



Biclustering Algorithms for Biological Data Analysis

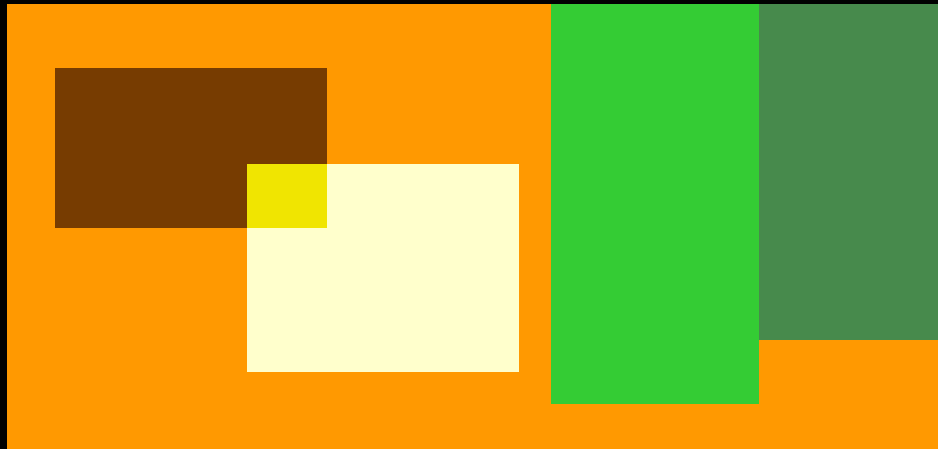
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Presentation by
Matthew Hibbs



What is Biclustering?

- Given an $n \times m$ matrix, A , find a set of submatrices, B_k , such that the contents of each B_k follow a desired pattern
- Row/Column order need not be consistent between different B_k s



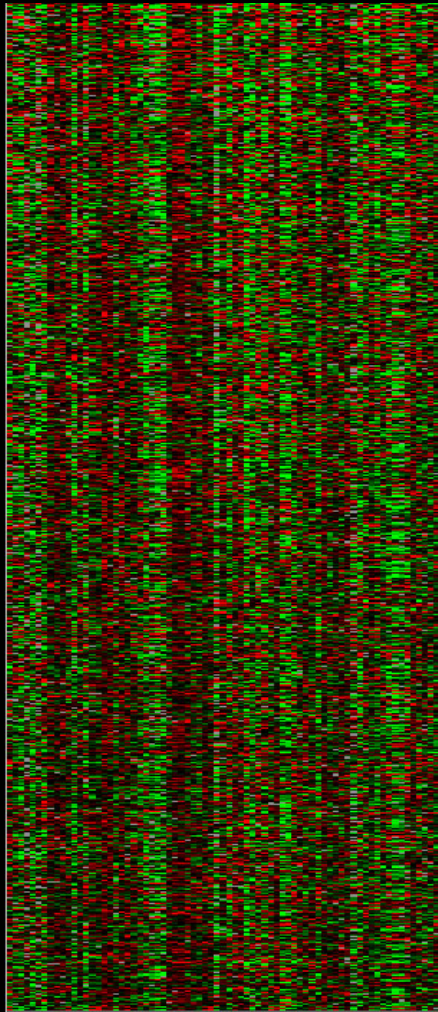


Why Biclusters?

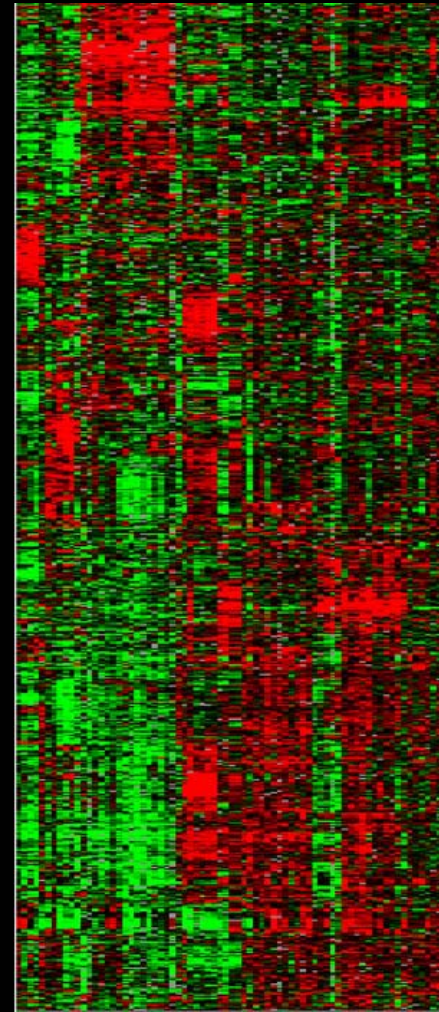
- Genes not regulated under all conditions
- Genes regulated by multiple factors/processes concurrently
- Key to determine function of genes
- Key to determine classification of conditions



