

# Drawing Clusterings of Bipartite Graphs

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## Abstract

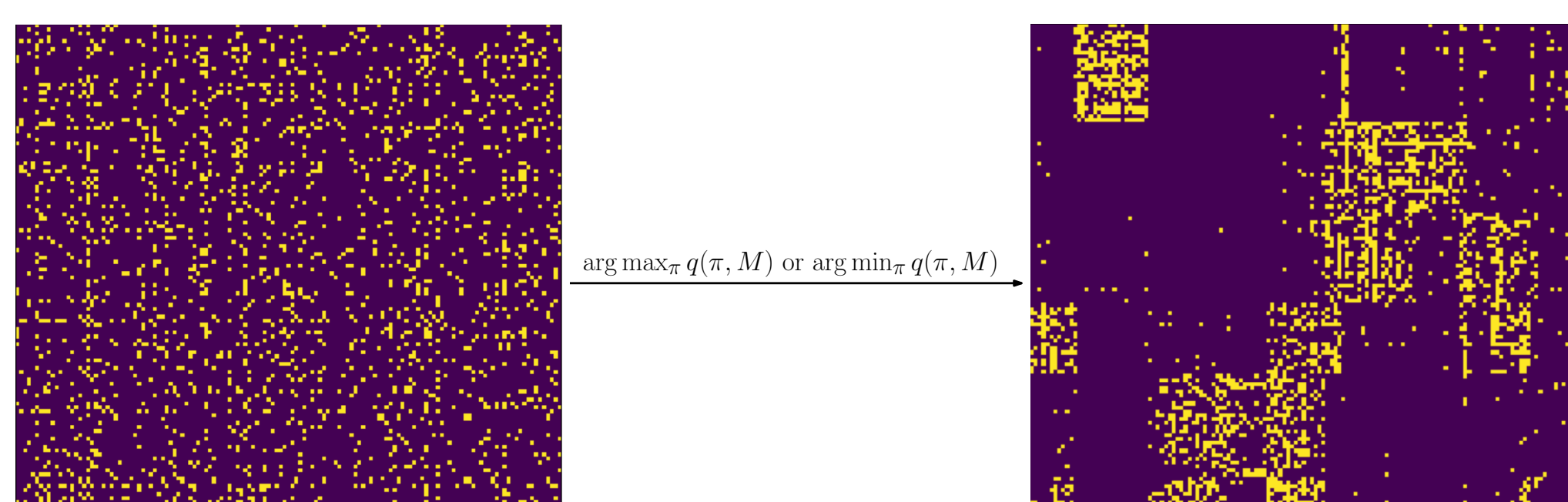
We study the drawing of a given *overlapping* clusterings of bipartite graphs. Our approach does not require a (dis-)similarity function between the clusters that shall be visualized. We present:

- An algorithm for drawing overlapping clusters
- A pre-processing routine that decreases the computational complexity
- A novel objective function to assess the drawing quality

