

Advanced Topics on Algorithms  
2025/2026

# Clustering is Hard Only When it Doesn't Matter

Lecturer: Alessandro Straziota

In previous episodes...

Why do we need algorithm analysis?

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1. Performance Prediction

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But FWF is clearly worse than LRU!

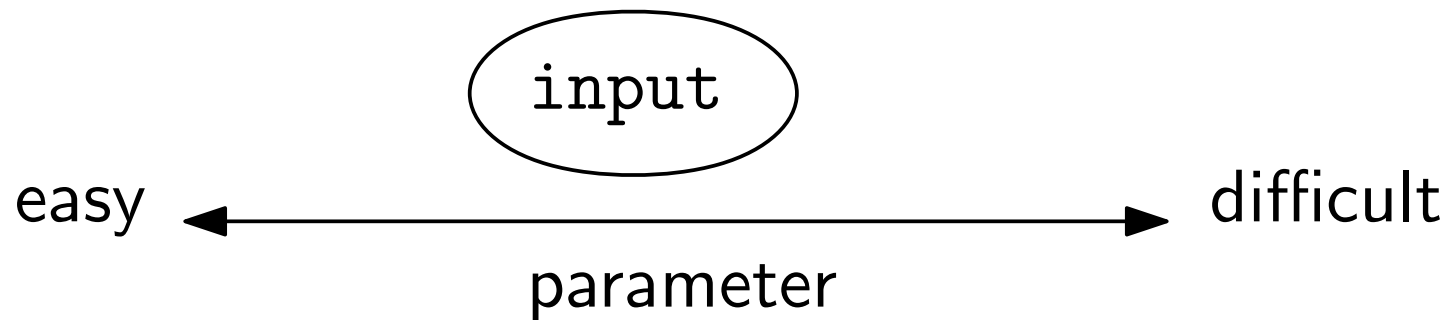
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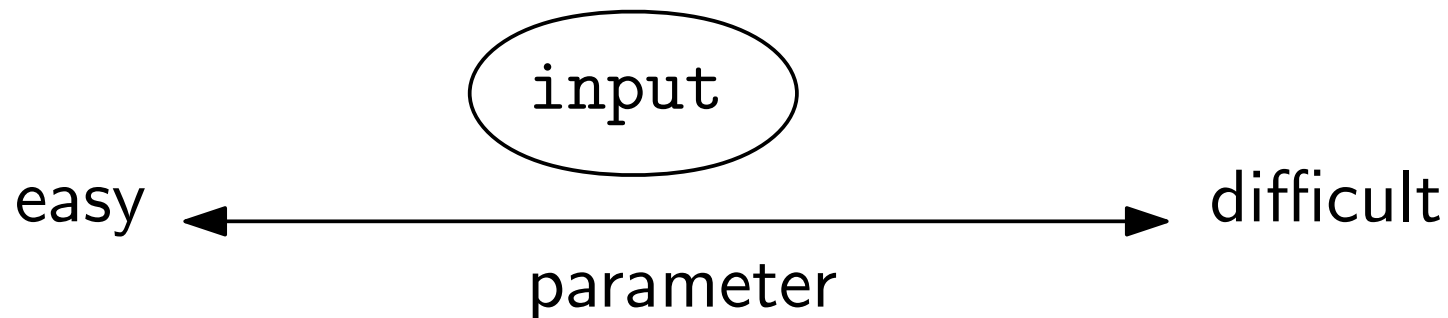
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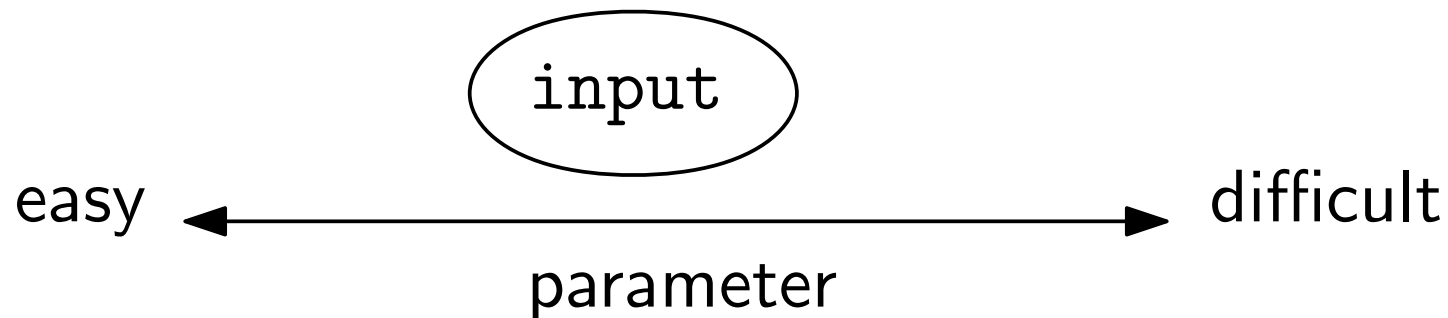


**Example (Working Set Model):** the maximum number of **distinct** page requests in every window length  $w$ .

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**Example (Working Set Model):** the maximum number of **distinct** page requests in every window length  $w$ .

**Claim.** LRU has a **page fault rate** strictly lower than FIFO.

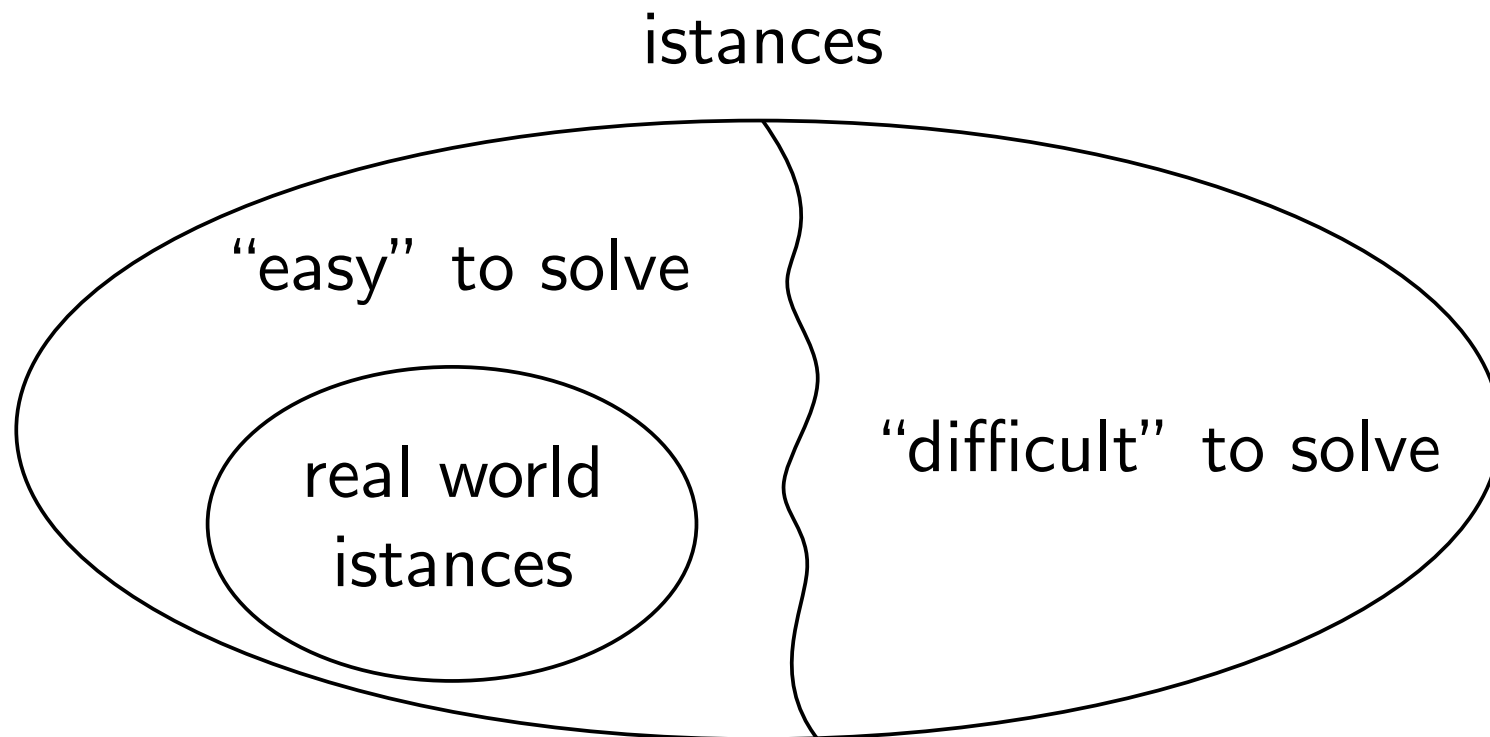
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**Insight:** in most applications we only care about instances in which there is a “meaningful solution”, that are computationally easier to solve than worst-case instances.

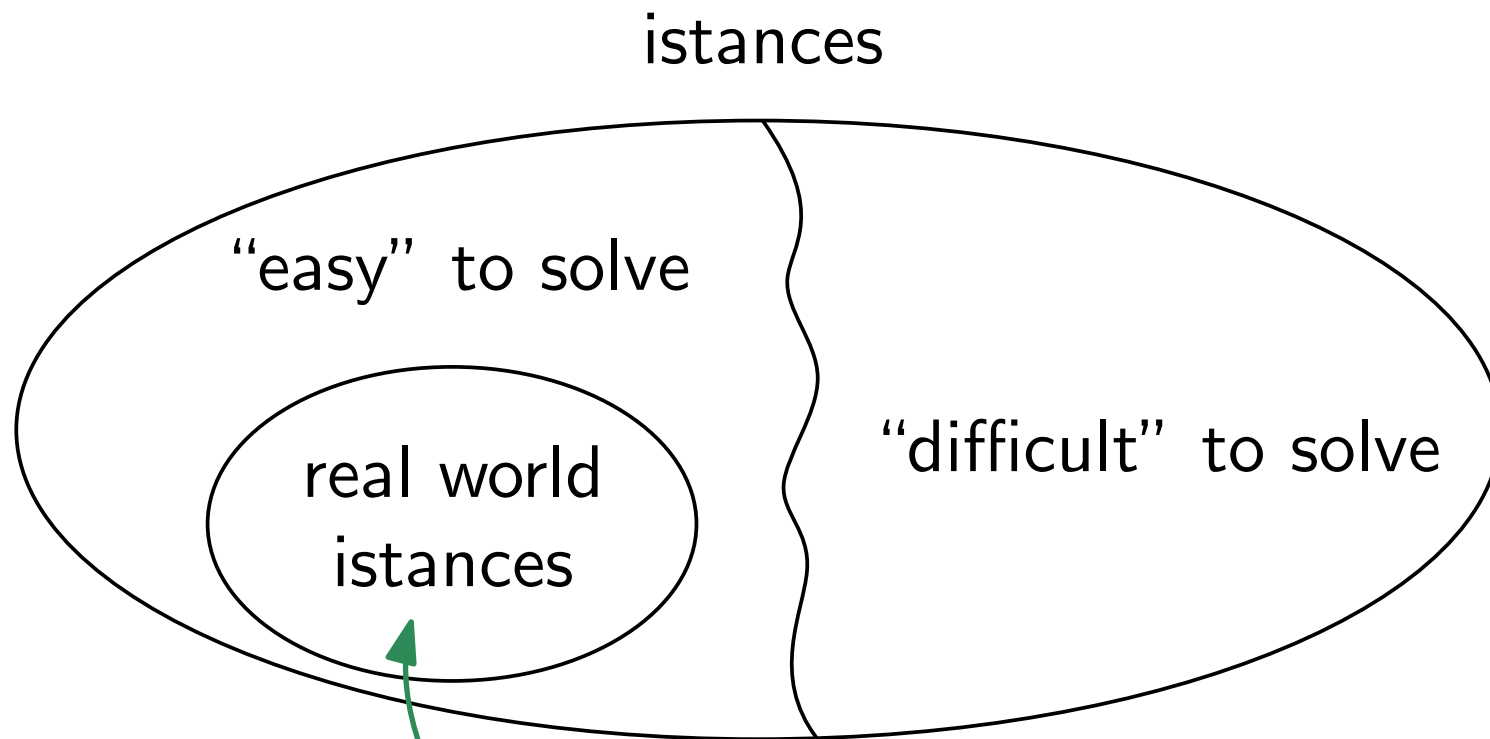
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we are interested in analyzing  
the algorithms here

Beyond Worst-Case Analysis  
Episode III

Clustering is Hard Only When it  
Doesn't Matter

# Clustering

**Input:** a set of data.

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documents



figures



genomes

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**Goal:** group homogeneous data into sets (**clusters**) based on their similarity.

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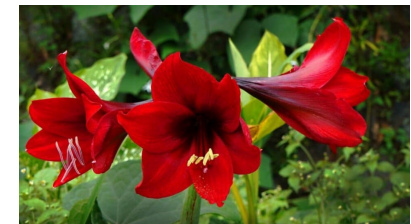
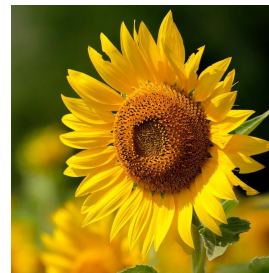
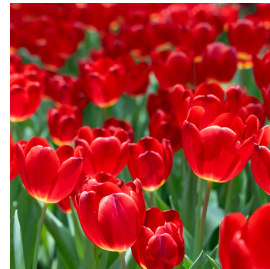


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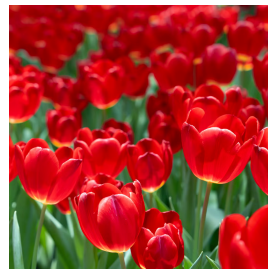
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Cluster 1



Cluster 2



Cluster 3



# Clustering

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... and this?

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... and what about this ???

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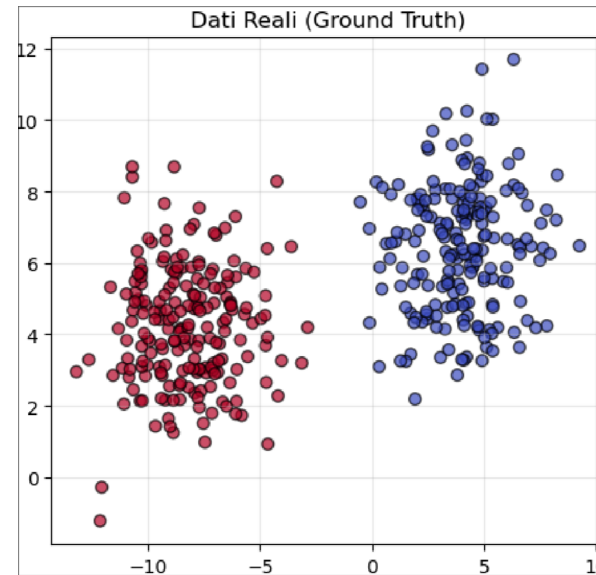
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vector representation

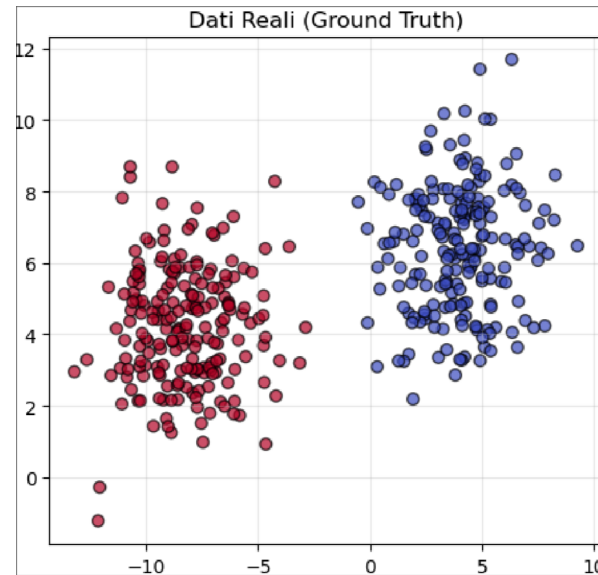
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**Distance function:**  $d : \mathcal{M} \times \mathcal{M} \rightarrow \mathbb{R}^+$  such that

- $d(x, x) = 0$
- $d(x, y) = d(y, x)$
- $d(x, y) \leq d(x, z) + d(z, y)$

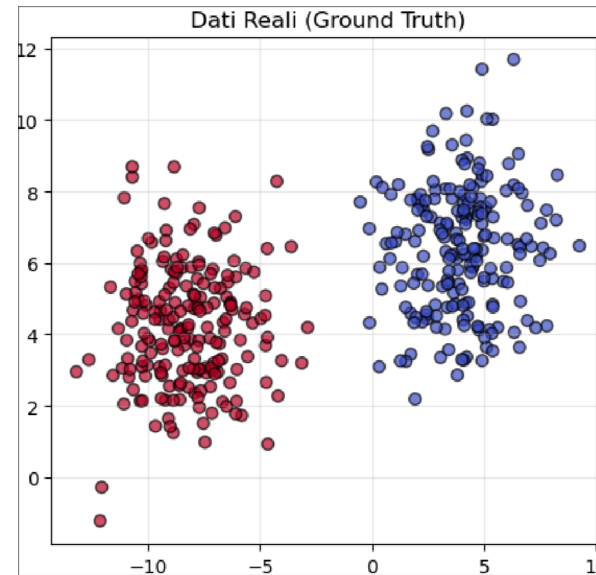
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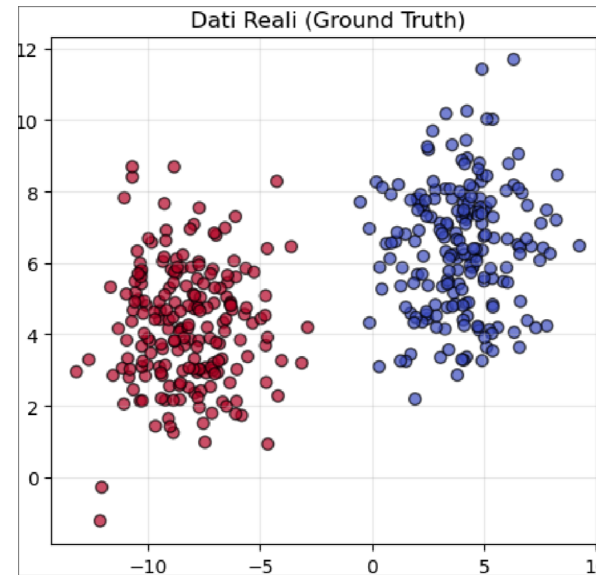
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Through an optimization problem!