Simple “Bicluster”



Unclustered



Clustered

Dataset from Garber et al.



Formal Definitions

- A contains rows X and columns Y
- $X = \{x_1, \dots, x_n\}$ $Y = \{y_1, \dots, y_n\}$
- $I \subseteq X, J \subseteq Y, A_{IJ} = (I, J) = \text{submatrix}$
- $I = \{i_1, \dots, i_k\}$ $J = \{j_1, \dots, j_s\}$

$$a_{iJ} = \frac{1}{|J|} \sum_{j \in J} a_{ij}$$

$$a_{IJ} = \frac{1}{|I||J|} \sum_{i \in I, j \in J} a_{ij}$$

$$a_{Ij} = \frac{1}{|I|} \sum_{i \in I} a_{ij}$$

$$a_{IJ} = \frac{1}{|I|} \sum_{i \in I} a_{iJ} = \frac{1}{|J|} \sum_{j \in J} a_{Ij}$$

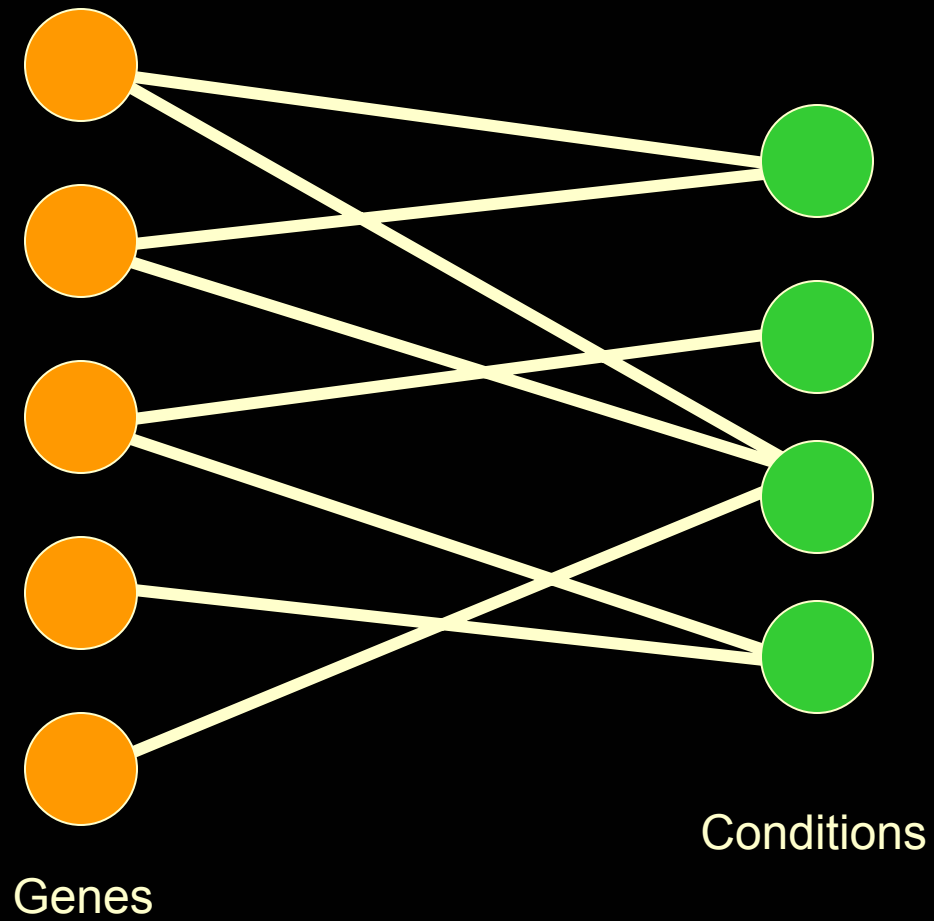


Bipartite Graph

- Matrix can be thought of as a Graph
- Rows are one set of vertices L , Columns are another set R
- Edges are weighted by the corresponding entries in the matrix
- If all weights are binary, biclustering becomes biclique finding