## Seriation Problem

*Goal:* Reorder the matrix to find “dense” blocks

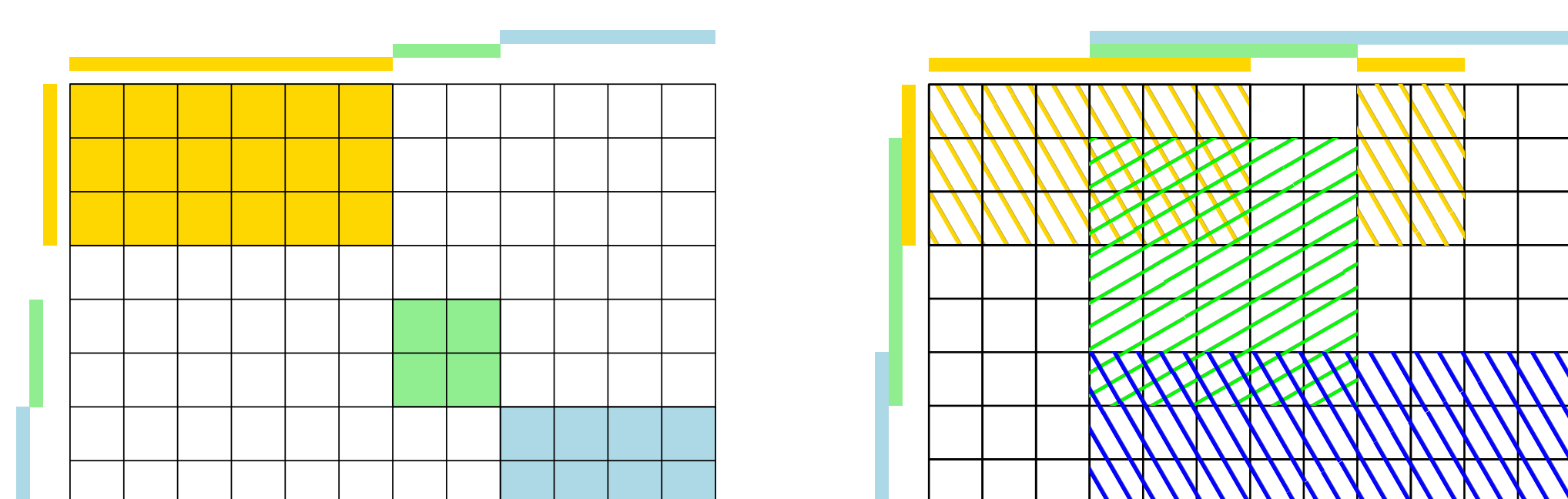
- Given a quality metric, find row and column permutations to optimize the visualization [2]
- *Pattern-agnostic:* no prior knowledge over the structure of the data
- Cannot visualize a *given* clustering



## Drawing Overlapping Clusterings

In a bipartite graph  $G = (R \cup C, E)$ , a *cluster* is defined by  $(R' \subseteq R, C' \subseteq C)$ . Clustering algorithms find dense subgraphs  $\{(R', C')\}_{i=1}^k$ .

- Tiles are colored according to which clusters the corresponding rows and columns belong to
- Projection over the rows and columns
- Complex clusterings appear in Data Mining [3, 4]



## Problem Summary

- *Input:*
  - The bipartite graph  $G$
  - A *complex clustering*, i.e., clusters  $\{(R'_i, C'_i)\}_{i=1}^k$
- *Output:*
  - A permutation of the rows and of the columns that visualizes the given clustering  $\{(R'_i, C'_i)\}_{i=1}^k$

To get the permutations, we maximize an objective function that measures the drawing quality:

$$\arg \max_{\pi_R, \pi_C} \sum_{i=0}^k S(\text{cluster}_i, (\pi_R, \pi_C)),$$

where

$$S(\text{cluster}) = \sum_{\text{rect} \in \mathcal{R}(\text{cluster})} \text{area}(\text{rect})^2.$$

It is founded on two properties:

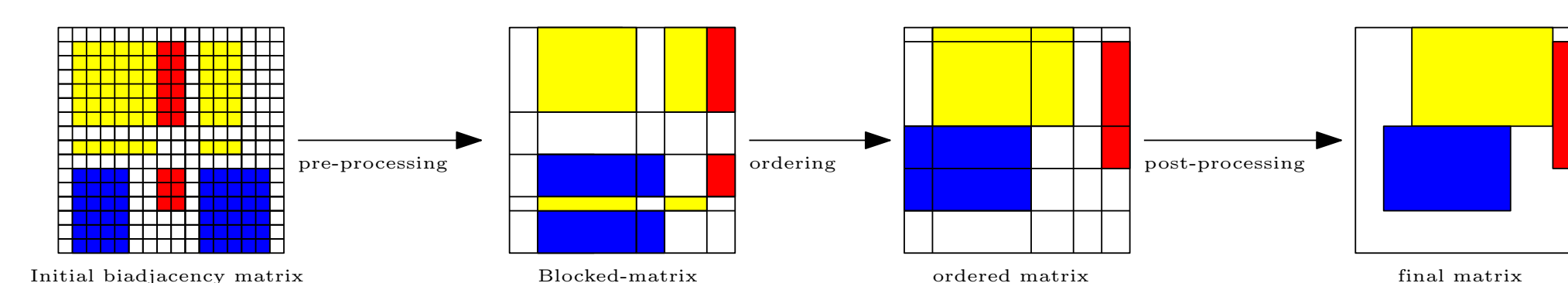
- The score of two clusters should be evaluated independently:

$$S\left(\begin{array}{|c|c|} \hline \text{diagonal} & \text{diagonal} \\ \hline \end{array}\right) = S\left(\begin{array}{|c|c|} \hline \text{diagonal} & \text{empty} \\ \hline \end{array}\right) + S\left(\begin{array}{|c|c|} \hline \text{empty} & \text{diagonal} \\ \hline \end{array}\right)$$