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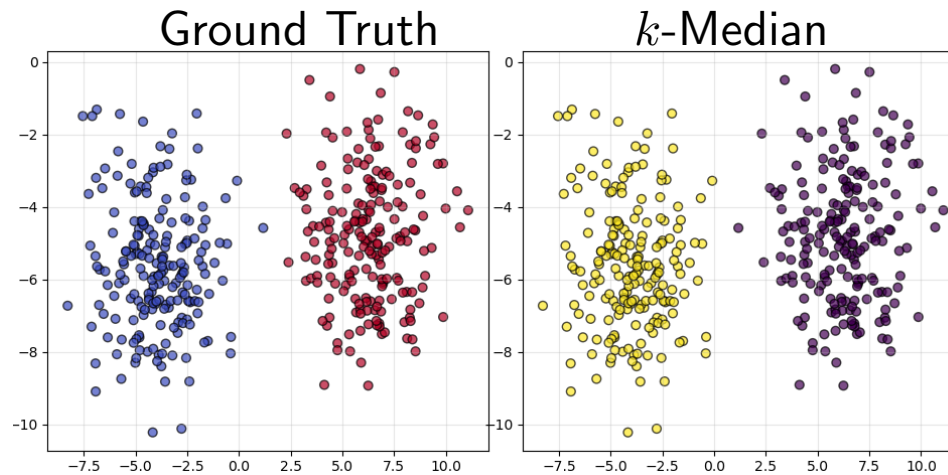
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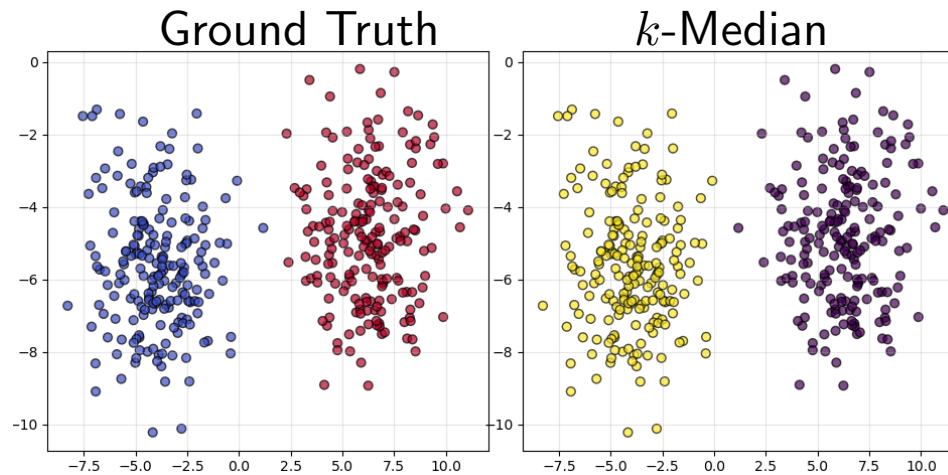
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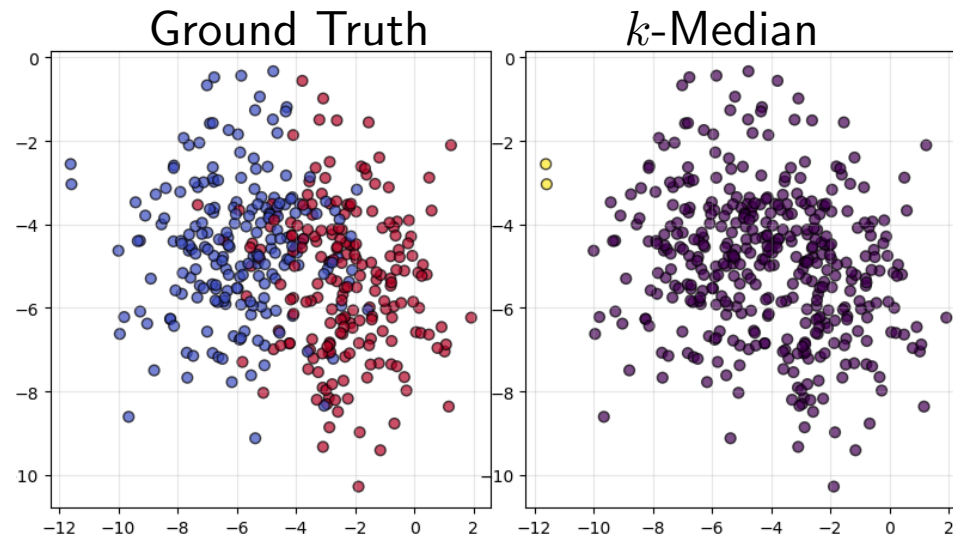


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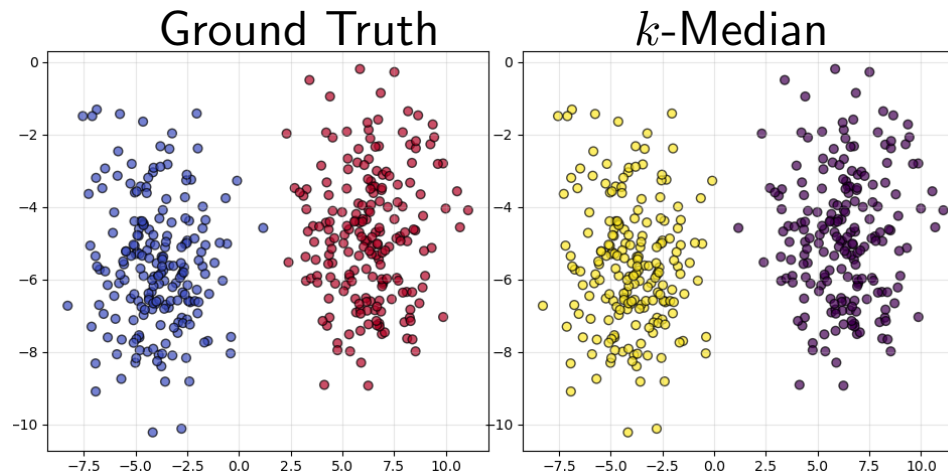


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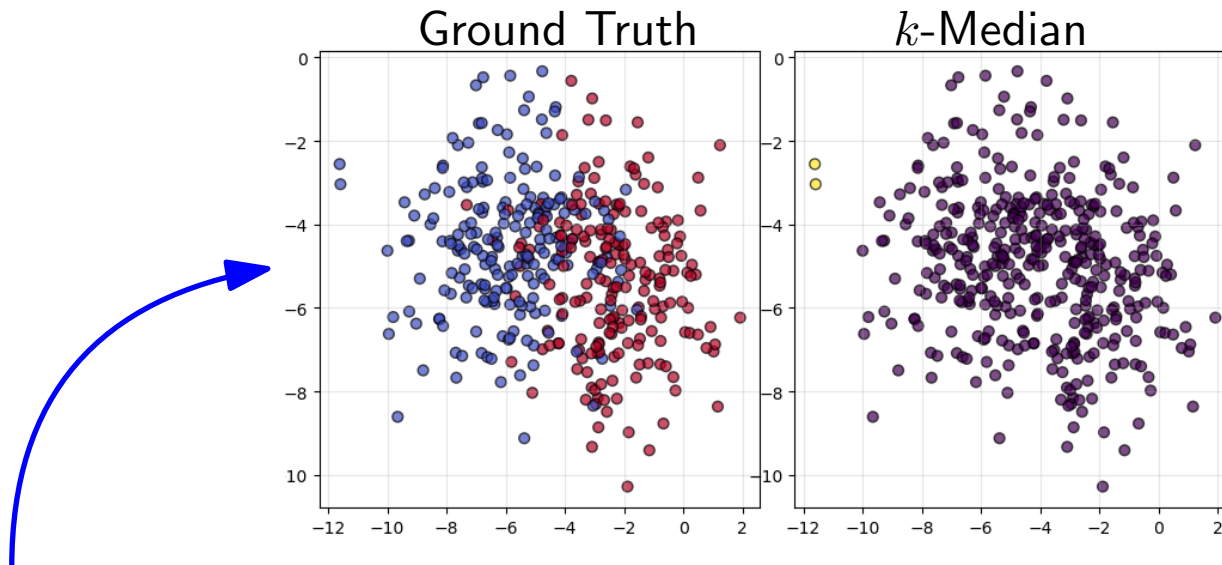


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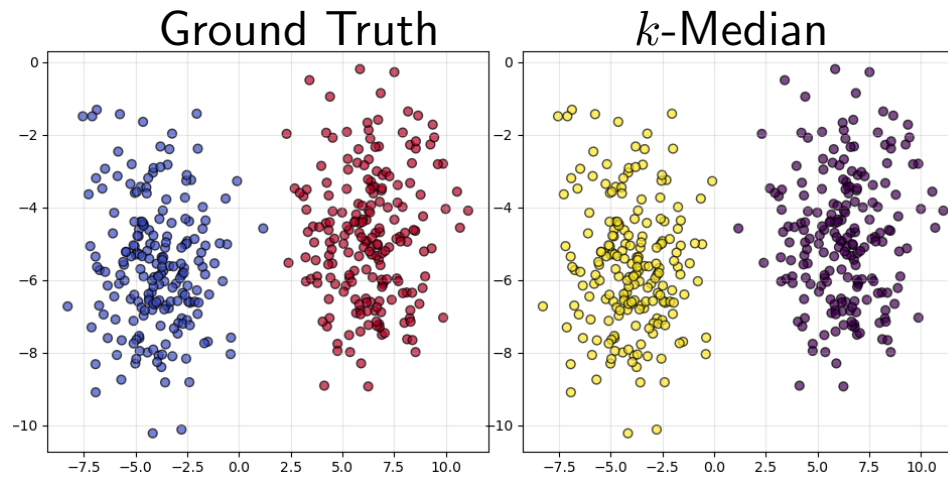
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**Good news:** it's not an interesting case :)

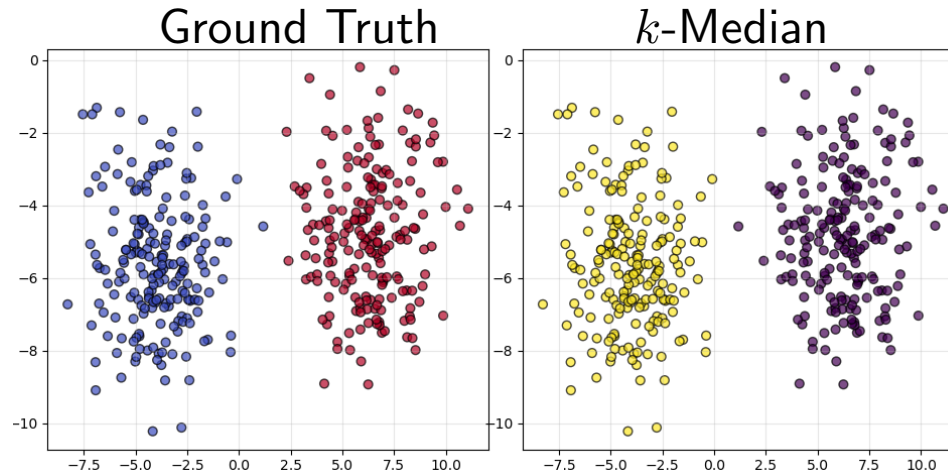
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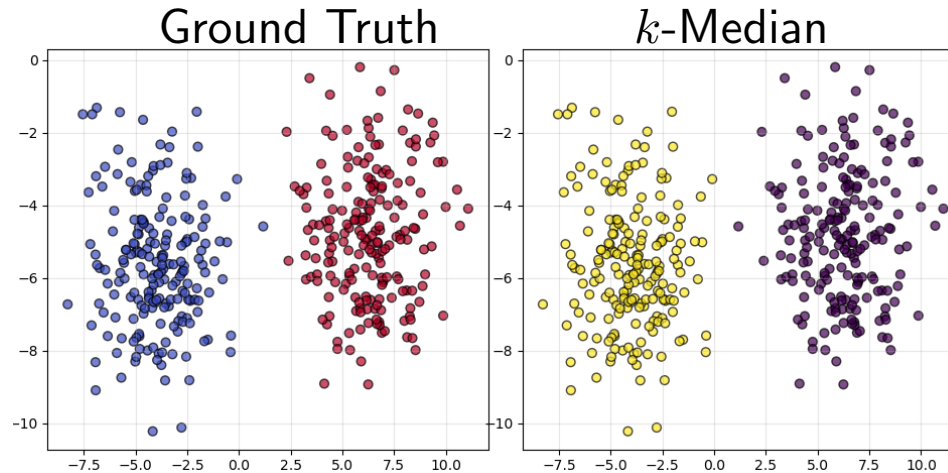
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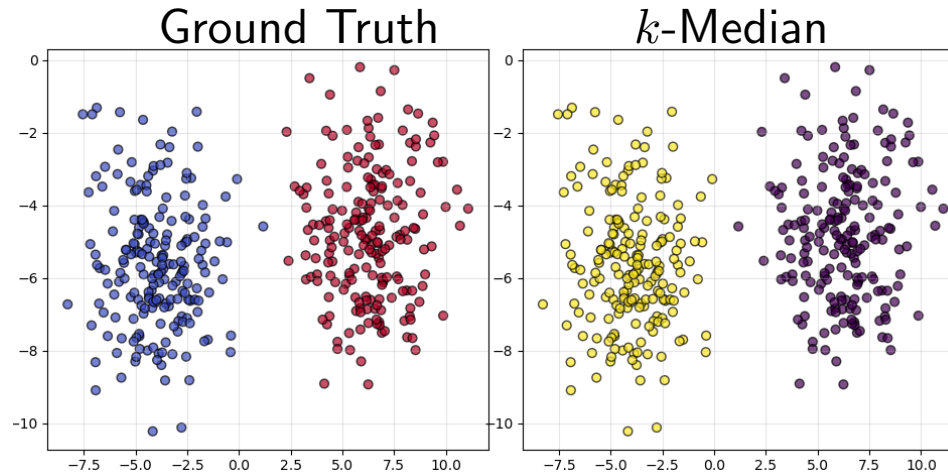


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clustering is hard only when it doesn't matter!

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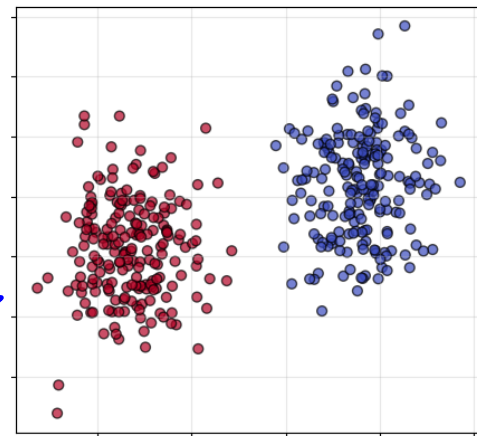
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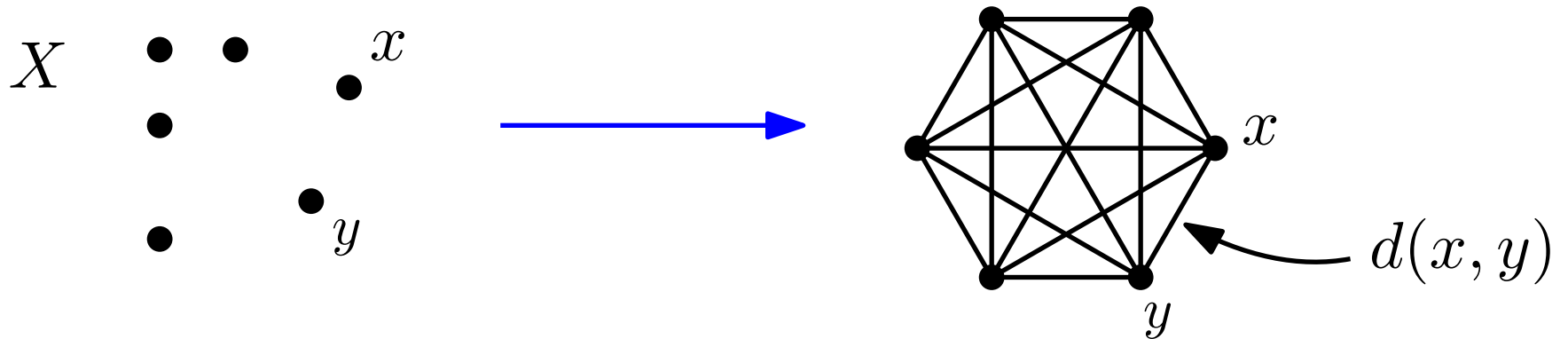
**Intuition:** the clusters are well separated, so even changing the metric (provided it is not too different) the solution  $S^*$  remains optimal (and unique).

interesting instance



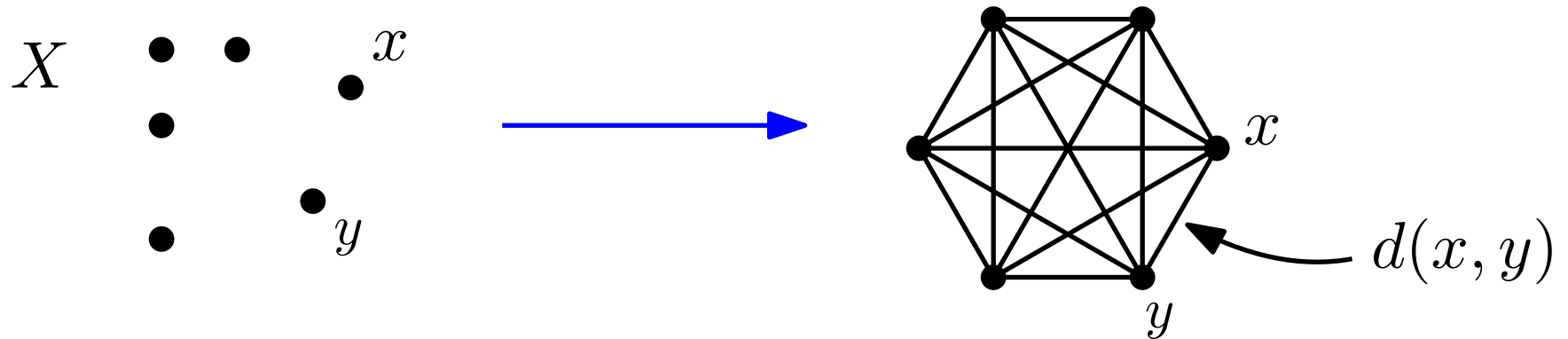
# Single-Link Algorithm

Step 1. Think the input  $(X, d)$  as a complete graph with vertices  $X$  and edge weights given by  $d$ .