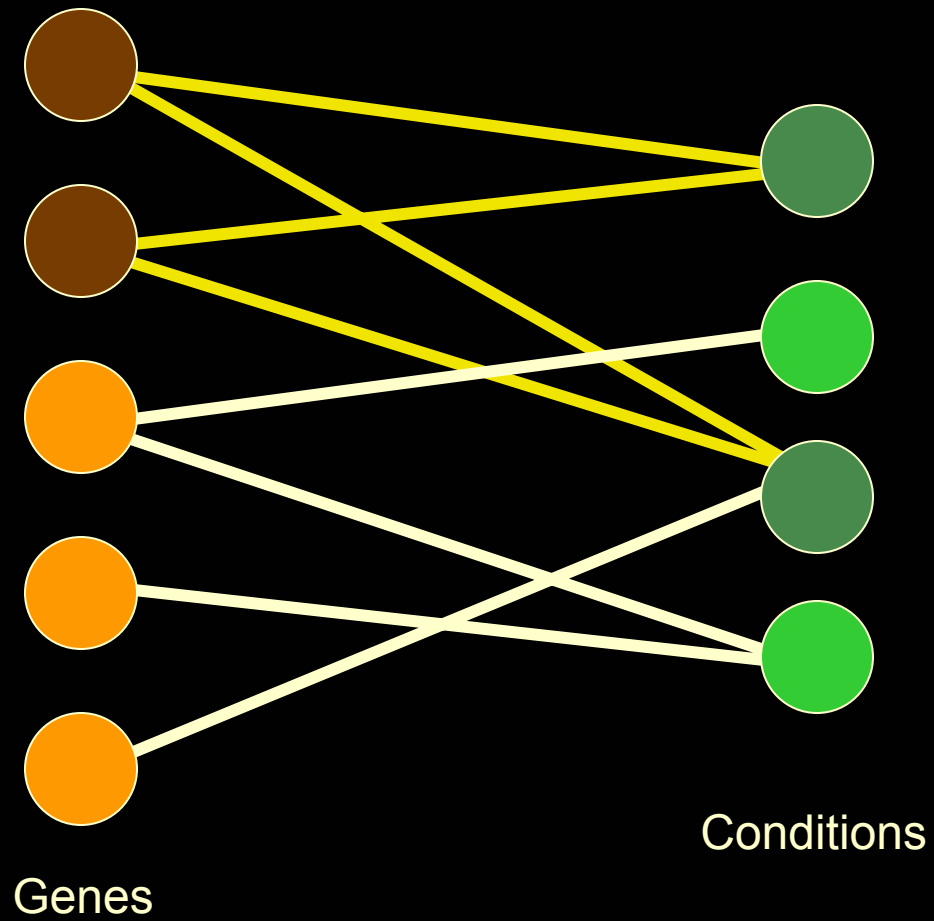


NP-complete





NP-complete





Ordering an Algorithm

- Biclustor Type
- Biclustor Structure
- Algorithmic Approach





Ordering an Algorithm

- Bicluster Type
- Bicluster Structure
- Algorithmic Approach





Bicluster Types

- Constant values
- Constant values on rows or columns
- Coherent values
- Coherent evolutions