- A cluster is well drawn when it appears in the drawing as a large consecutive rectangle

$$S\left(\begin{array}{|c|c|} \hline \text{blue} & \text{white} \\ \hline \end{array}\right) > S\left(\begin{array}{|c|c|} \hline \text{blue} & \text{blue} \\ \hline \end{array}\right) > S\left(\begin{array}{|c|c|} \hline \text{white} & \text{white} \\ \hline \end{array}\right)$$

## Algorithm Overview

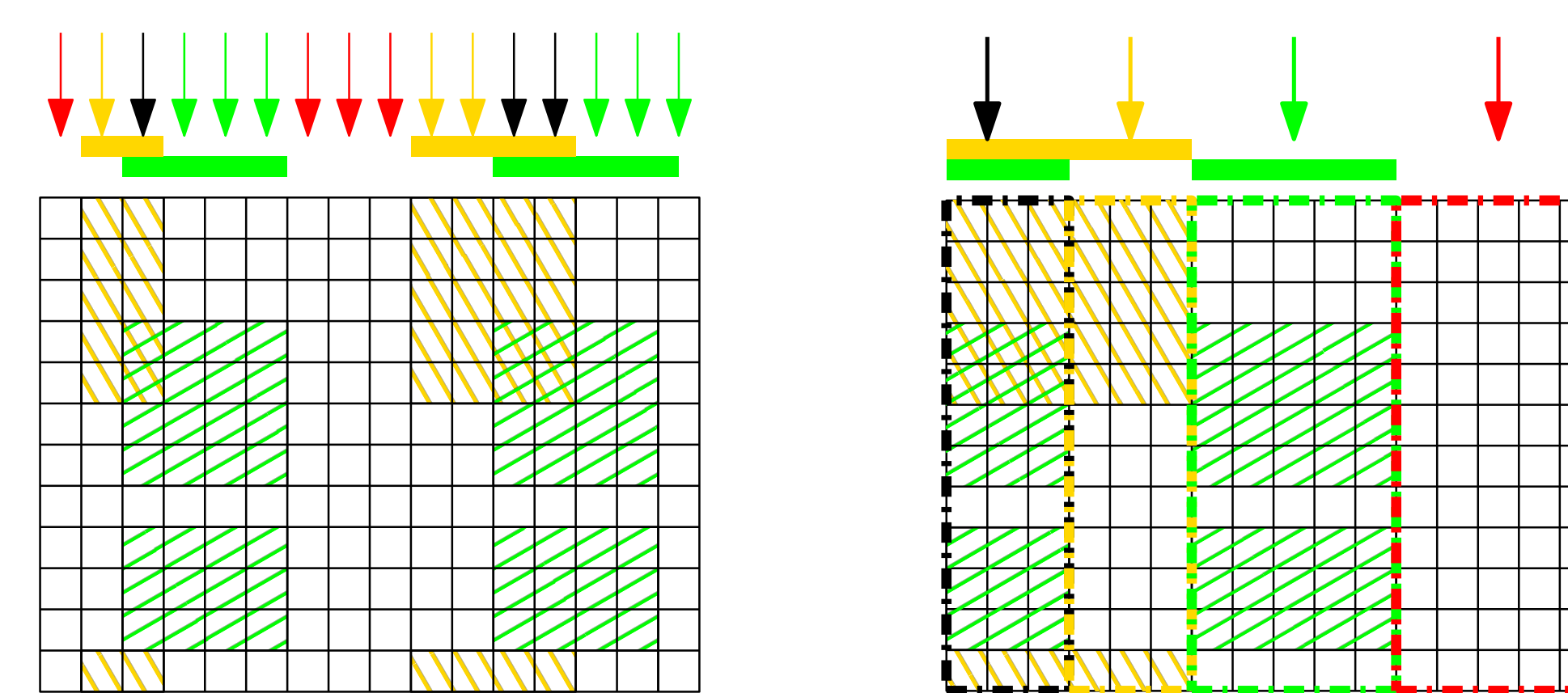


- *Pre-processing:* Reduce the computational complexity by creating *blocks* of rows and columns
- *Ordering:* Provide an ordering of the blocks to draw clusters as good as possible. There are two components in this step:
  - *Objective function:* Assert the quality of the ordering
  - *Optimization algorithm:* Find the best permutation possible to maximize the objective function
- *Post-processing:* Augment the ordering of the previous phase to get a better global picture

## Pre-processing

*Goal:* Utilize the clustering information to reduce the computational complexity of the problem.