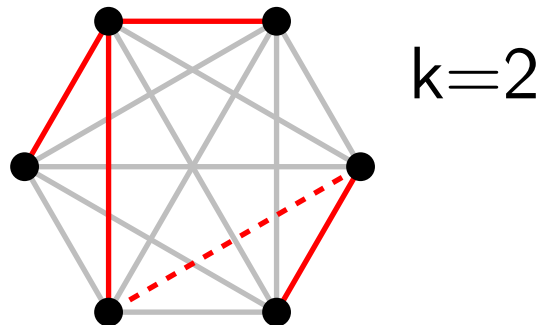


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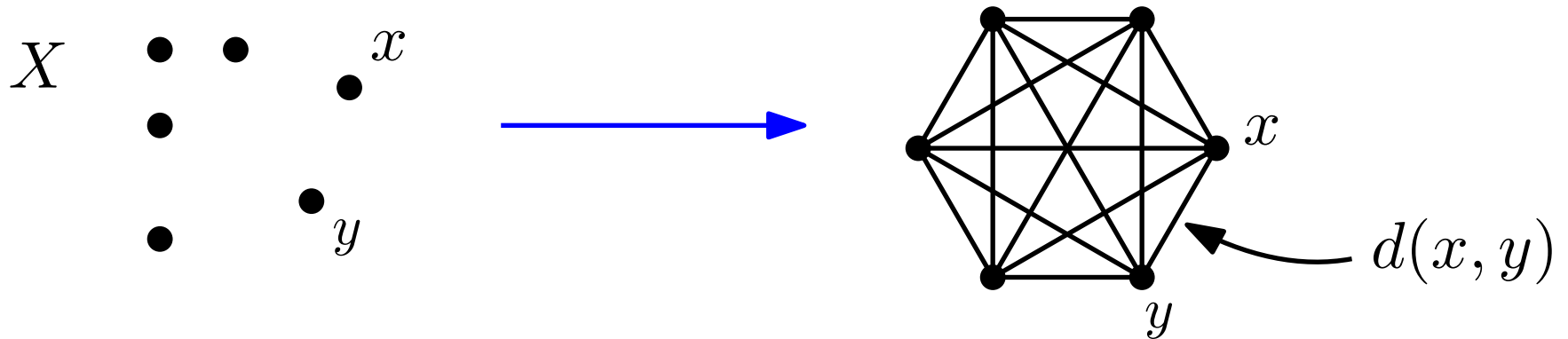


**Step 2.** runs Kruskal's minimum spanning tree (MST) algorithm, but stop when there are  $k$  connected components. That is, we skip the final  $k - 1$  edge additions of Kruskal's algorithm.

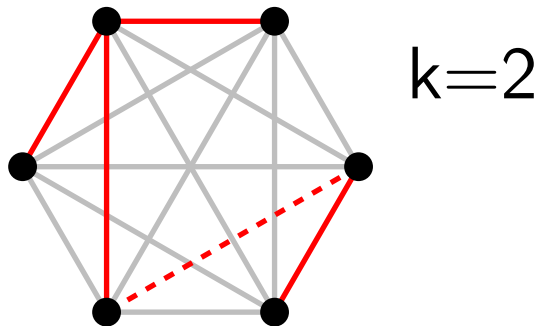


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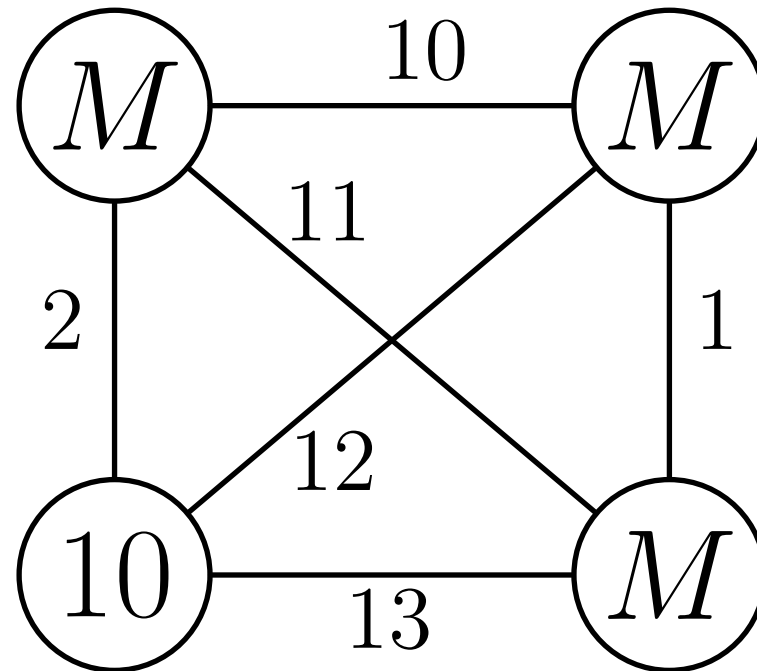


Does it give a good solution?

# Counterexample

$$k = 3, M \gg 10$$

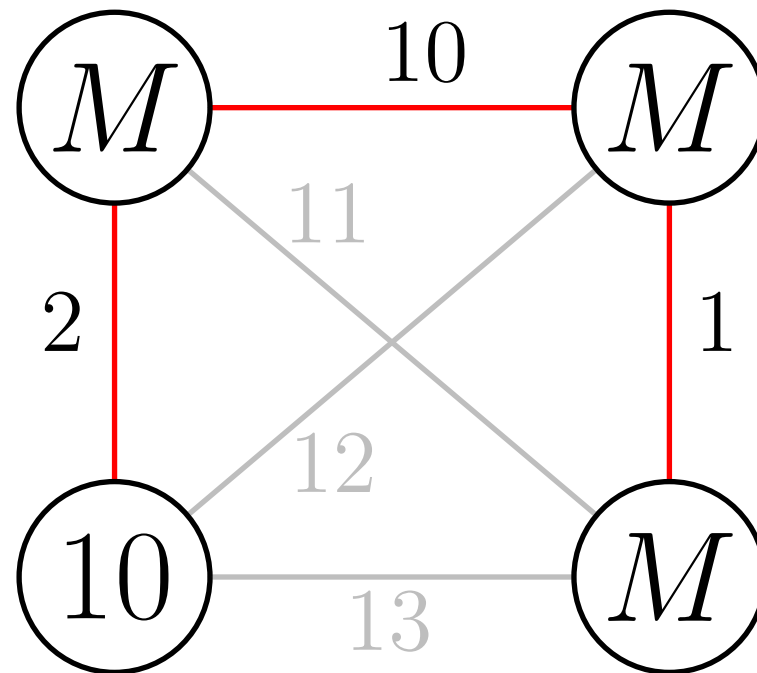
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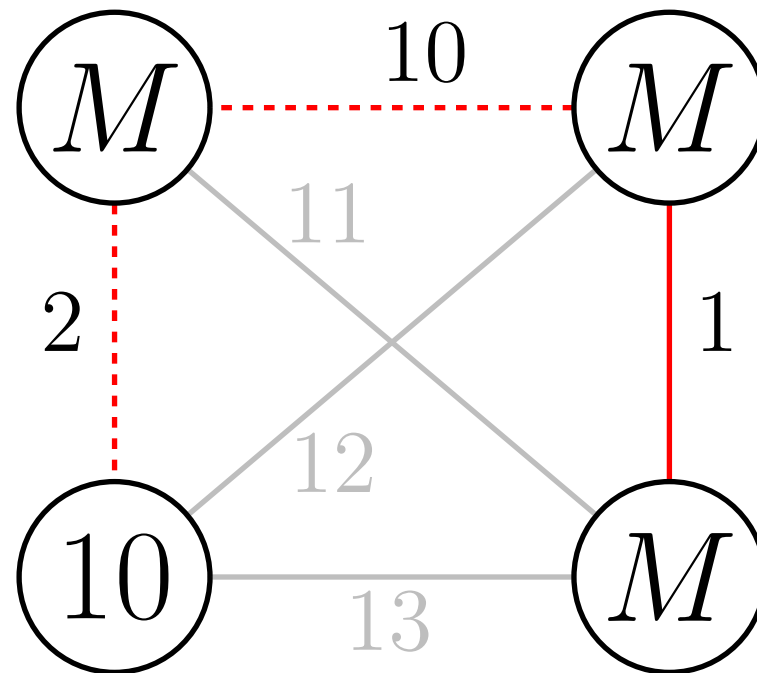
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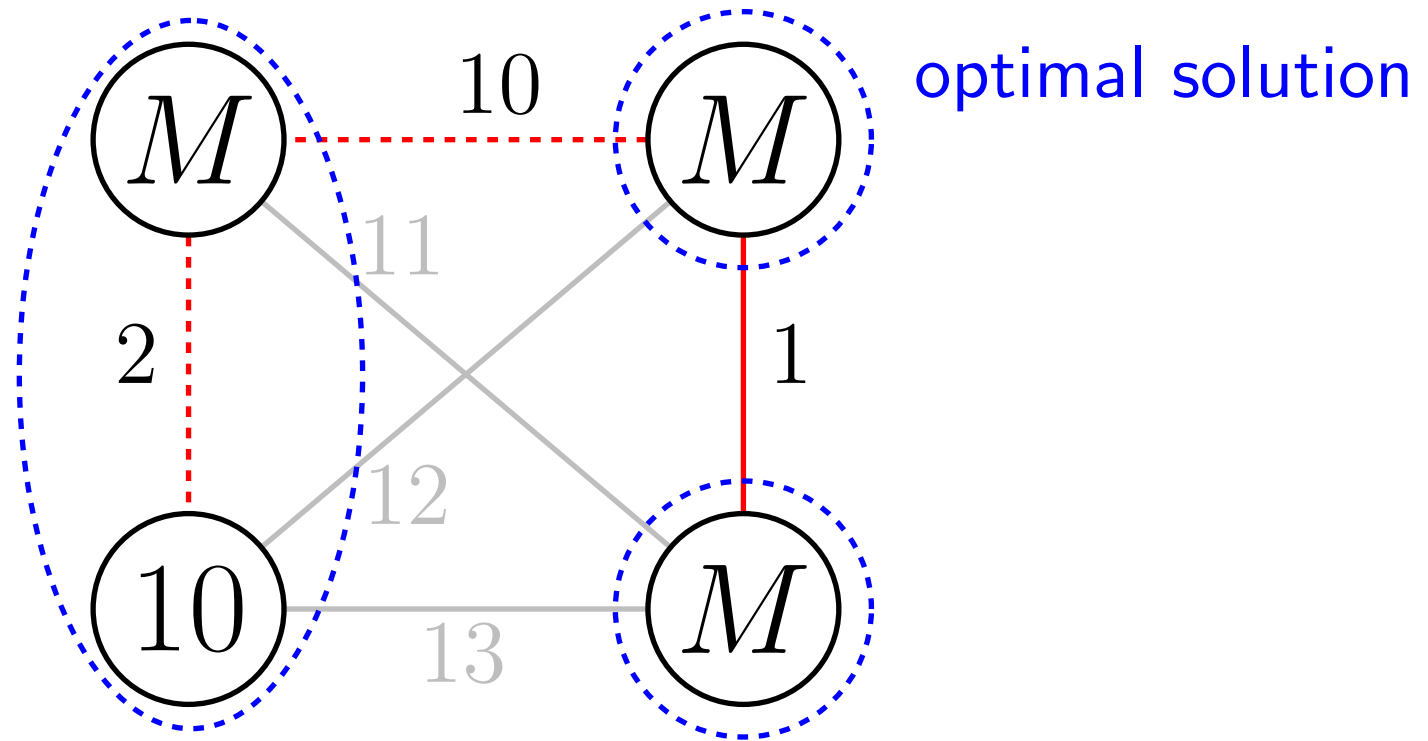
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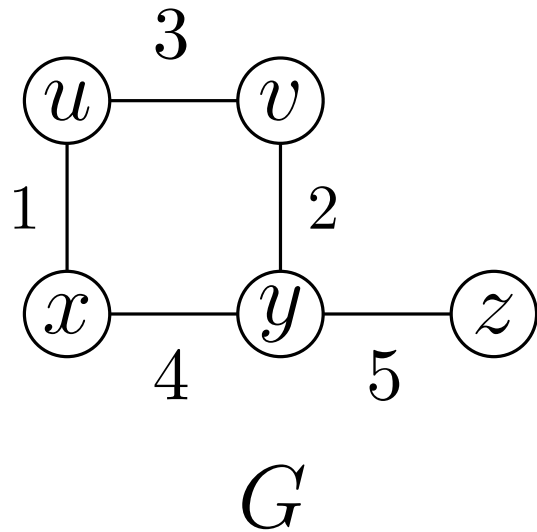
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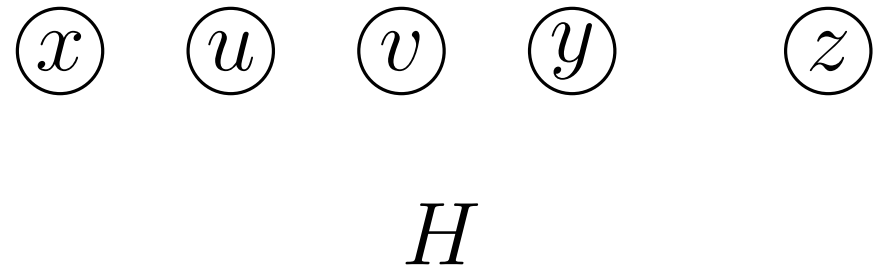
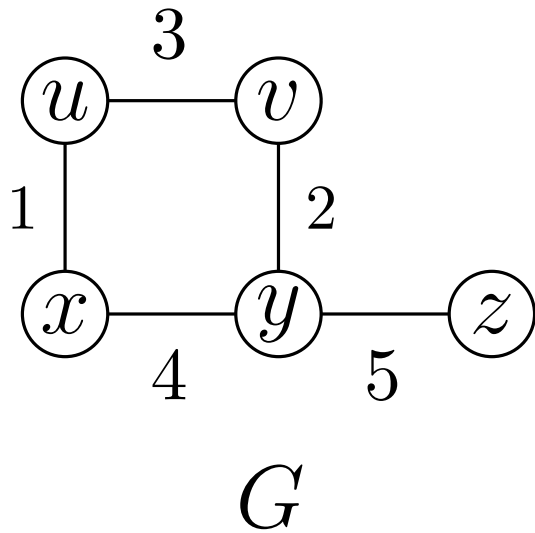
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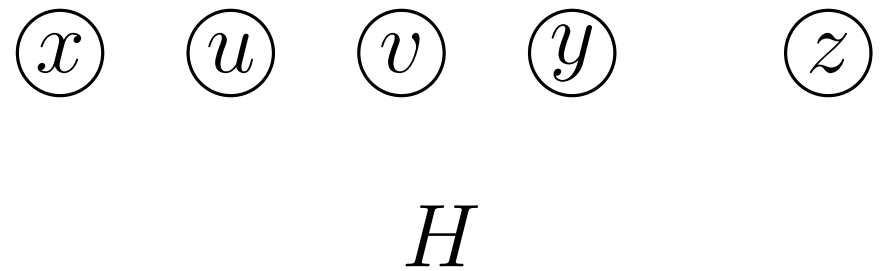
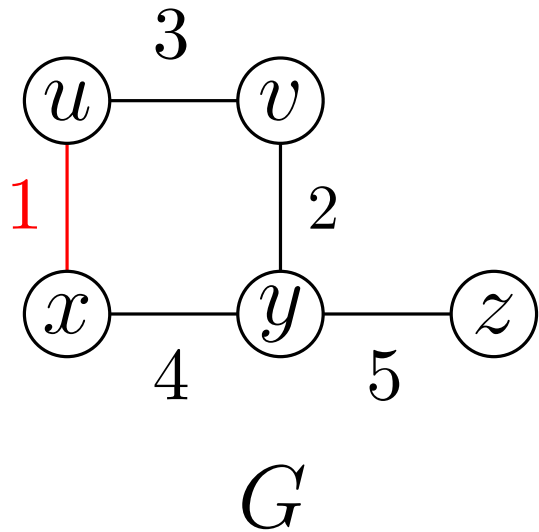
# Hierarchical Cluster Tree