1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0

1.0	1.0	1.0	1.0
2.0	2.0	2.0	2.0
3.0	3.0	3.0	3.0
4.0	4.0	4.0	4.0

1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0

1.0	2.0	5.0	0.0
2.0	3.0	6.0	1.0
4.0	5.0	8.0	3.0
5.0	6.0	9.0	4.0

1.0	2.0	0.5	1.5
2.0	4.0	1.0	3.0
4.0	8.0	2.0	6.0
3.0	6.0	1.5	4.5

S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1

S1	S1	S1	S1
S2	S2	S2	S2
S3	S3	S3	S3
S4	S4	S4	S4

S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4

70	13	19	10
49	40	49	35
40	20	27	15
90	15	20	12

↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖



Constant Values

Perfect: $a_{ij} = \mu$ for all $i \in I$ and $j \in J$
Block Clustering, minimize *variance*:

$$VAR(I, J) = \sum_{i \in I, j \in J} (a_{ij} - a_{IJ})^2.$$

1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0

1.0	1.0	1.0	1.0
2.0	2.0	2.0	2.0
3.0	3.0	3.0	3.0
4.0	4.0	4.0	4.0

1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0

1.0	2.0	5.0	0.0
2.0	3.0	6.0	1.0
4.0	5.0	8.0	3.0
5.0	6.0	9.0	4.0

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2.0	4.0	1.0	3.0
4.0	8.0	2.0	6.0
3.0	6.0	1.5	4.5

S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1

S1	S1	S1	S1
S2	S2	S2	S2
S3	S3	S3	S3
S4	S4	S4	S4

S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4

70	13	19	10
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↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖



Constant Values on Rows/Cols

Perfect constant Rows:

$$a_{ij} = \mu + \alpha_i,$$

$$a_{ij} = \mu \times \alpha_i,$$

Perfect constant Columns:

$$a_{ij} = \mu + \beta_j,$$

$$a_{ij} = \mu \times \beta_j,$$

1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0

1.0	1.0	1.0	1.0
2.0	2.0	2.0	2.0
3.0	3.0	3.0	3.0
4.0	4.0	4.0	4.0

1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0

1.0	2.0	5.0	0.0
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4.0	5.0	8.0	3.0
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3.0	6.0	1.5	4.5

S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1

S1	S1	S1	S1
S2	S2	S2	S2
S3	S3	S3	S3
S4	S4	S4	S4

S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4

70	13	19	10
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↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖



Constant Values on Rows/Cols

- Normalize rows/cols → constant value
- Noise makes perfect biclusters rare
 - δ -valid ks-patterns (Califano et al.)

$$\max(a_{ij}) - \min(a_{ij}) < \delta, \forall j \in J$$

1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0

1.0	1.0	1.0	1.0
2.0	2.0	2.0	2.0
3.0	3.0	3.0	3.0
4.0	4.0	4.0	4.0

1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0

1.0	2.0	5.0	0.0
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S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1

S1	S1	S1	S1
S2	S2	S2	S2
S3	S3	S3	S3
S4	S4	S4	S4

S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4

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90	15	20	12

↗	↗	↘	↗
↖	↖	↗	↖
↗	↗	↘	↗
↖	↖	↗	↖



Coherent values

Perfect additive model:

$$a_{ij} = \mu + \alpha_i + \beta_j$$

Perfect multiplicative model:

$$a_{ij} = \mu' \times \alpha'_i \times \beta'_j$$

$$\mu = \log(\mu'), \alpha_i = \log(\alpha'_i), \beta_j = \log(\beta'_j)$$

1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0

1.0	1.0	1.0	1.0
2.0	2.0	2.0	2.0
3.0	3.0	3.0	3.0
4.0	4.0	4.0	4.0

1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0

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S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1

S1	S1	S1	S1
S2	S2	S2	S2
S3	S3	S3	S3
S4	S4	S4	S4

S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4

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90	15	20	12

↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖



Coherent values

Perfect δ -bicluster: $a_{ij} = a_{iJ} + a_{Ij} - a_{IJ}$

(Cheng & Church) Residue: $r(a_{ij}) = a_{ij} - a_{iJ} - a_{Ij} + a_{IJ}$

Mean squared residue: $H(I, J) = \frac{1}{|I||J|} \sum_{i \in I, j \in J} r(a_{ij})^2$

1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0

1.0	1.0	1.0	1.0
2.0	2.0	2.0	2.0
3.0	3.0	3.0	3.0
4.0	4.0	4.0	4.0

1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0

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5.0	6.0	9.0	4.0

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2.0	4.0	1.0	3.0
4.0	8.0	2.0	6.0
3.0	6.0	1.5	4.5

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S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1

S1	S1	S1	S1
S2	S2	S2	S2
S3	S3	S3	S3
S4	S4	S4	S4

S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4

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↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖



Overlapping Coherent Values

Plaid Model or General Additive Model (Lazzeroni and Owen)

$$a_{ij} = \sum_{k=0}^K \theta_{ijk} \rho_{ik} \kappa_{jk} \quad \frac{1}{2} \sum_{i=1}^n \sum_{j=1}^m (a_{ij} - \theta_{ij0} - \sum_{k=1}^K \theta_{ijk} \rho_{ik} \kappa_{jk})^2$$

$$\theta_{ijk} = \mu_k, \mu_k + \alpha_{ik}, \mu_k + \beta_{jk}, \text{ or } \mu_k + \alpha_{ik} + \beta_{jk}$$

1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	3.0	3.0
1.0	1.0	3.0	3.0
		2.0	2.0
		2.0	2.0
		2.0	2.0
		2.0	2.0

1.0	1.0	1.0	1.0
2.0	2.0	2.0	2.0
3.0	3.0	8.0	8.0
4.0	4.0	10.0	10.0
		7.0	7.0
		8.0	8.0
		8.0	8.0
		8.0	8.0

1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	8.0	10.0
1.0	2.0	8.0	10.0
		5.0	6.0
		5.0	6.0
		7.0	8.0
		7.0	8.0

1.0	2.0	5.0	0.0
2.0	3.0	6.0	1.0
4.0	5.0	9.0	5.0
5.0	6.0	11.0	7.0
		4.0	5.0
		5.0	6.0
		8.0	3.0
		9.0	4.0



Overlapping Coherent Values

Gaussian Distribution with variance depending on
row, column, and bicluster variance

$$\sum_{i=1}^n \sum_{j=1}^m \frac{(a_{ij} - \theta_{ij0} - \sum_{k=1}^K \theta_{ijk} \rho_{ik} \kappa_{jk})^2}{2(\sigma_{iJ}^2 + \sigma_{Ij}^2 + \sigma_{IJ}^2)}$$

1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	3.0	3.0
1.0	1.0	3.0	3.0
		2.0	2.0
		2.0	2.0
		2.0	2.0
		2.0	2.0

1.0	1.0	1.0	1.0
2.0	2.0	2.0	2.0
3.0	3.0	8.0	8.0
4.0	4.0	10.0	10.0
		7.0	7.0
		8.0	8.0
		8.0	8.0
		8.0	8.0

1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	8.0	10.0
1.0	2.0	8.0	10.0
		5.0	6.0
		5.0	6.0
		7.0	8.0
		7.0	8.0

1.0	2.0	5.0	0.0
2.0	3.0	6.0	1.0
4.0	5.0	9.0	5.0
5.0	6.0	11.0	7.0
		4.0	5.0
		5.0	6.0
		8.0	3.0
		9.0	4.0



Coherent Evolutions

- Order-Preserving Submatrix (OPSM, Ben-Dor et al.)
- Order-Preserving Cluster (OP-Cluster, Liu and Wang)
- Rank-based approaches

1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0

1.0	1.0	1.0	1.0
2.0	2.0	2.0	2.0
3.0	3.0	3.0	3.0
4.0	4.0	4.0	4.0

1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0

1.0	2.0	5.0	0.0
2.0	3.0	6.0	1.0
4.0	5.0	8.0	3.0
5.0	6.0	9.0	4.0

1.0	2.0	0.5	1.5
2.0	4.0	1.0	3.0
4.0	8.0	2.0	6.0
3.0	6.0	1.5	4.5

S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1

S1	S1	S1	S1
S2	S2	S2	S2
S3	S3	S3	S3
S4	S4	S4	S4

S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4

70	13	19	10
49	40	49	35
40	20	27	15
90	15	20	12

↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖



Coherent Evolutions

- Quantized expression levels into states
- Maximize conserved rows/cols (Murali and Kasif)

1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0

1.0	1.0	1.0	1.0
2.0	2.0	2.0	2.0
3.0	3.0	3.0	3.0
4.0	4.0	4.0	4.0

1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0

1.0	2.0	5.0	0.0
2.0	3.0	6.0	1.0
4.0	5.0	8.0	3.0
5.0	6.0	9.0	4.0

1.0	2.0	0.5	1.5
2.0	4.0	1.0	3.0
4.0	8.0	2.0	6.0
3.0	6.0	1.5	4.5

S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1

S1	S1	S1	S1
S2	S2	S2	S2
S3	S3	S3	S3
S4	S4	S4	S4

S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4

70	13	19	10
49	40	49	35
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↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖



Coherent Evolutions

- Identify “significant conditions” with respect to normal levels
- Construct a bipartite graph containing only these edges
- bicluster is biclique (simple SAMBA, Tanay et al.)