- Form *blocks* of columns (and rows) that belong exactly to the same set of clusters



*Consequence:* We only need to reorder the blocks! This reorders the rows and columns implicitly.

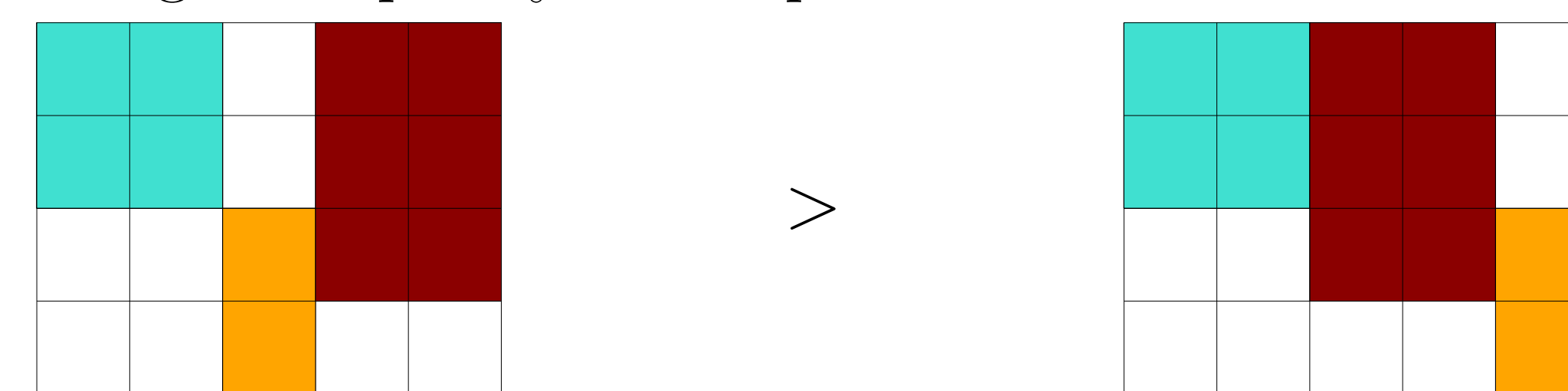
## Ordering

*Goal:* Compute an ordering of the blocks to draw the clusters as good as possible.

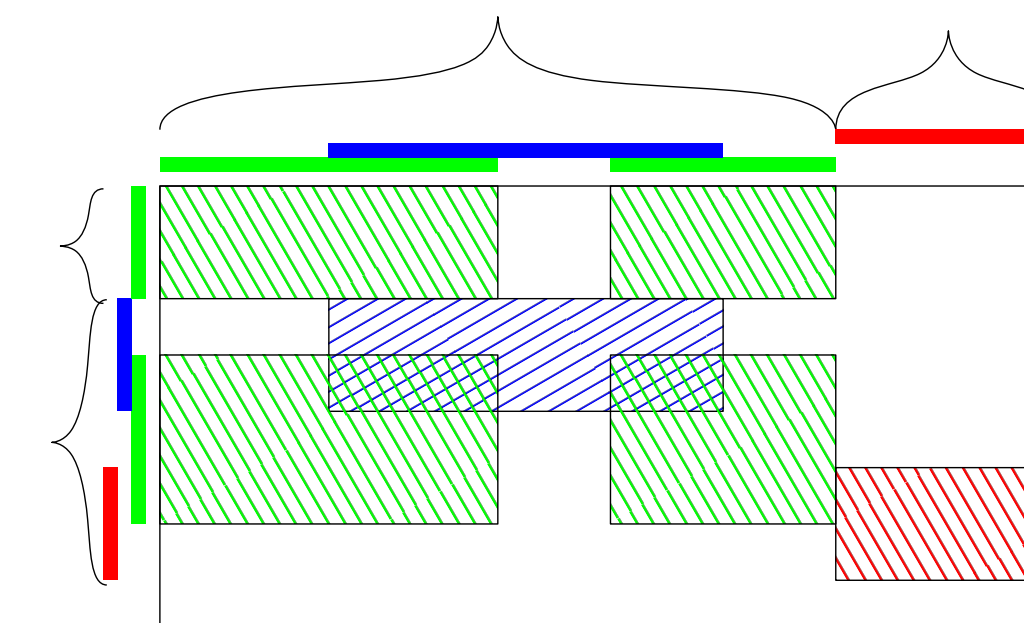
- We maximize the objective function detailed on the left column