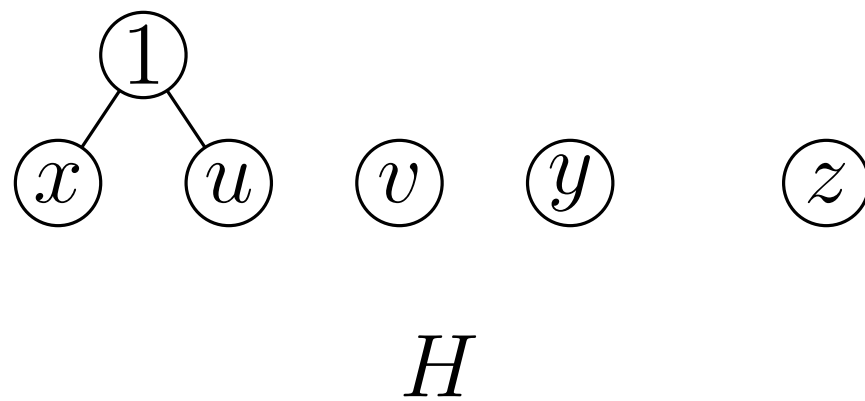
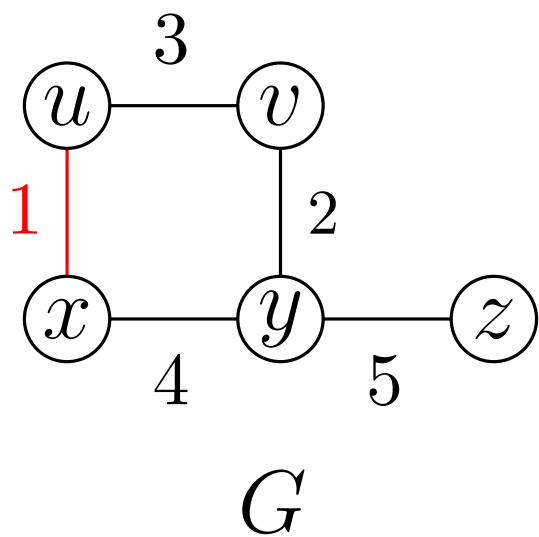
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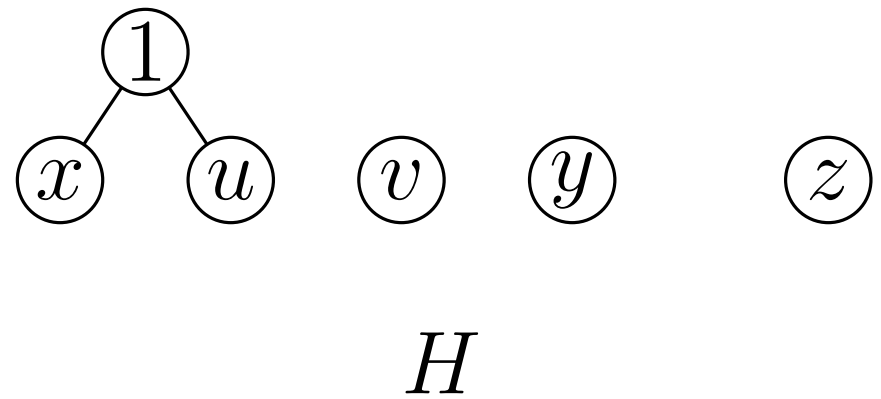
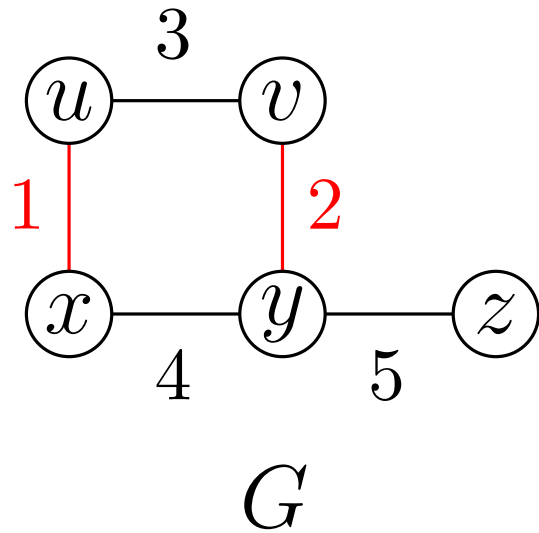
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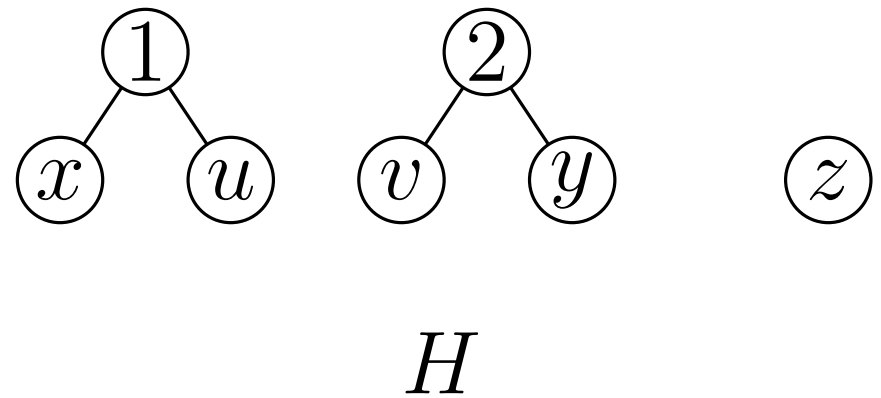
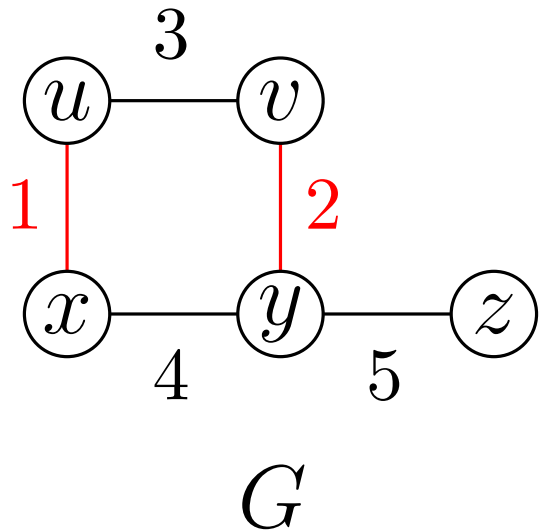
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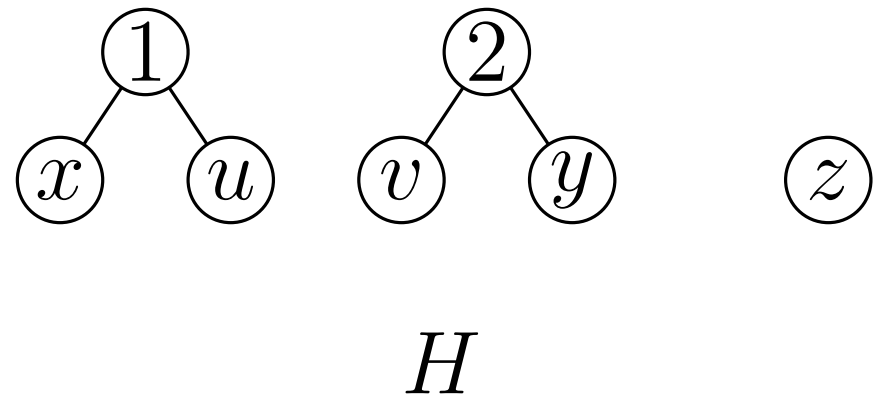
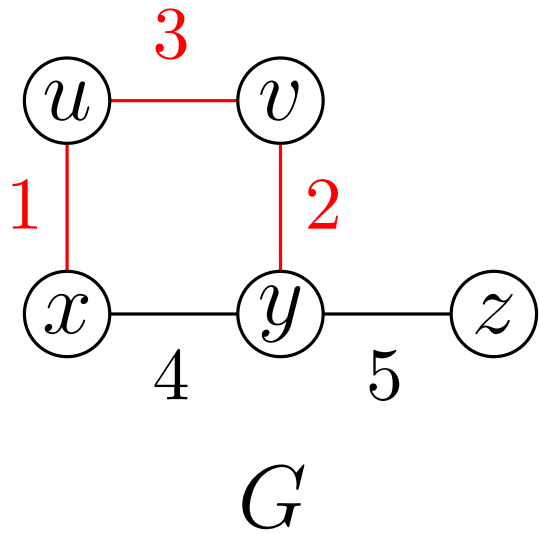
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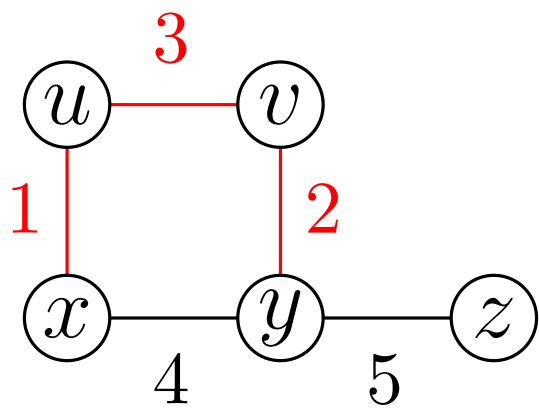
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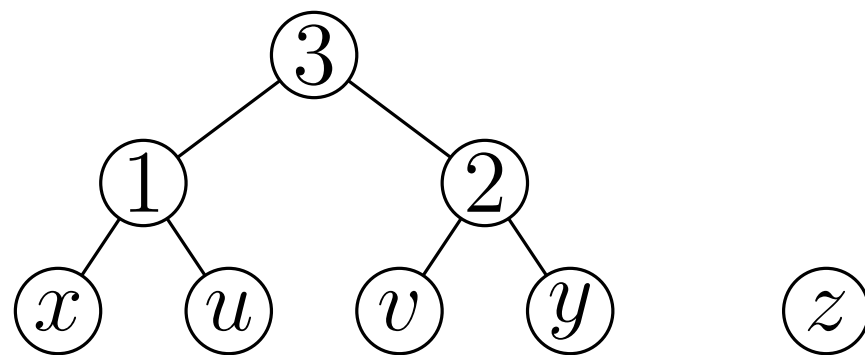
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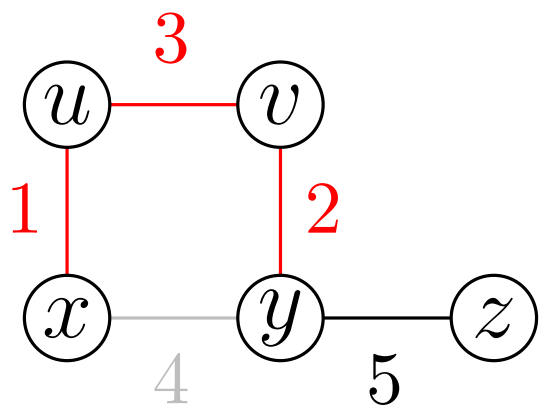


$G$

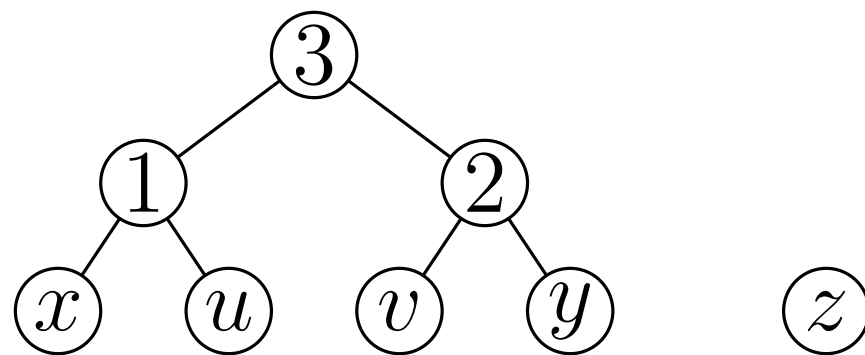


$H$

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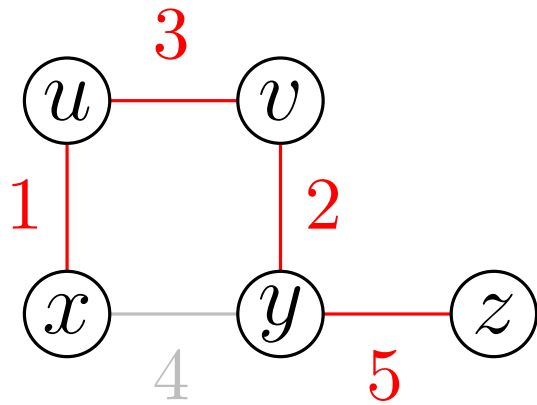


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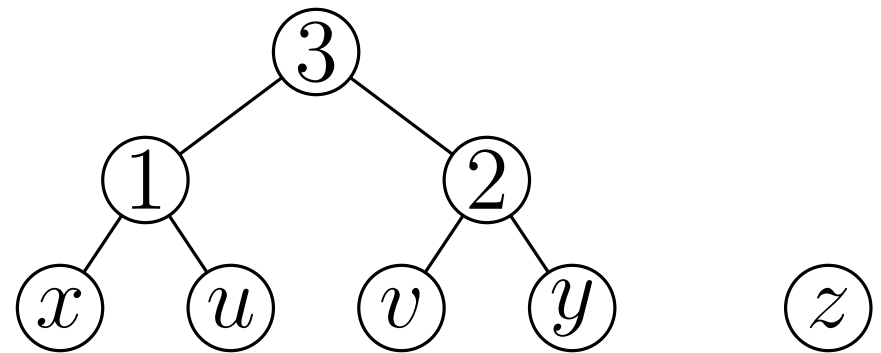


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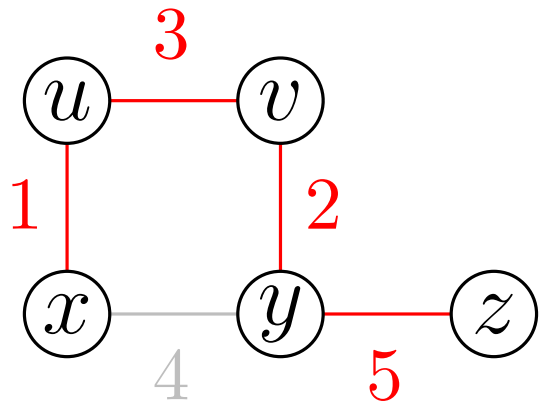


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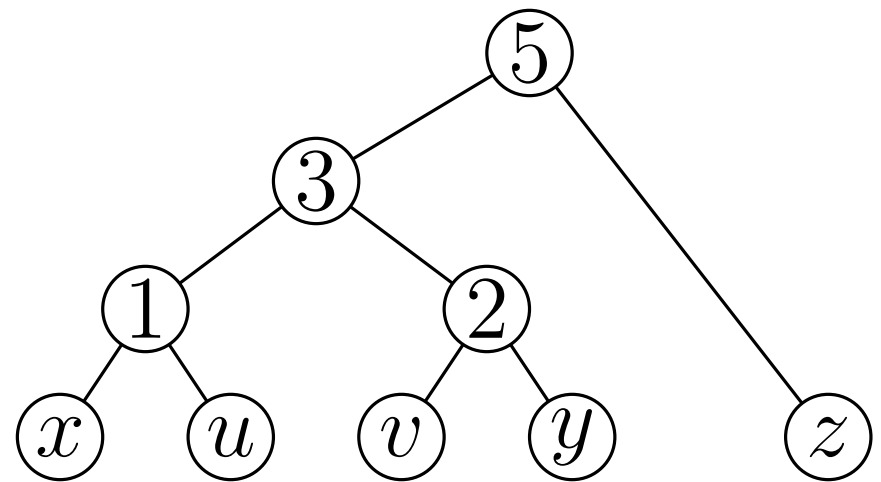


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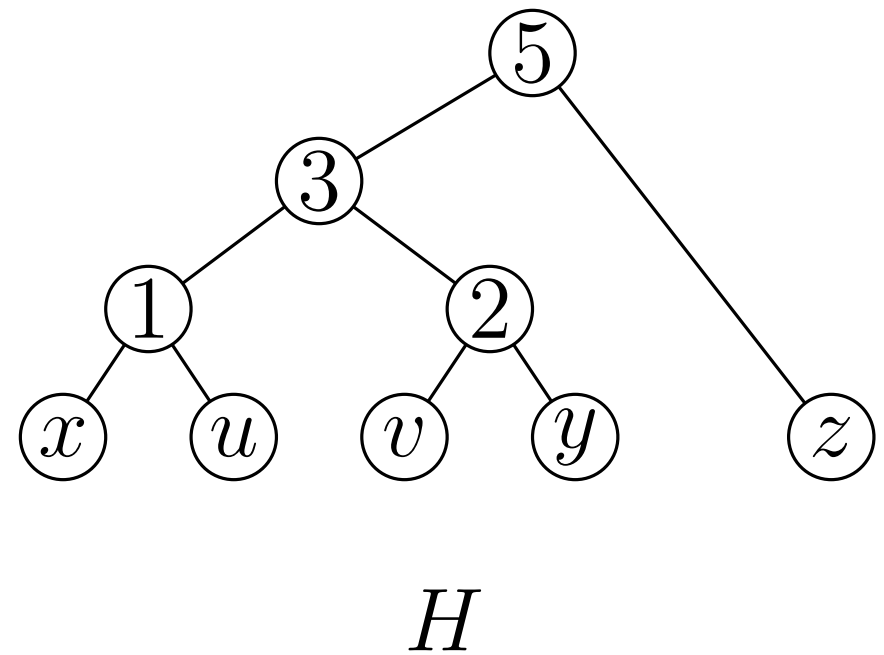
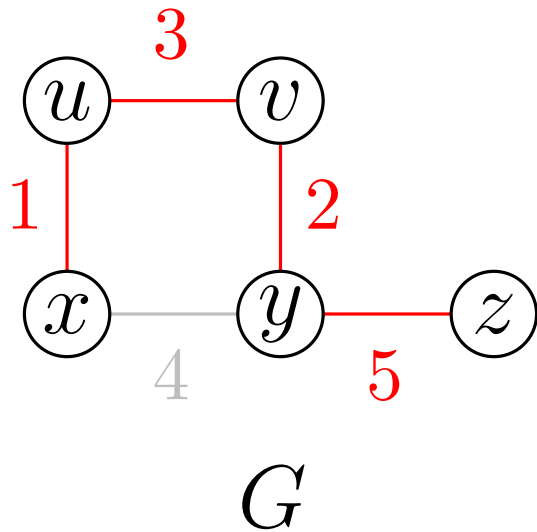
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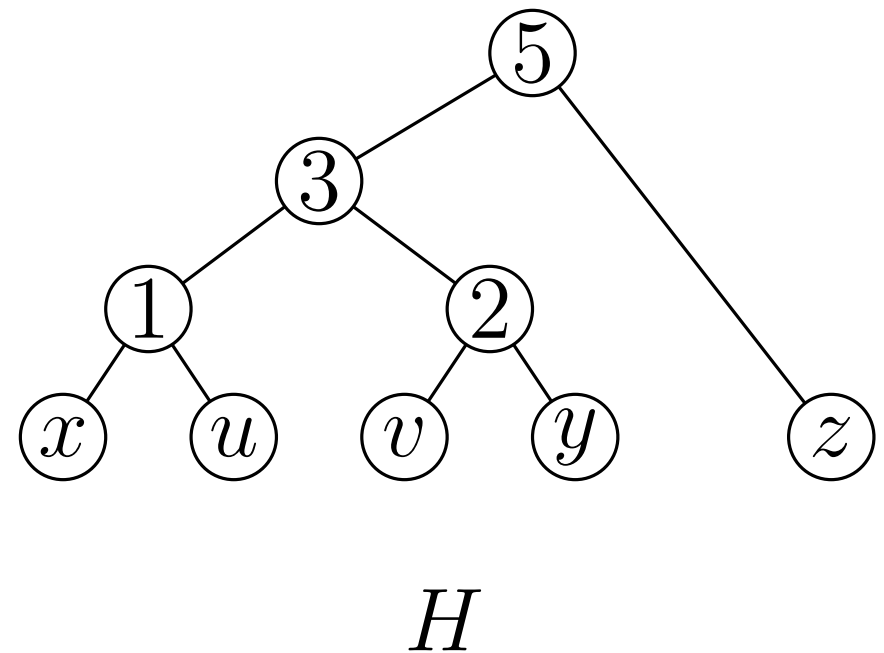
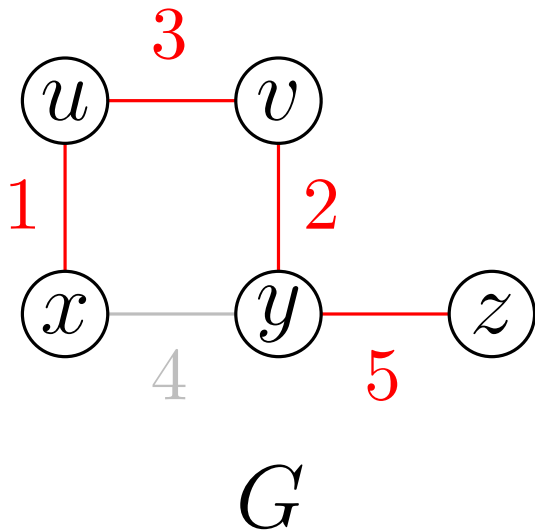
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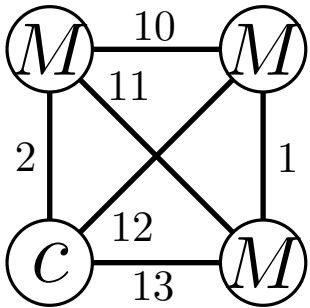
**Property 2:** the (sets of leaves of) subtrees of  $H$  correspond exactly to the connected components that appear at some point in the execution of Kruskal's algorithm.