1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0

1.0	1.0	1.0	1.0
2.0	2.0	2.0	2.0
3.0	3.0	3.0	3.0
4.0	4.0	4.0	4.0

1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0

1.0	2.0	5.0	0.0
2.0	3.0	6.0	1.0
4.0	5.0	8.0	3.0
5.0	6.0	9.0	4.0

1.0	2.0	0.5	1.5
2.0	4.0	1.0	3.0
4.0	8.0	2.0	6.0
3.0	6.0	1.5	4.5

S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1

S1	S1	S1	S1
S2	S2	S2	S2
S3	S3	S3	S3
S4	S4	S4	S4

S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4

70	13	19	10
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↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖
↖	↖	↖	↖



Coherent Evolutions

- Label “significant conditions” as up or down regulated
- Select columns that have the same or opposite effect
- (refined SAMBA, Tanay et al.)

1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0
1.0	1.0	1.0	1.0

1.0	1.0	1.0	1.0
2.0	2.0	2.0	2.0
3.0	3.0	3.0	3.0
4.0	4.0	4.0	4.0

1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0
1.0	2.0	3.0	4.0

1.0	2.0	5.0	0.0
2.0	3.0	6.0	1.0
4.0	5.0	8.0	3.0
5.0	6.0	9.0	4.0

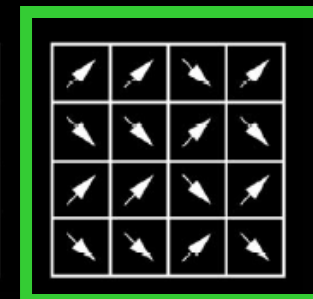
1.0	2.0	0.5	1.5
2.0	4.0	1.0	3.0
4.0	8.0	2.0	6.0
3.0	6.0	1.5	4.5

S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1
S1	S1	S1	S1

S1	S1	S1	S1
S2	S2	S2	S2
S3	S3	S3	S3
S4	S4	S4	S4

S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4
S1	S2	S3	S4

70	13	19	10
49	40	49	35
40	20	27	15
90	15	20	12





Ordering an Algorithm

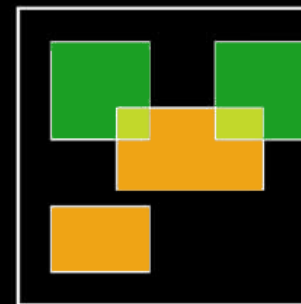
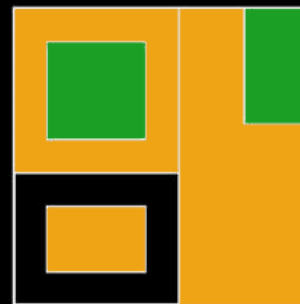
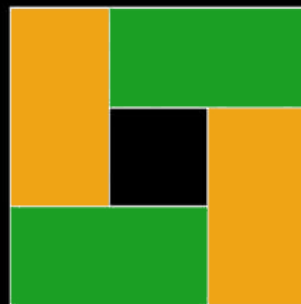
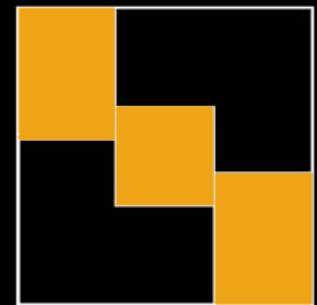
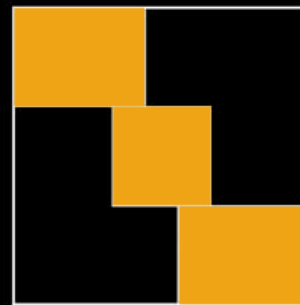
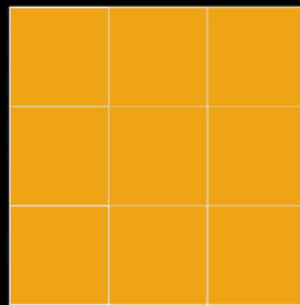
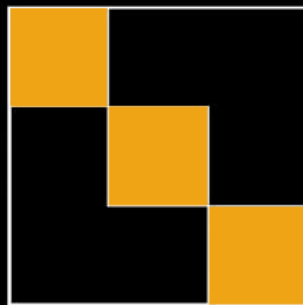
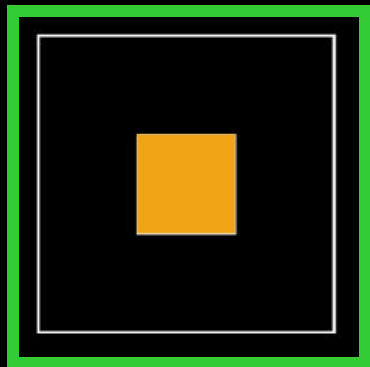
- Biclust^{er} Type
- Biclust^{er} Structure
- Algorithmic Approach