## Post-processing

*Goal:* Reorder *groups of* blocks such that the objective function does not decrease, but we increase the global quality of the picture.

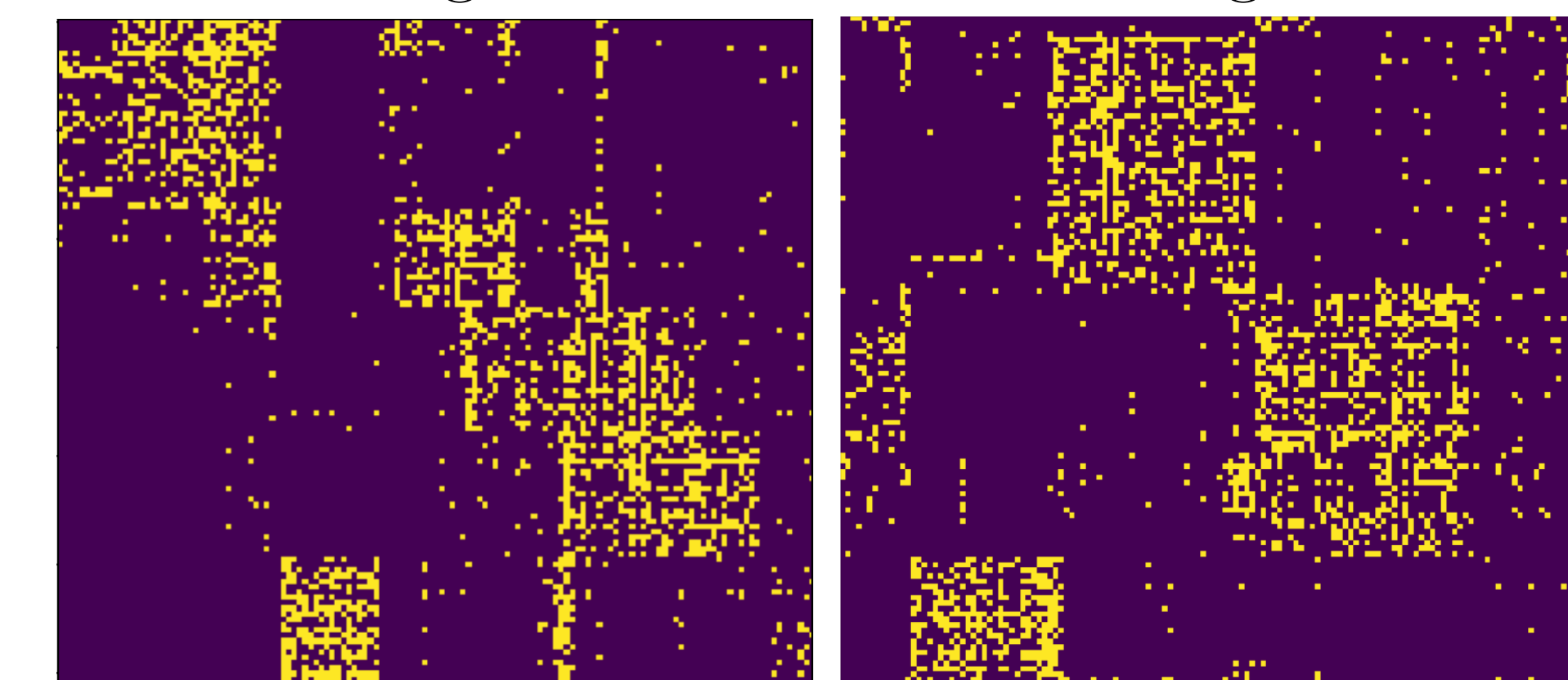


→ Partition the columns so that any pair of columns that have a common cluster are in the same set