# Where Does Single-Link Fail?

$$k = 3$$

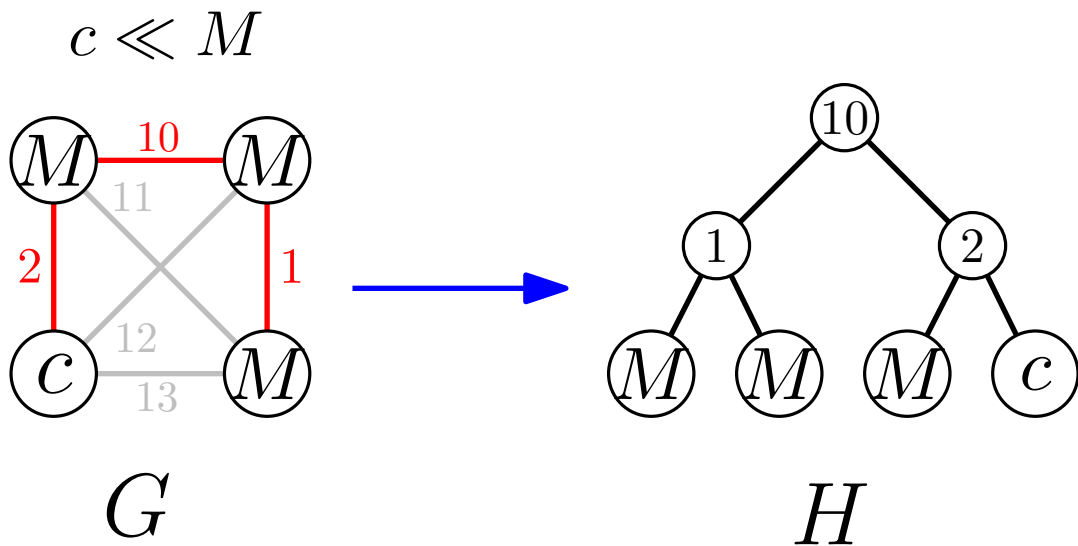
$$c \ll M$$



$G$

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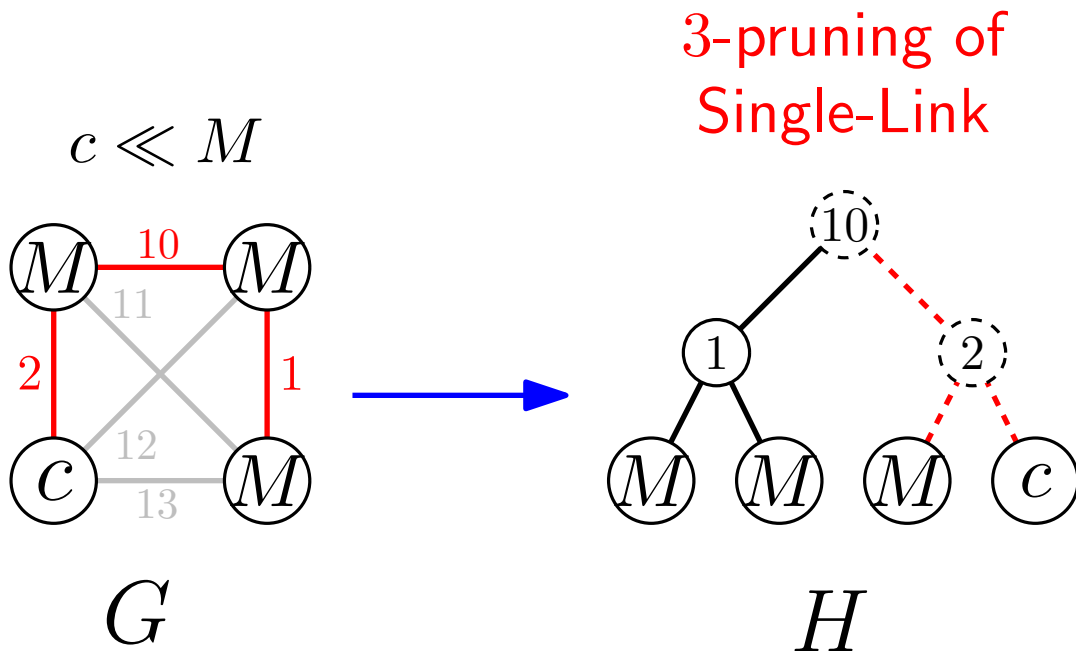
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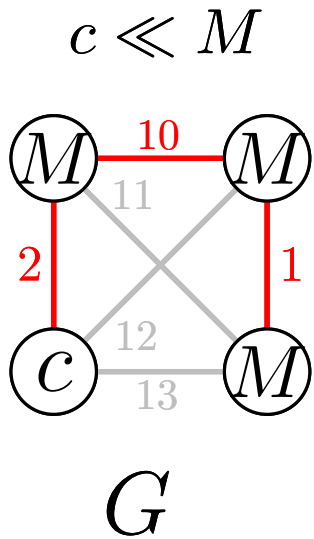
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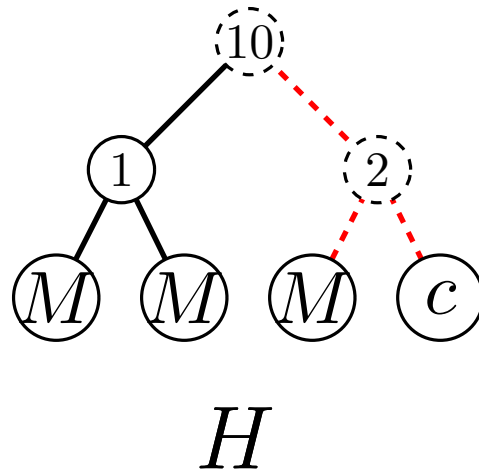
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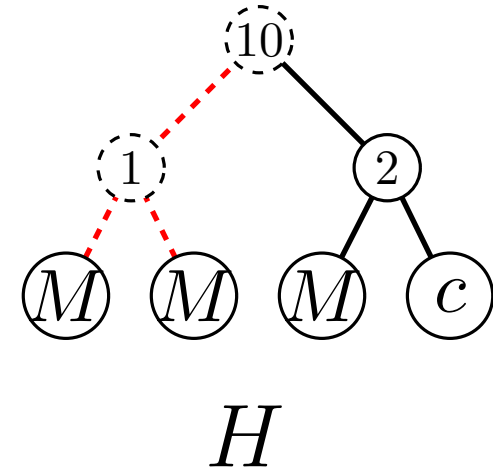
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3-pruning of  
Single-Link



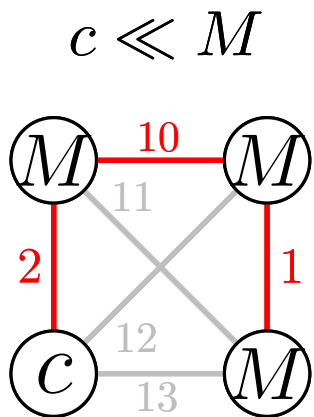
optimal  
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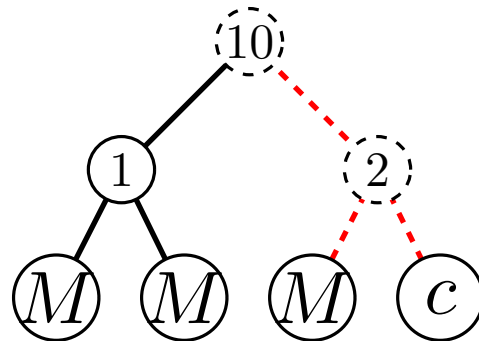
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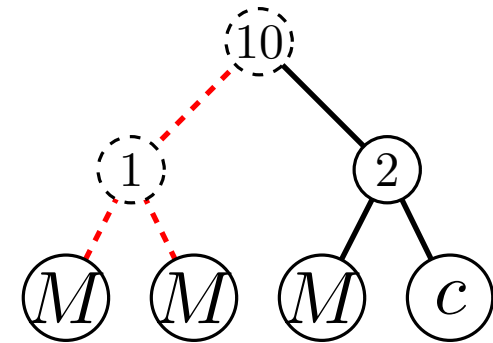
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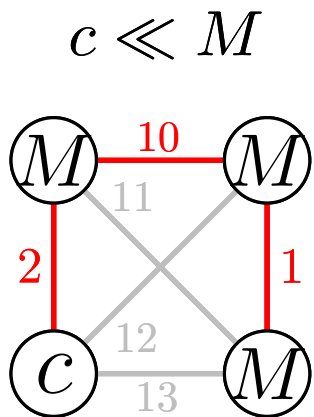
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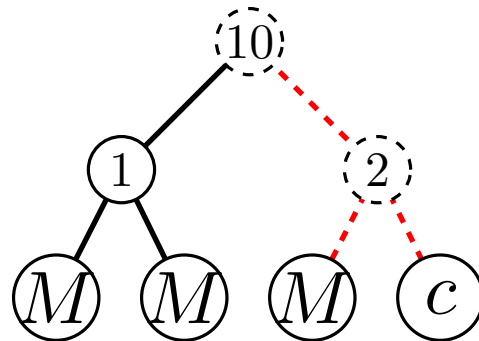
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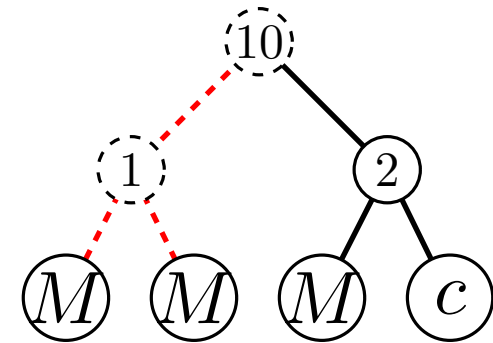
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Analysis

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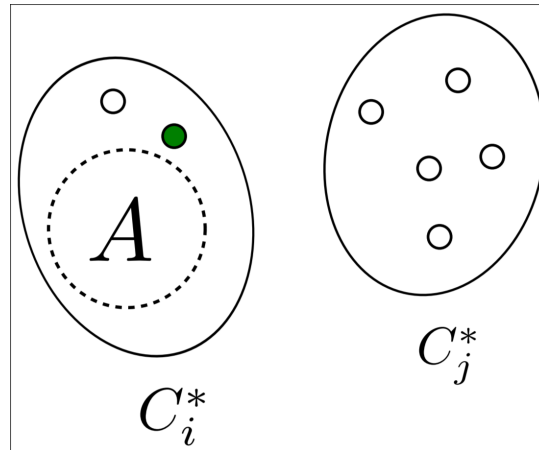
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(b) for every  $i$ , and every strict subset  $A \subset C_i^*$ , the point  $x^* = \arg \max_{x \in X \setminus A} d(x, A)$  of  $X \setminus A$  closest to  $A$  lies in  $C_i^*$



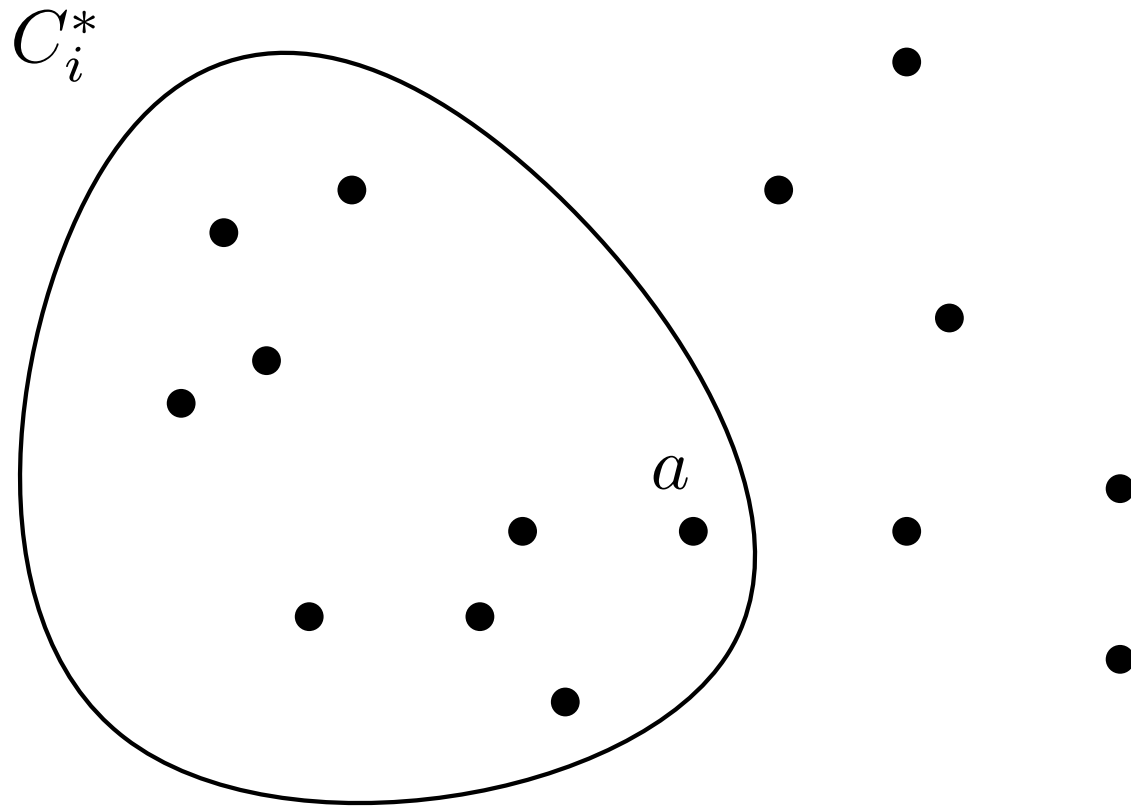
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$$(b) \implies (a)$$

Assume  $(b)$  is true.