Bicluster Structure

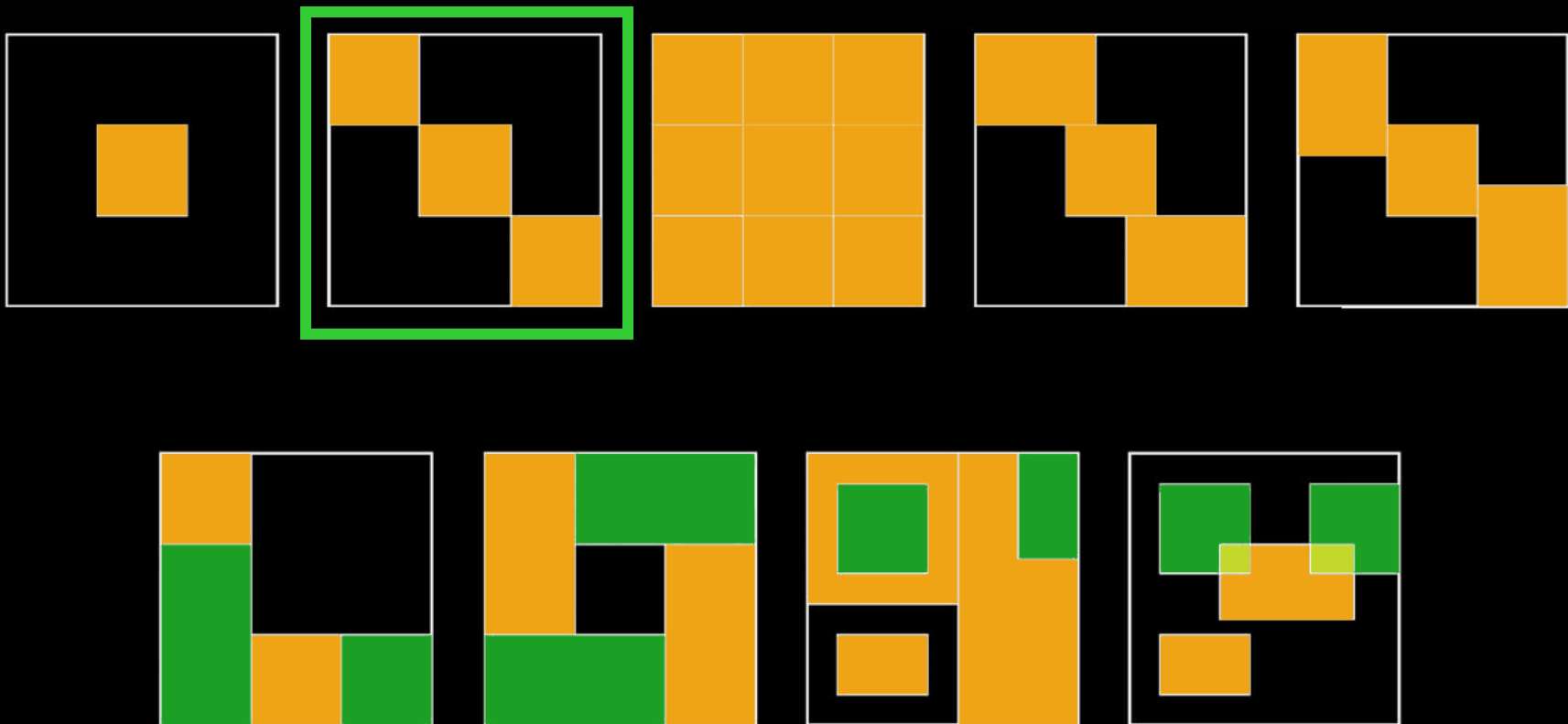
Single Bicluster





Bicluster Structure