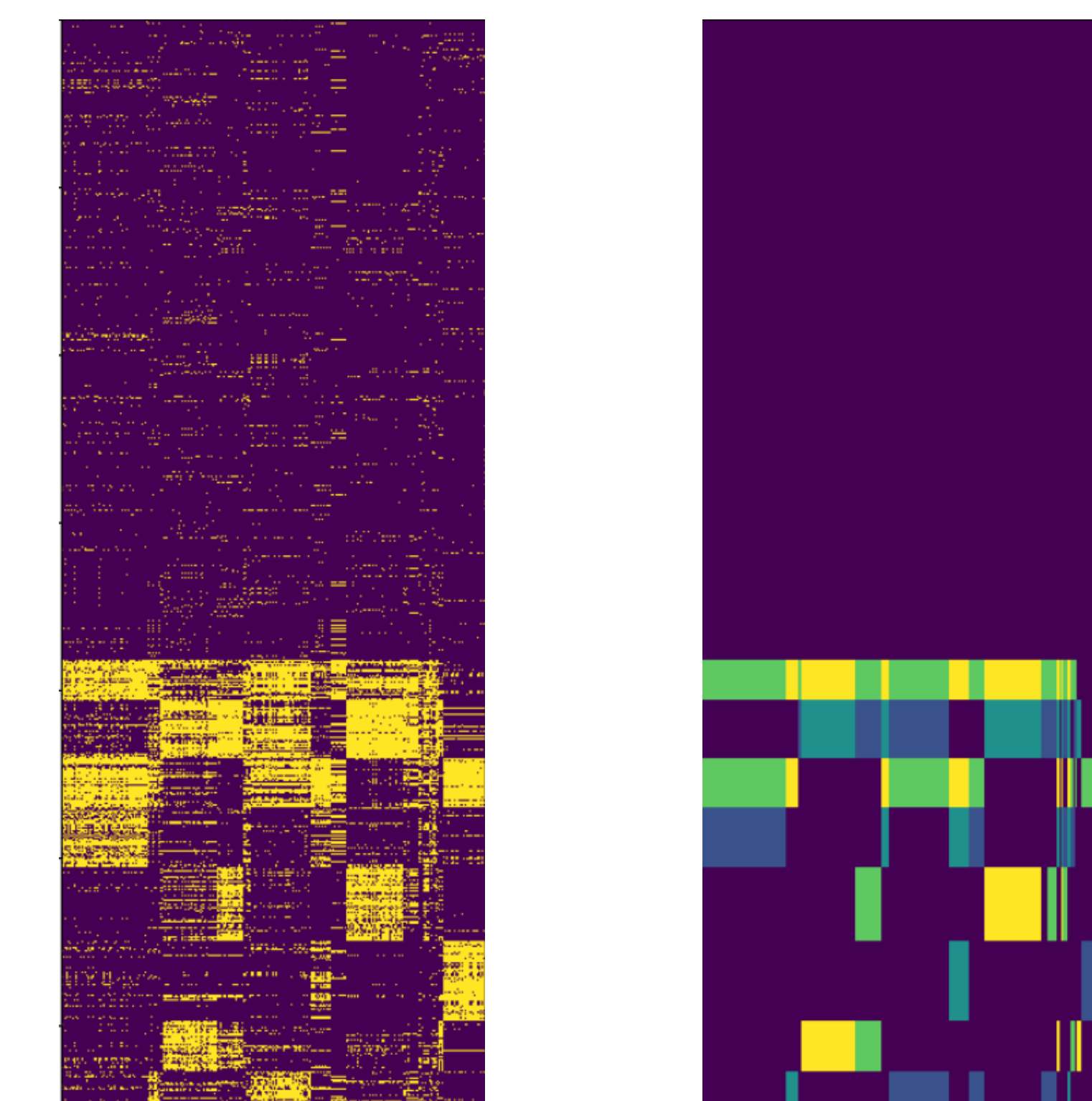


## Results

- Use the visualization to compare clusterings PCV algorithm Basso algorithm



- Assess the local imperfections of a clustering



## References

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- [4] S.C. Madeira and A.L. Oliveira. Biclustering algorithms for biological data analysis: a survey. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(1):24–45, 2004.

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