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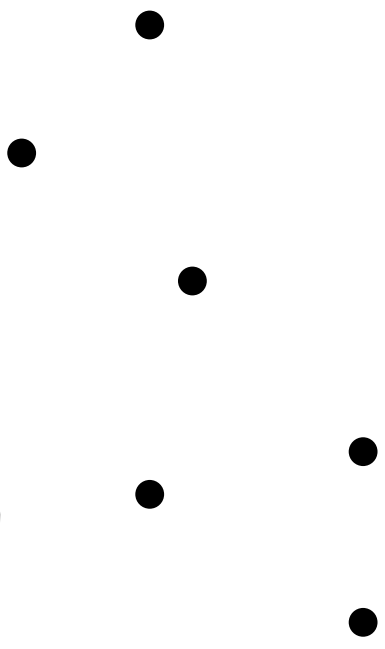
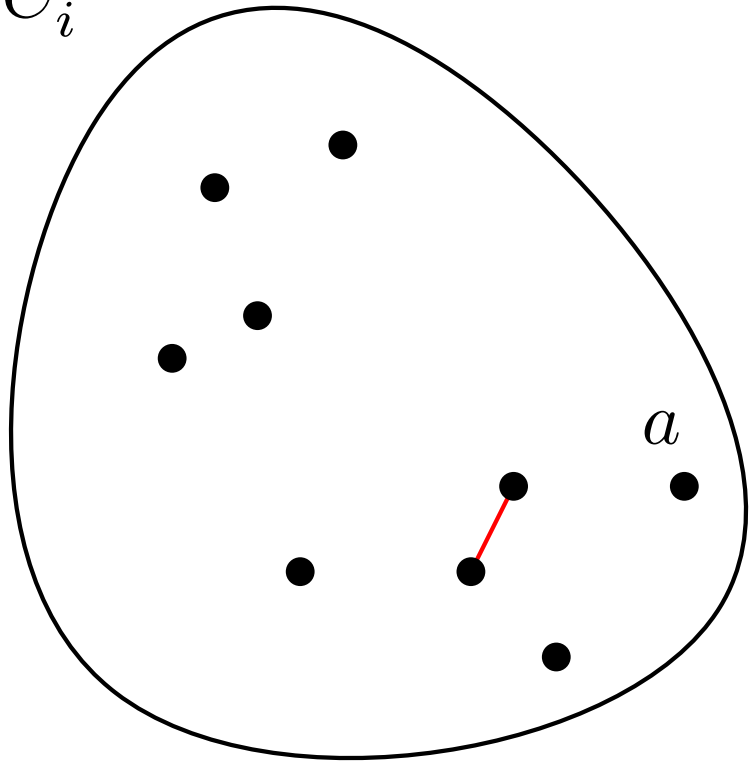
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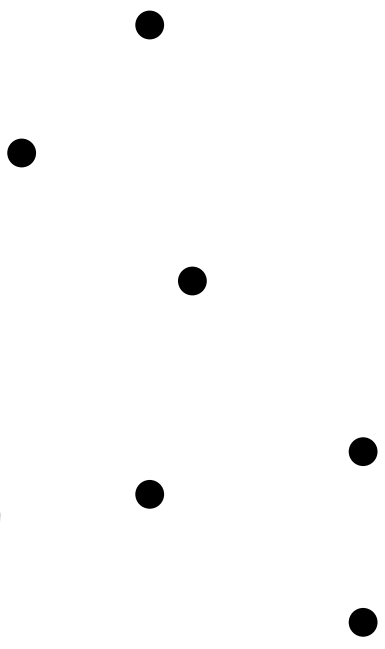
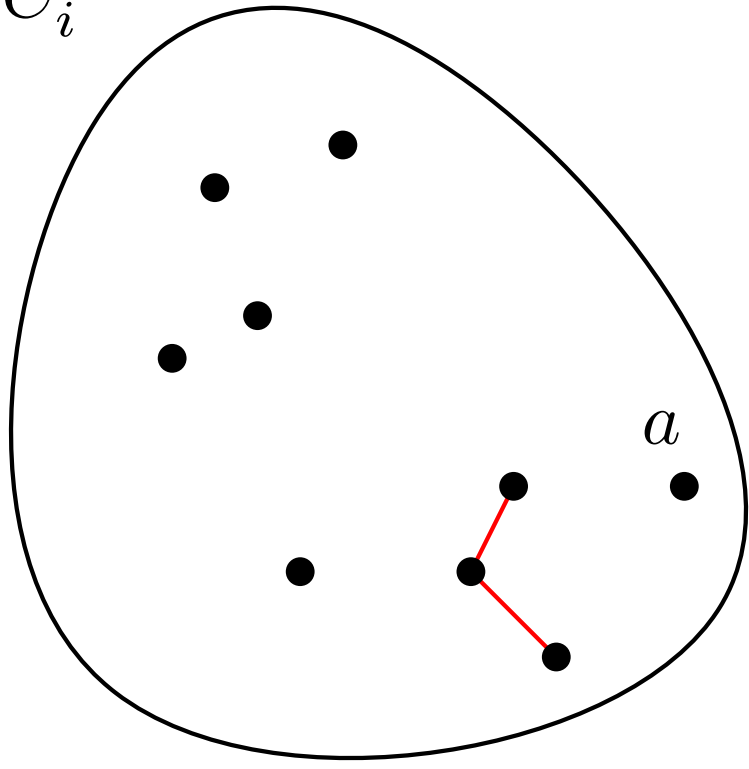
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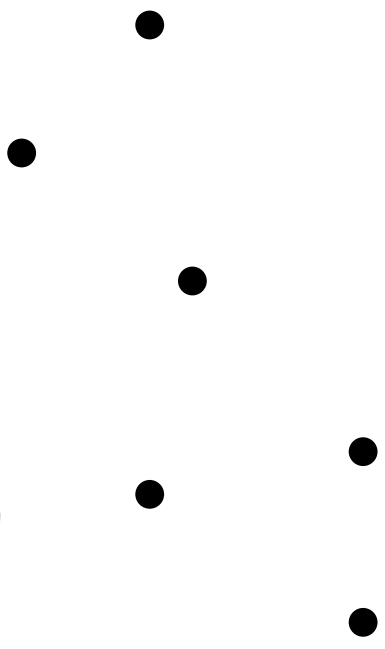
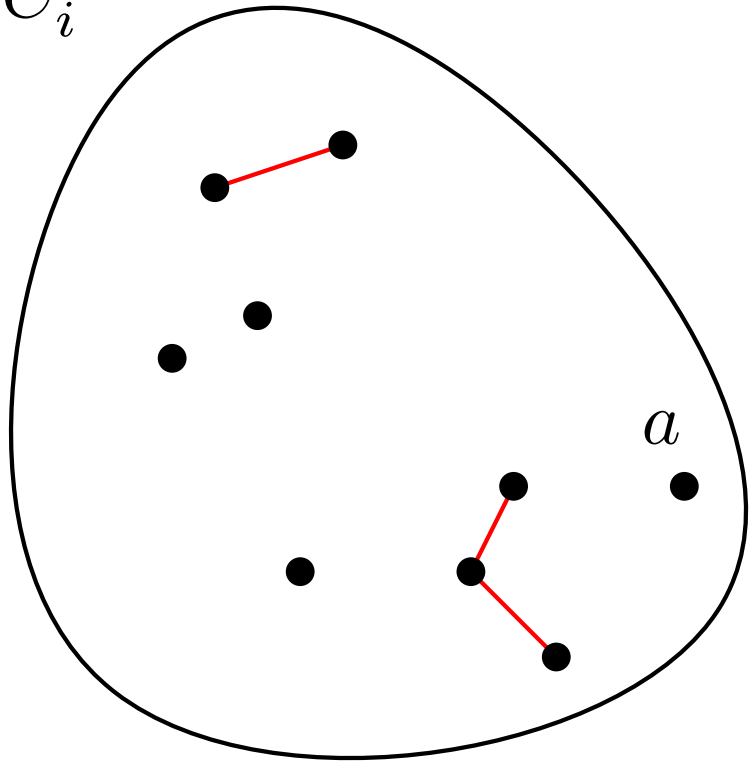
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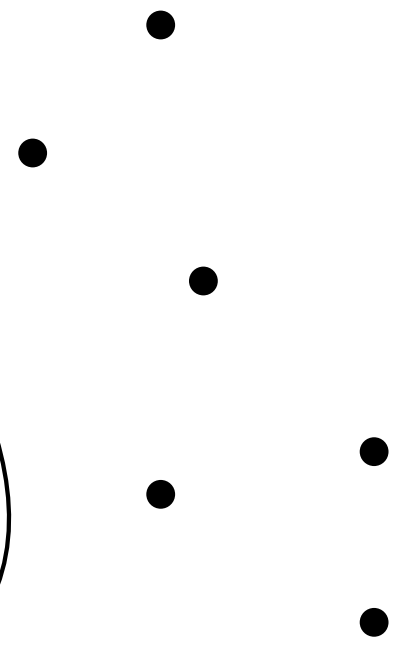
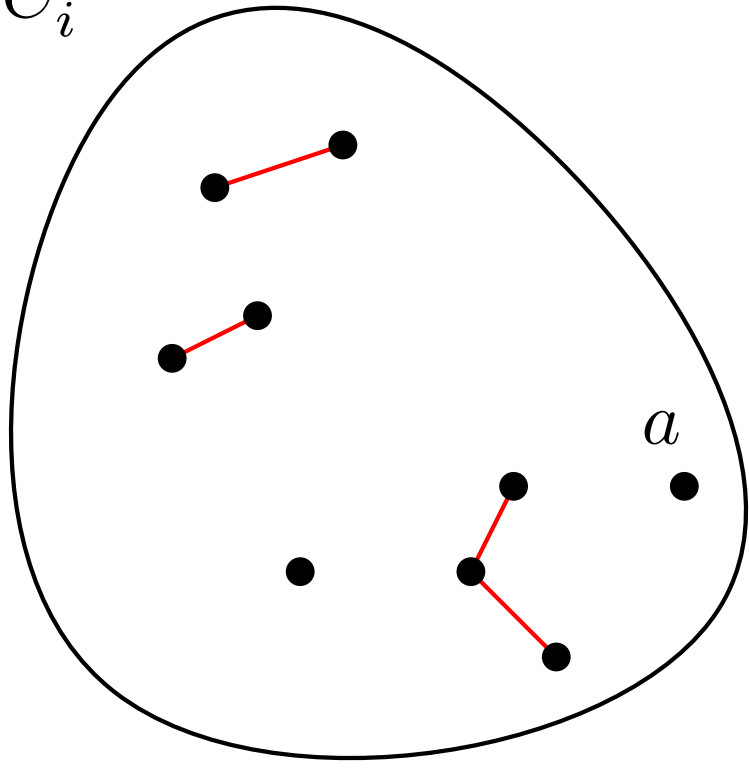
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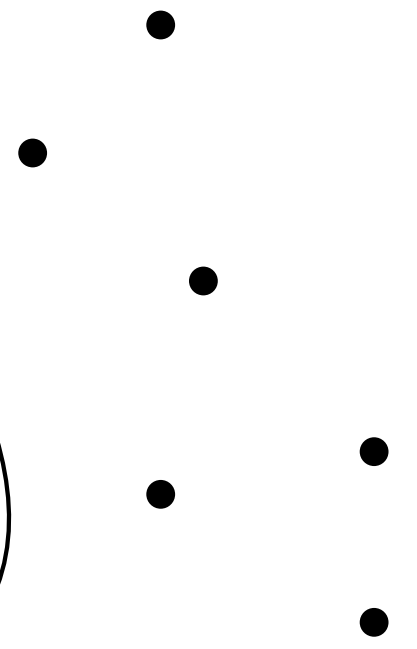
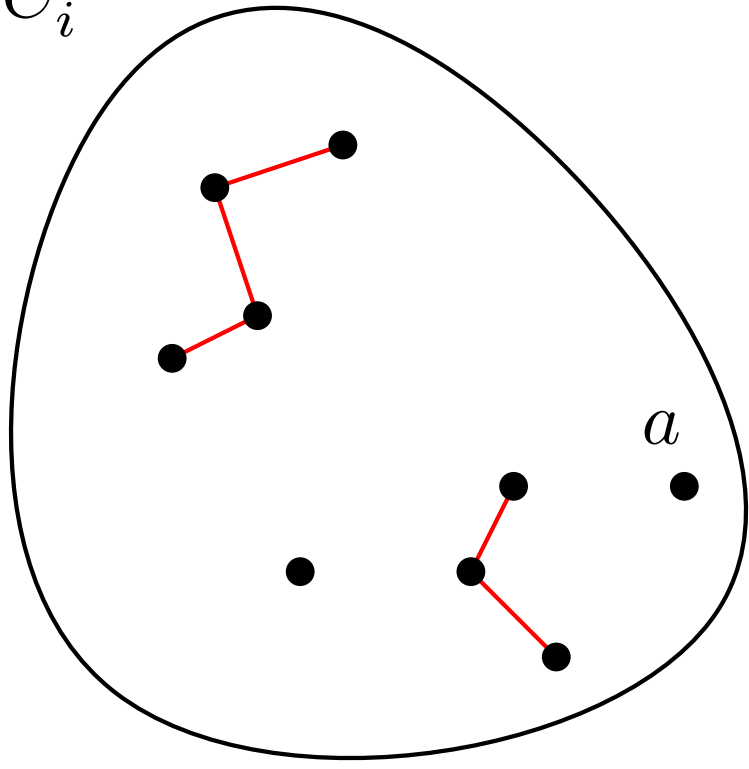
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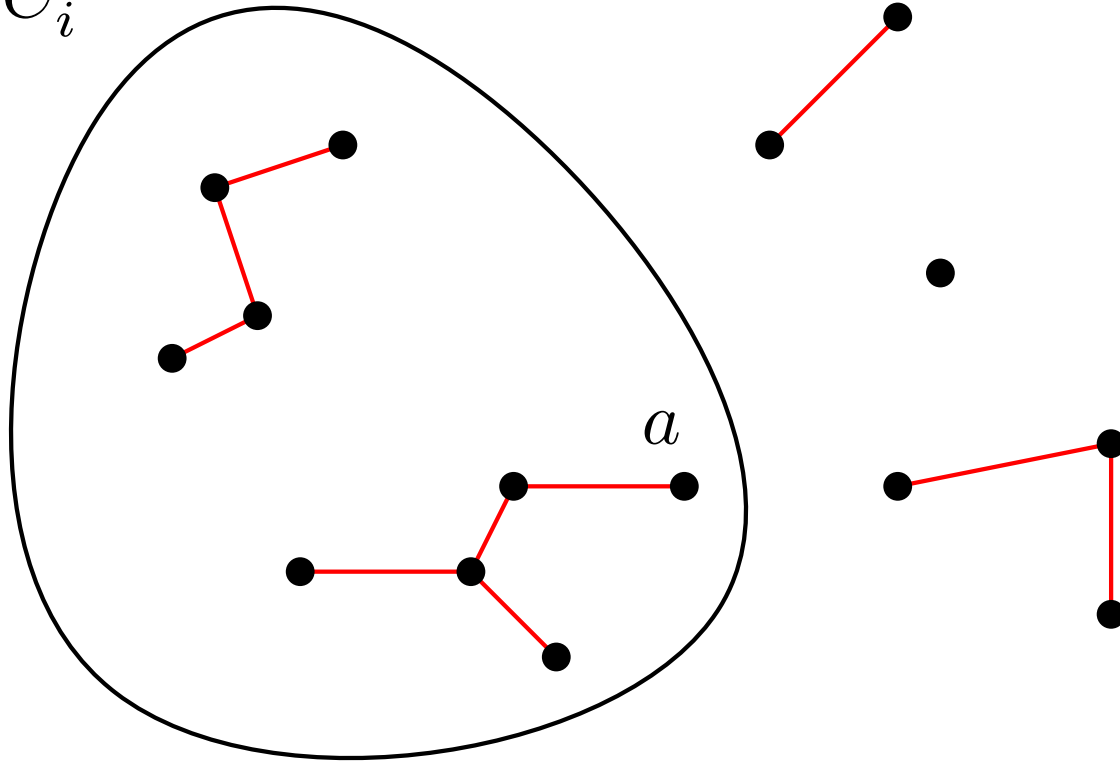
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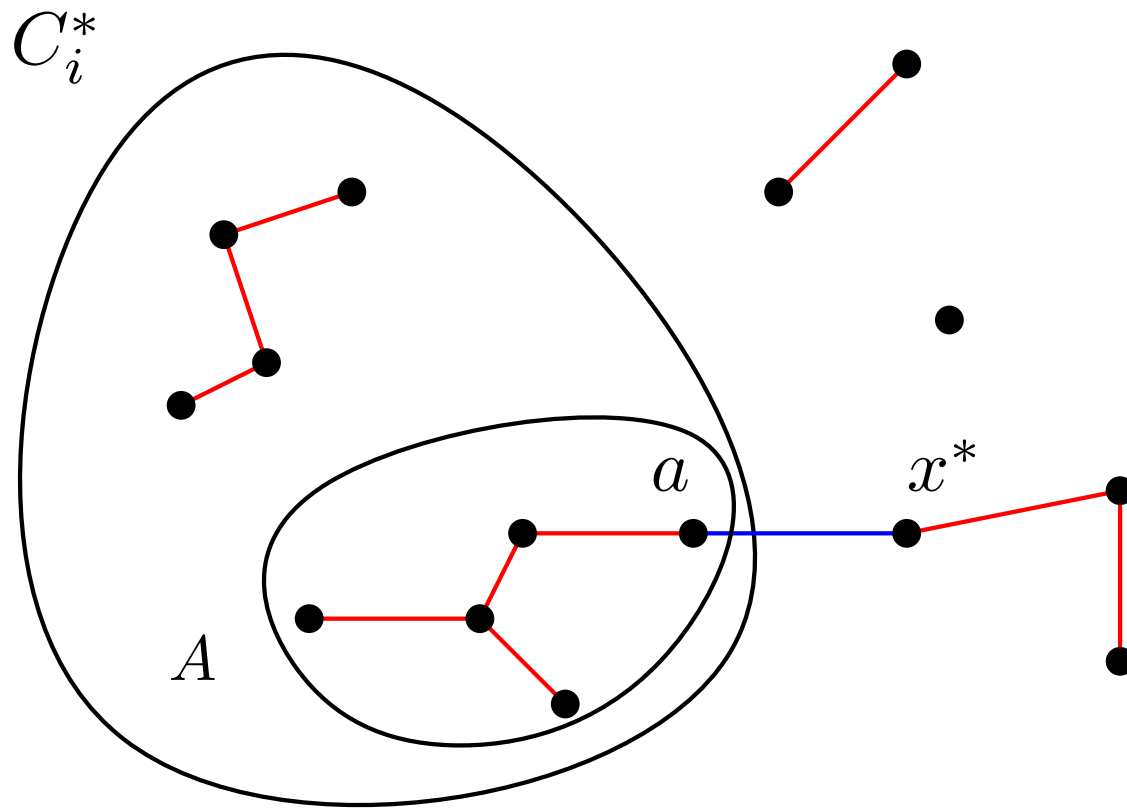
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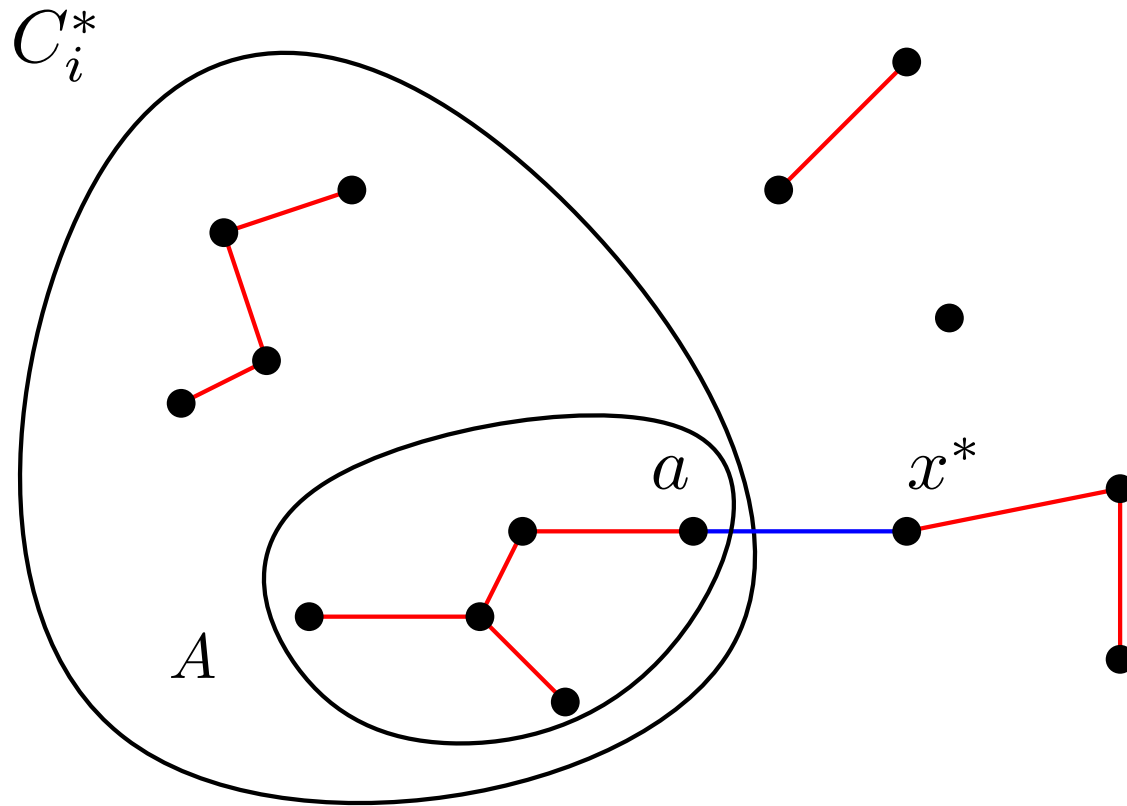
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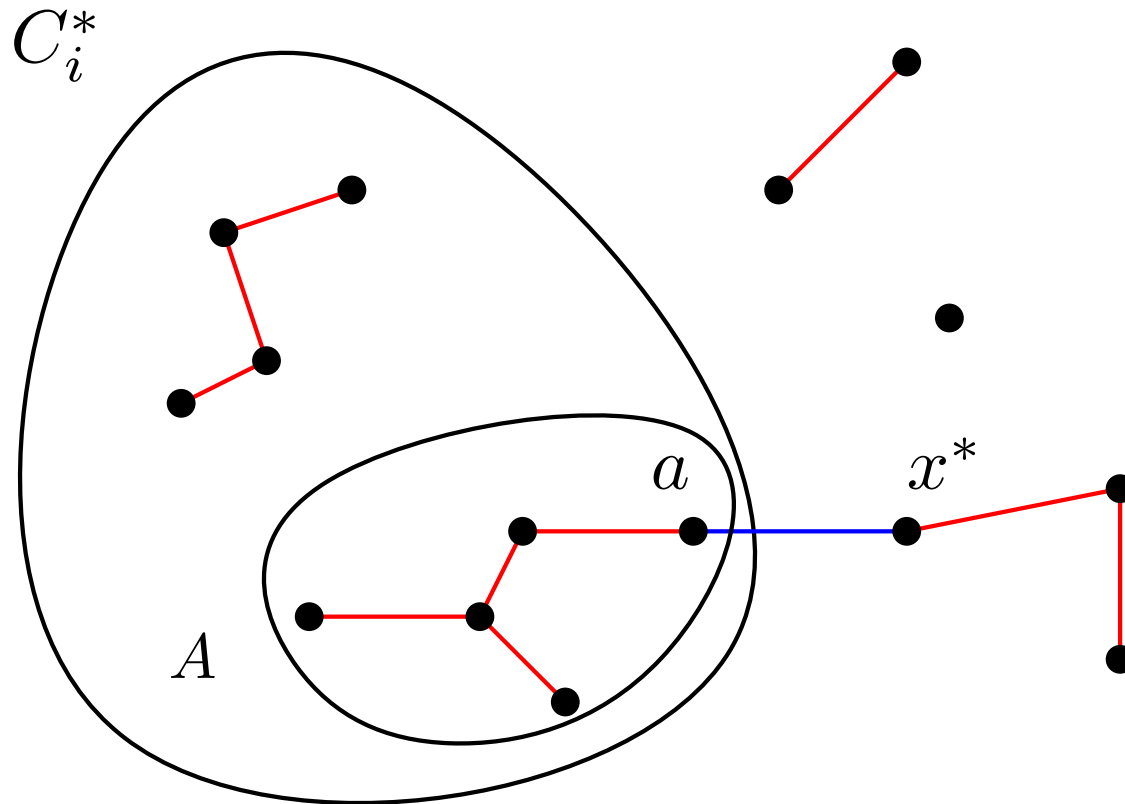
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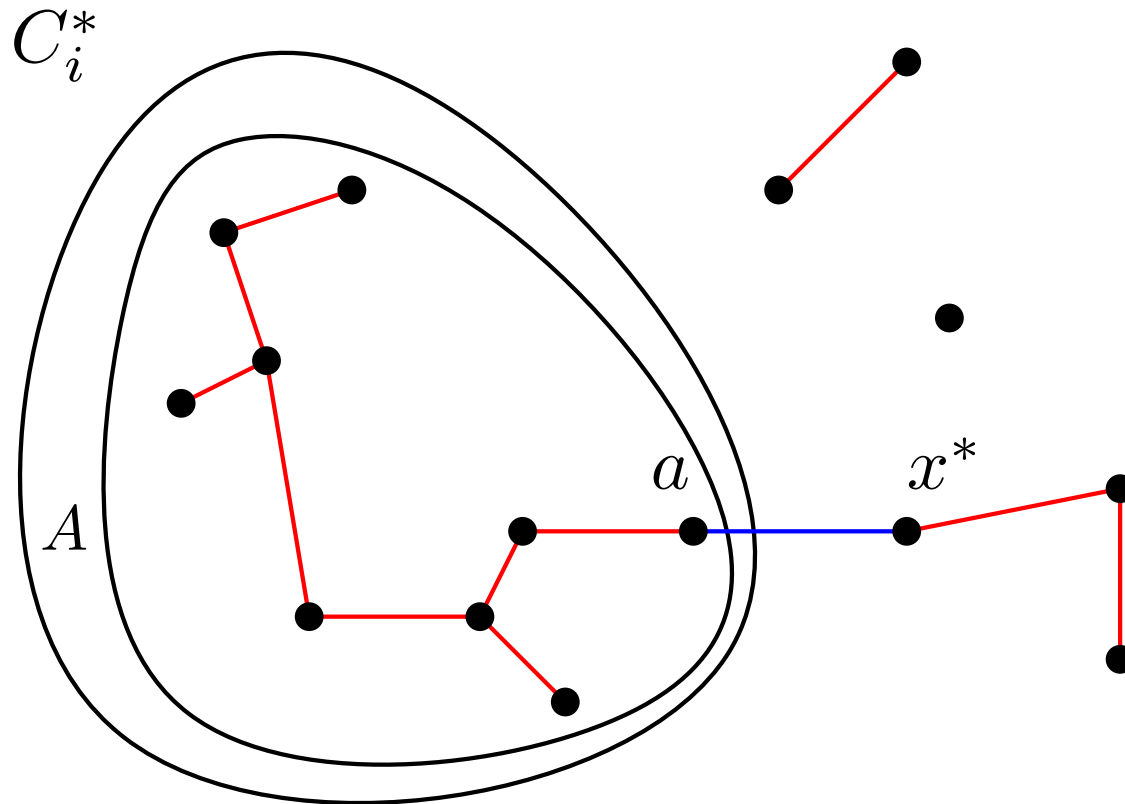


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$\implies A \not\subset C_i^* \implies A = C_i^* \implies C_i^*$  appears as a connected component during Kruskal.

