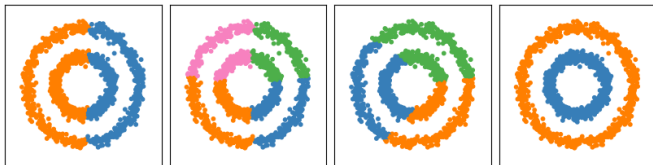


	g_1	g_2	g_3	g_4	g_5	g_6	g_7	g_8	g_9	g_{10}
g_1	0.0	8.1	9.2	7.7	9.3	2.3	5.1	10.2	6.1	7.0
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distance matrix

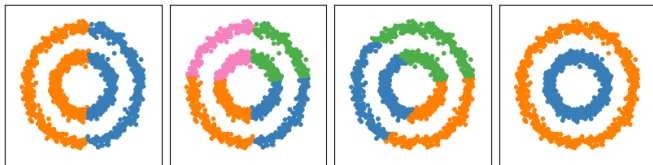
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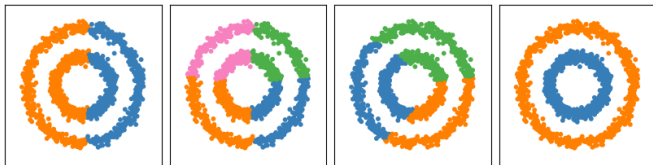


We need to define a quality criterion.

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Also: **how many** clusters do we want to find?

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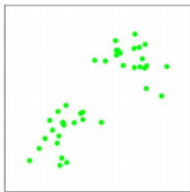
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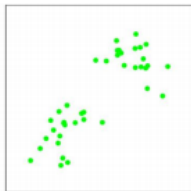
Termination criterion: For example, when the centroids stop changing.

k -means algorithm: Example

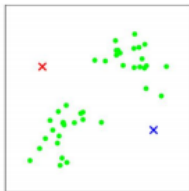


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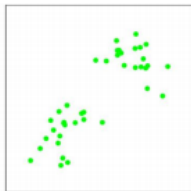


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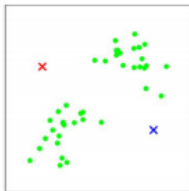


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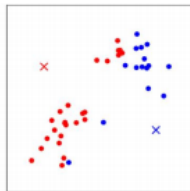
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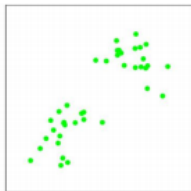


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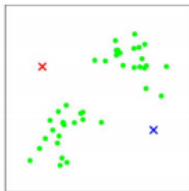


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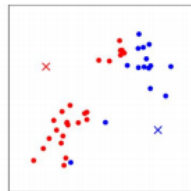
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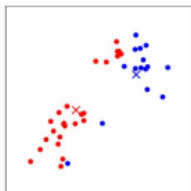
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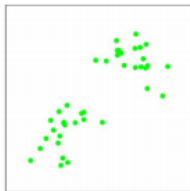


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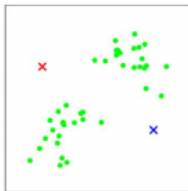


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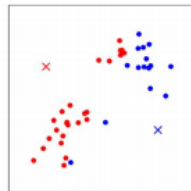
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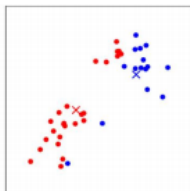
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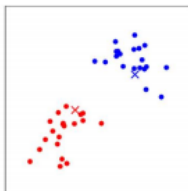
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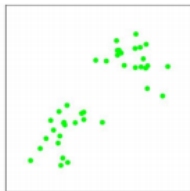


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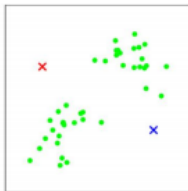


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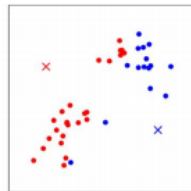
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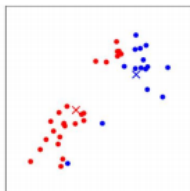
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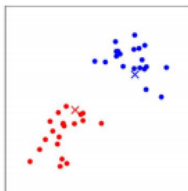
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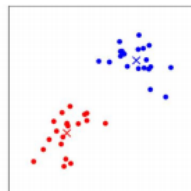
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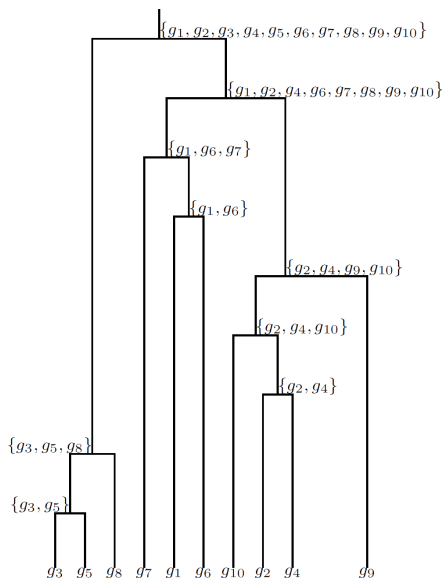
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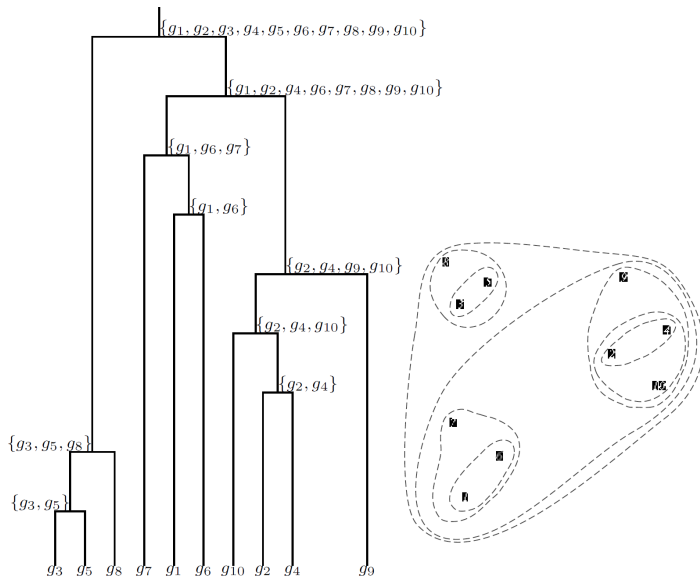
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Termination: Check if the cluster assignment does not change anymore, or if centroids stop moving significantly.

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- In general, the i -th cluster combines the two closest clusters from the $(i - 1)$ -th cluster.

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At the end, we have one large cluster that contains all the others.

Exercises

Implement the k -means clustering algorithm.

Test for different values of k with the given data (see course webpage).

Send me your code + some screenshots of your results.

Suggested reading

Chapters 10.1, 10.2 and 10.3 of:

“An Introduction to Bioinformatics Algorithms”, Jones and Pevzner