## Proof of (b)

**Claim 1.** In every  $\gamma$ -stable instance with  $\gamma \geq 3$ , for every point  $x \in C_i^*$  we have

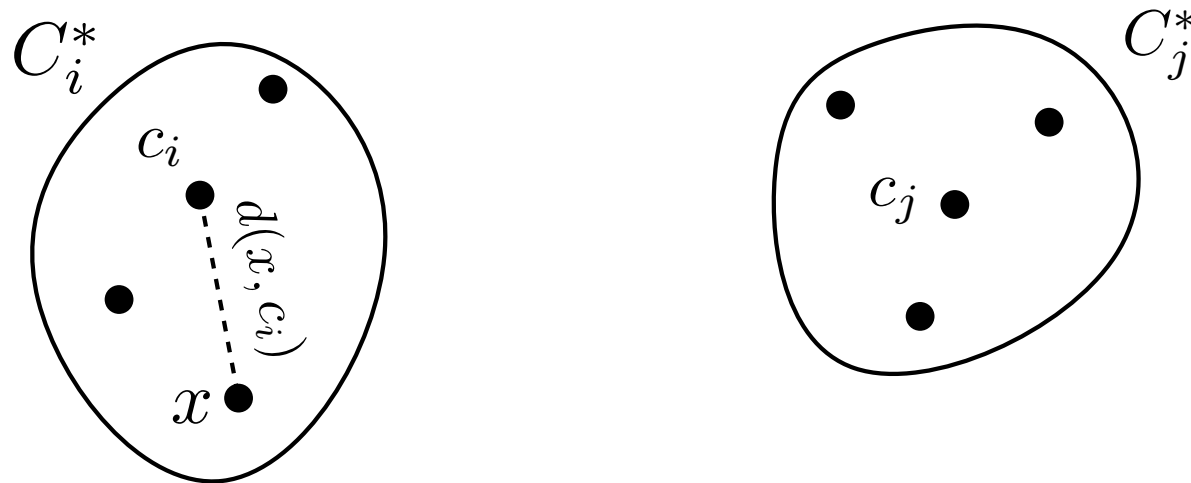
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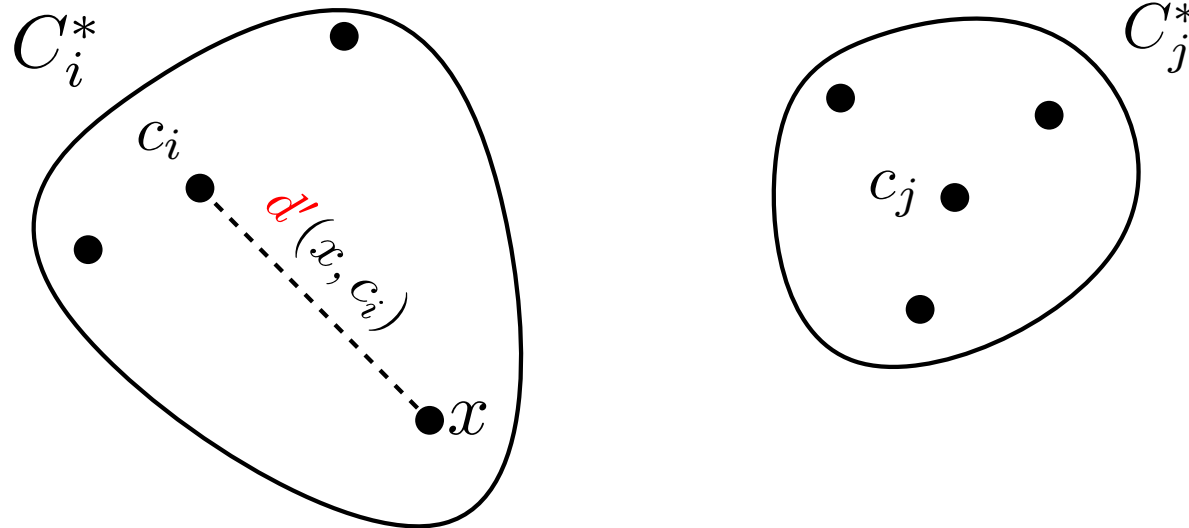


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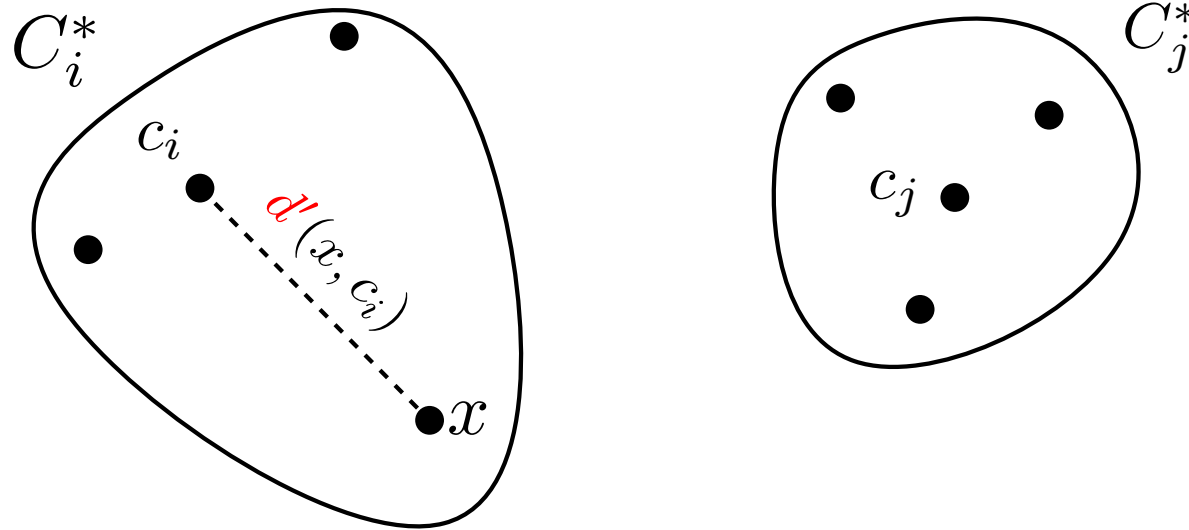
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$$d(x, c_j) = d'(x, c_j) > d'(x, c_i) = \gamma d(x, c_i) \geq 3d(x, c_i)$$



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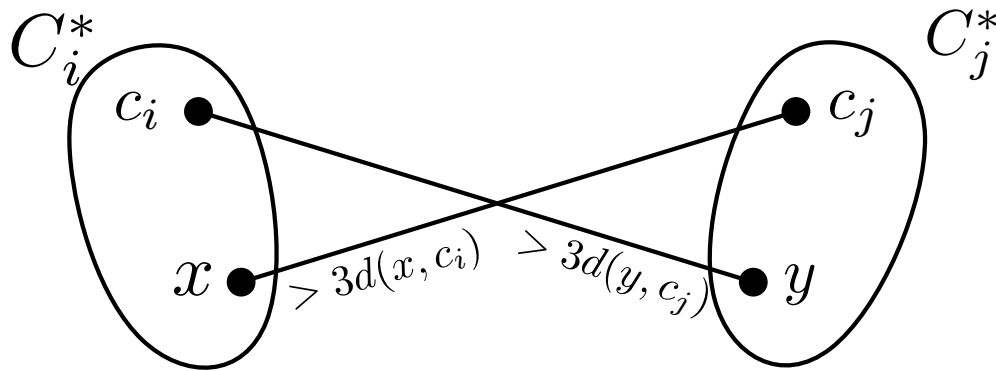
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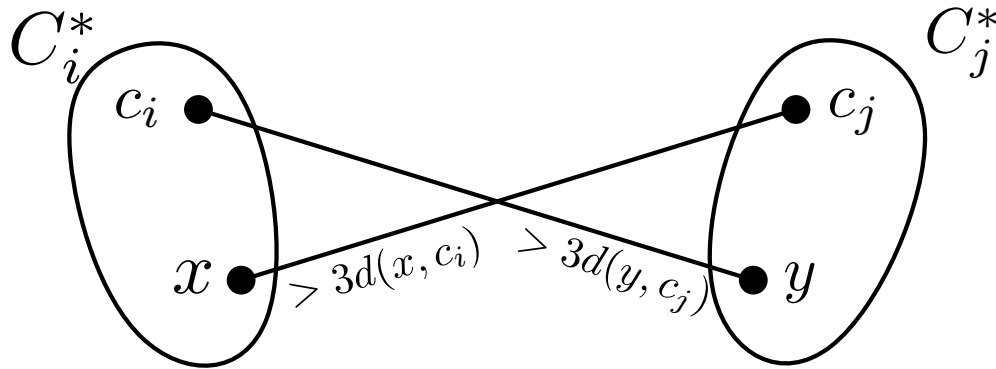
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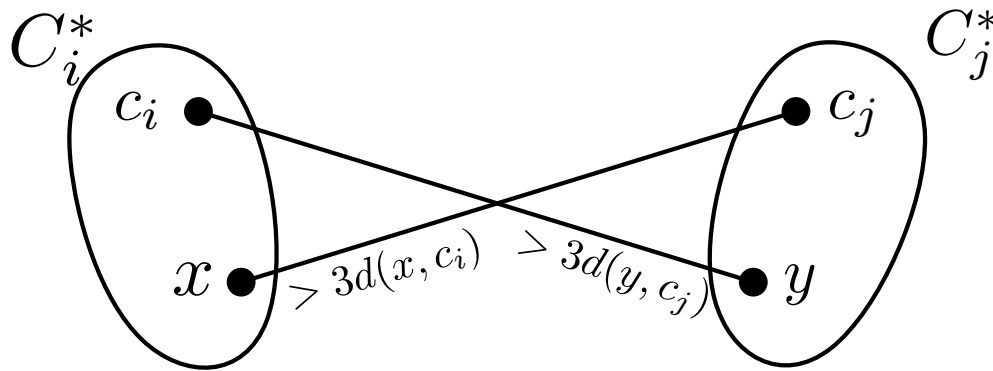
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rearranging:  $d(x, y) > 2d(x, c_i)$

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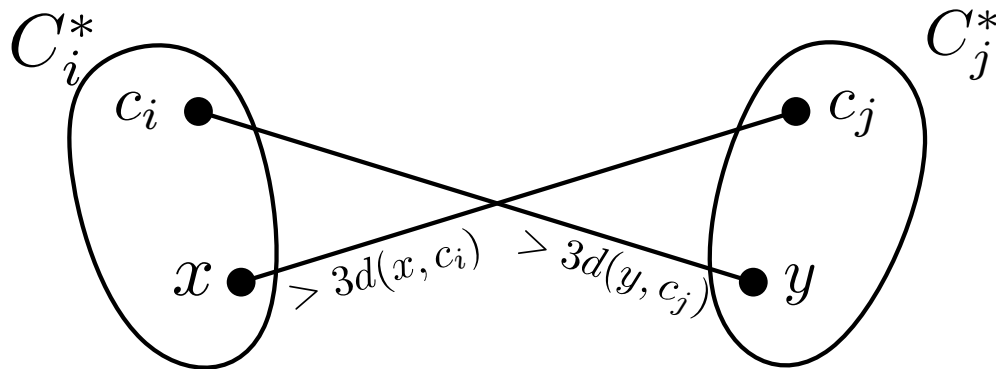
**Claim 2.** For every  $x \in C_i^*$  and  $y \in C_j^*$ , with  $j \neq i$ , we have

$$d(x, y) > 2 \max\{d(x, c_i), d(y, c_j)\}.$$

triangular inequality

claim 1

$$d(x, y) + d(x, c_i) \geq d(x, c_j) > 3d(x, c_i)$$



rearranging:  $d(x, y) > 2d(x, c_i)$

by symmetry:  $d(x, y) > 2d(y, c_j)$

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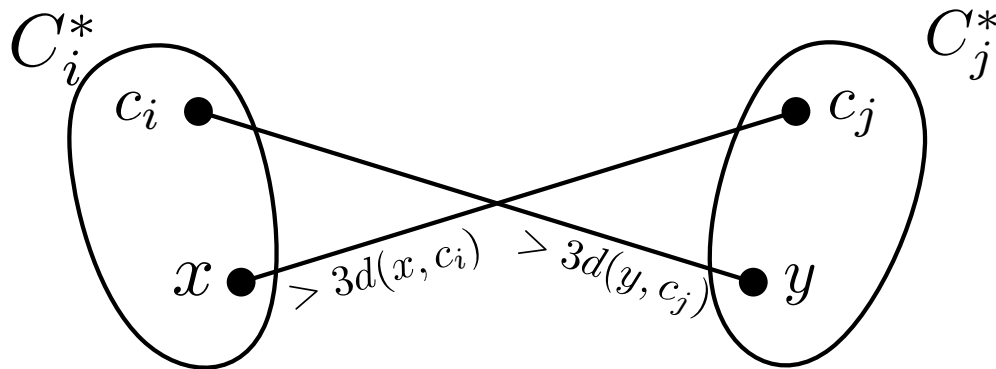
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We need to prove that, for every  $C_i^*$  and every strict subset  $A \subset C_i^*$ , the closest point in  $X \setminus A$  to  $A$  lies in  $C_i^*$ .

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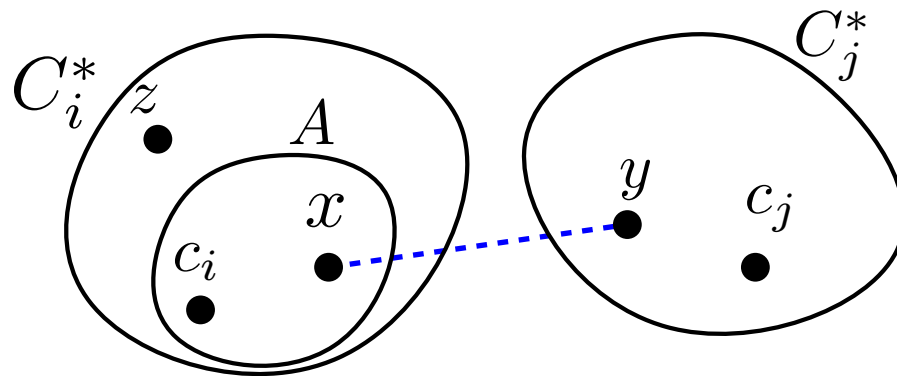
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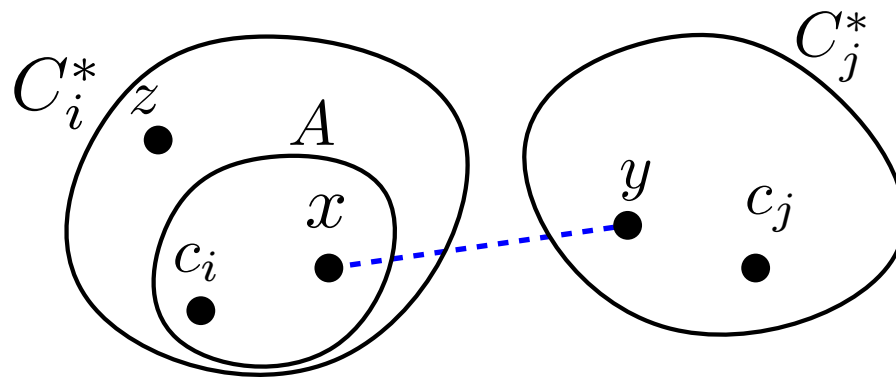
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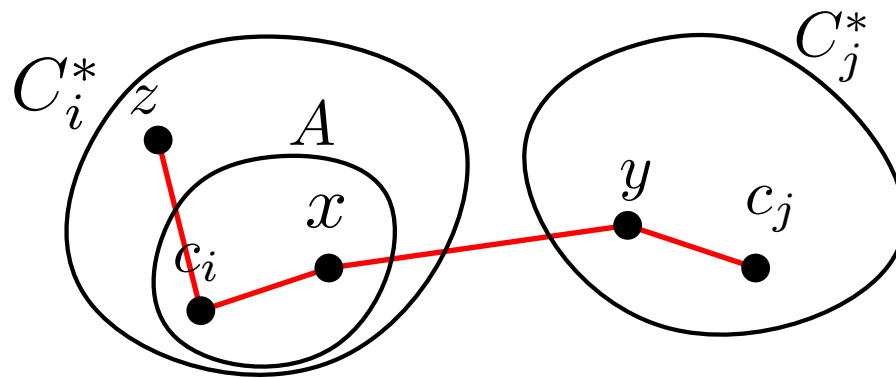
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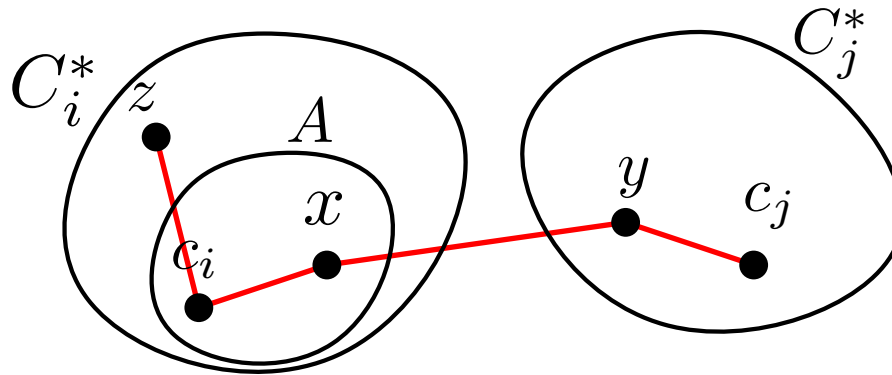
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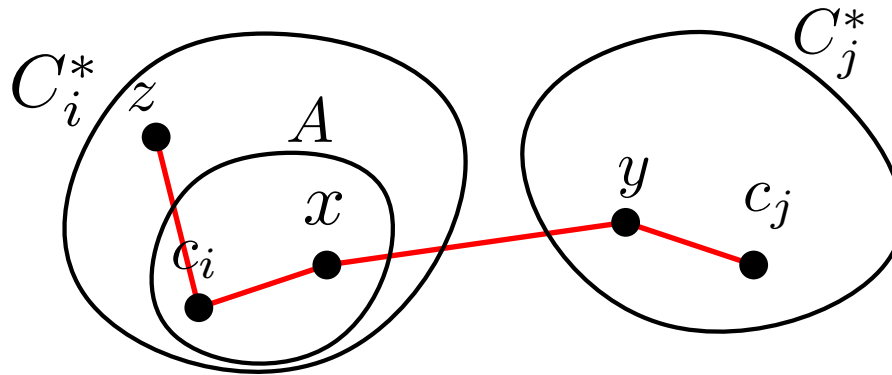
## Proof of (b)



triangular inequality

$$d(z, c_j) \leq d(z, c_i) + d(c_i, x) + d(x, y) + d(y, c_j)$$

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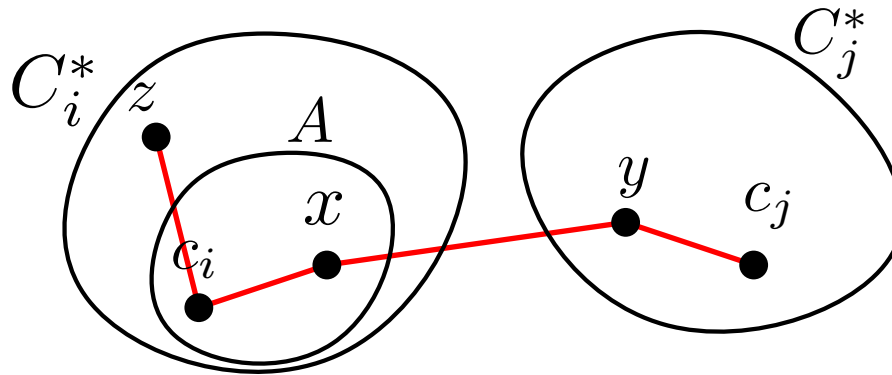


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$$\begin{aligned} d(z, c_j) &\leq d(z, c_i) + d(c_i, x) + d(x, y) + d(y, c_j) \\ &< \frac{1}{2}d(x, y) &< \frac{1}{2}d(x, y) \end{aligned}$$

calim 2

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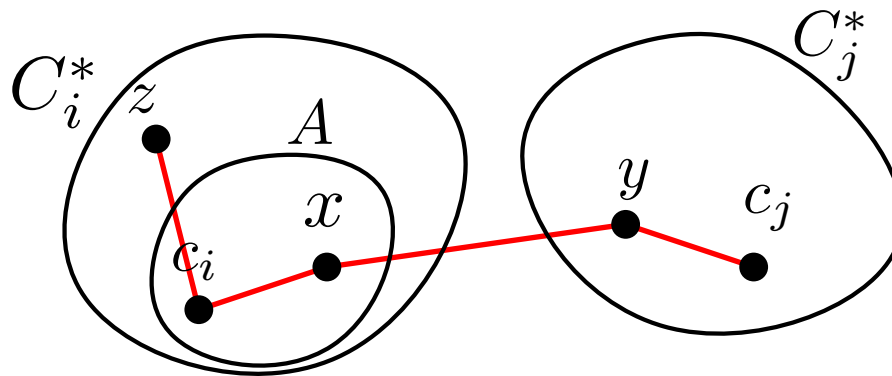


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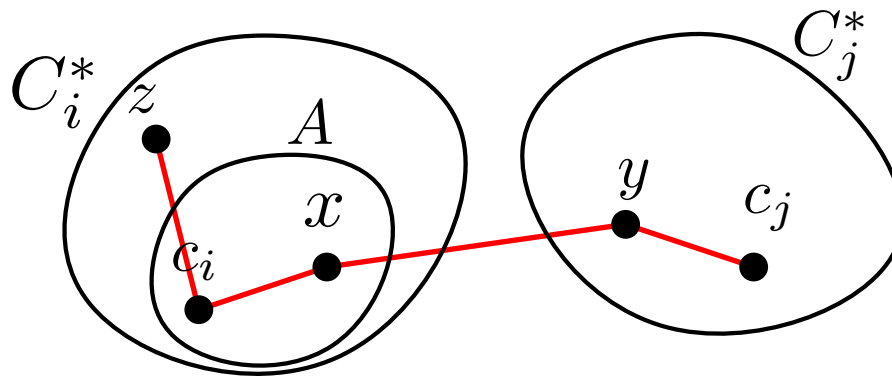
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Since  $c_i \in A$ ,  $z \notin A$ , and  $x, y$  are the closest point between  $A$  and  $C_j$ , we have

$$d(x, y) < d(z, c_i)$$

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triangular inequality

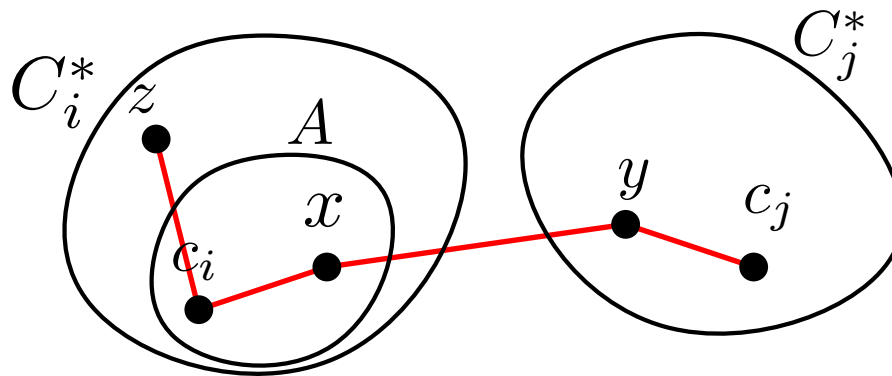
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$\implies (X, d)$  is not  $\gamma$ -stable (**absurd!**)



# Other Stability Definitions

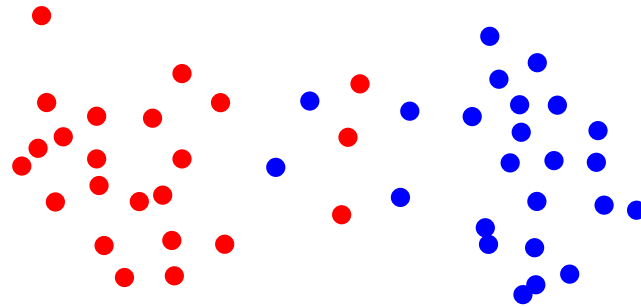
# Other Stability Definitions

**Def. (Approximation Stability)** The target clustering of a  $k$ -median instance is  $(c, \varepsilon)$ -approximation stable if every  $c$ -approximate  $k$ -clustering is  $\varepsilon$ -accurate, meaning that it agrees with the target clustering on at least a  $1 - \varepsilon$  fraction of the points.

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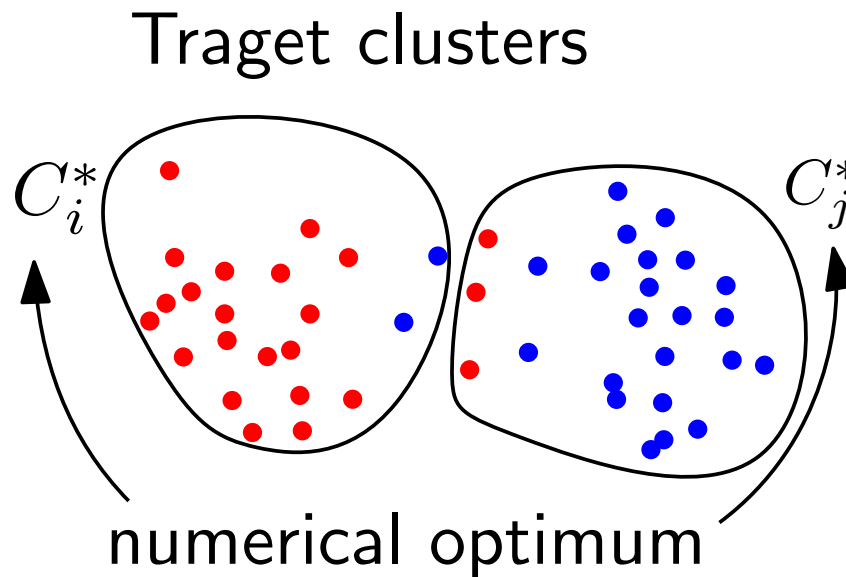
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Target clusters



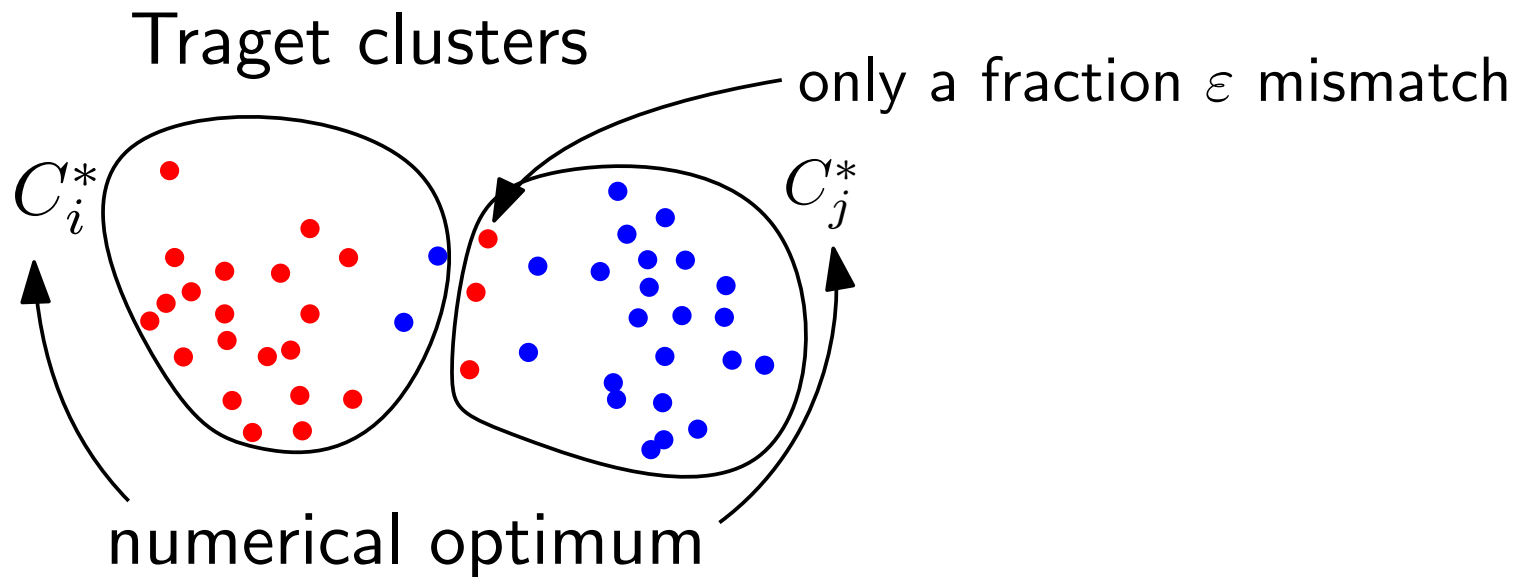
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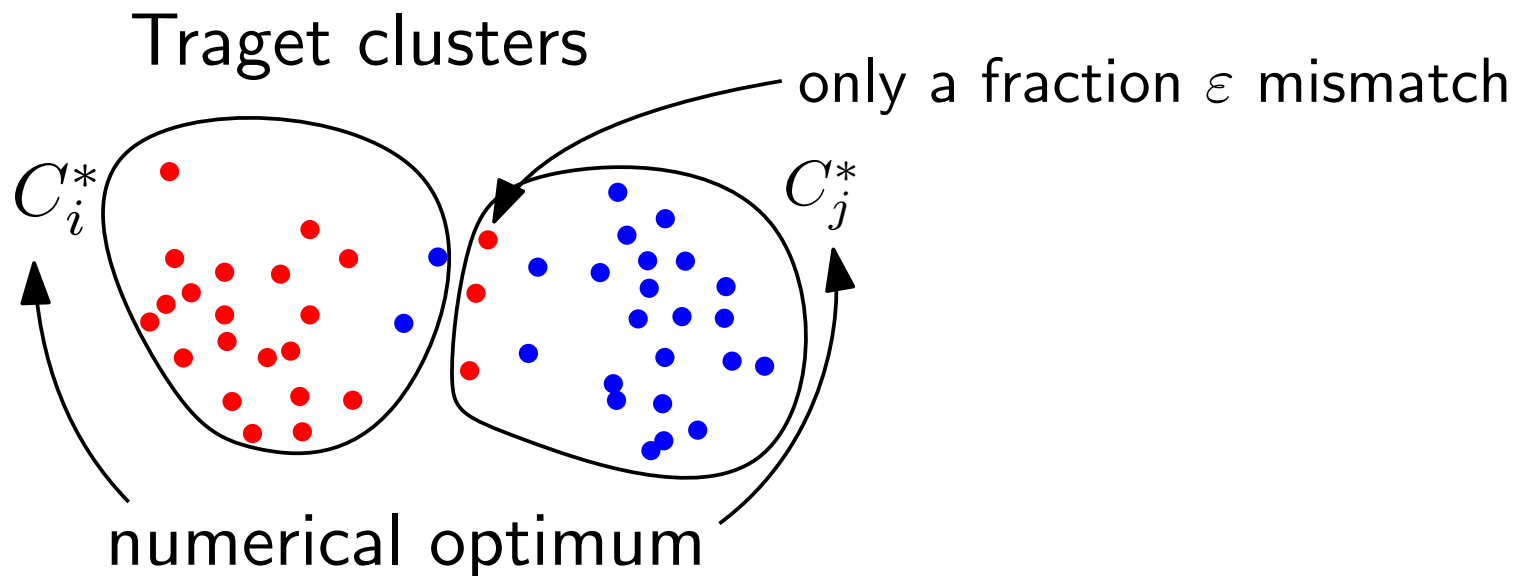
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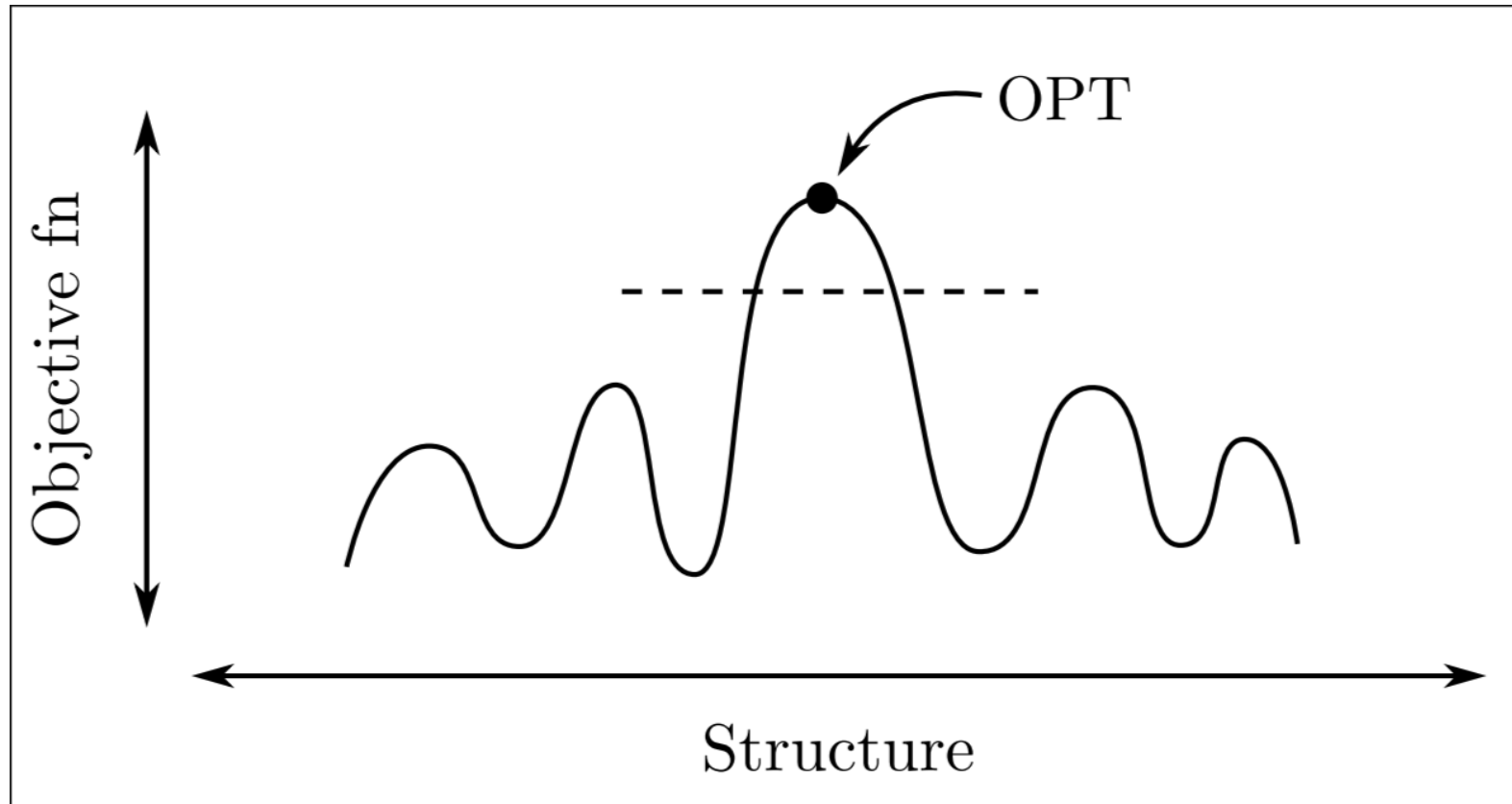
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**Theorem.** For every pair  $\alpha, \varepsilon > 0$  of constants, there is a polynomial-time algorithm that, for every  $(1 + \alpha, \varepsilon)$ -approximation stable  $k$ -median instance, recovers a  $k$ -clustering that agrees with the target clustering on all but an  $O(\varepsilon/\alpha)$  fraction of the points.

# Other Stability Definitions



**Intuition:** Numerical near-optimality implies structural near-optimality.