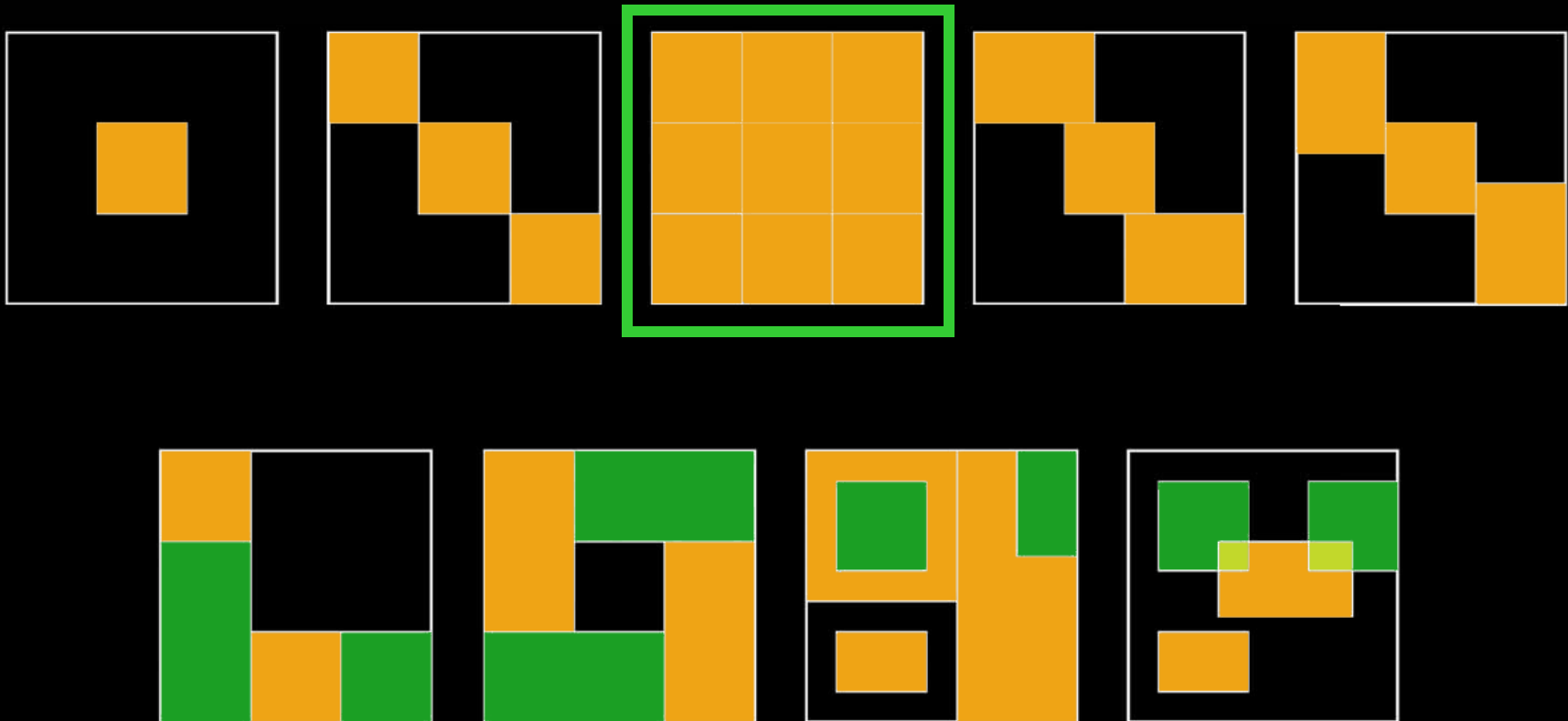
Exclusive row and column bicluster





Bicluster Structure

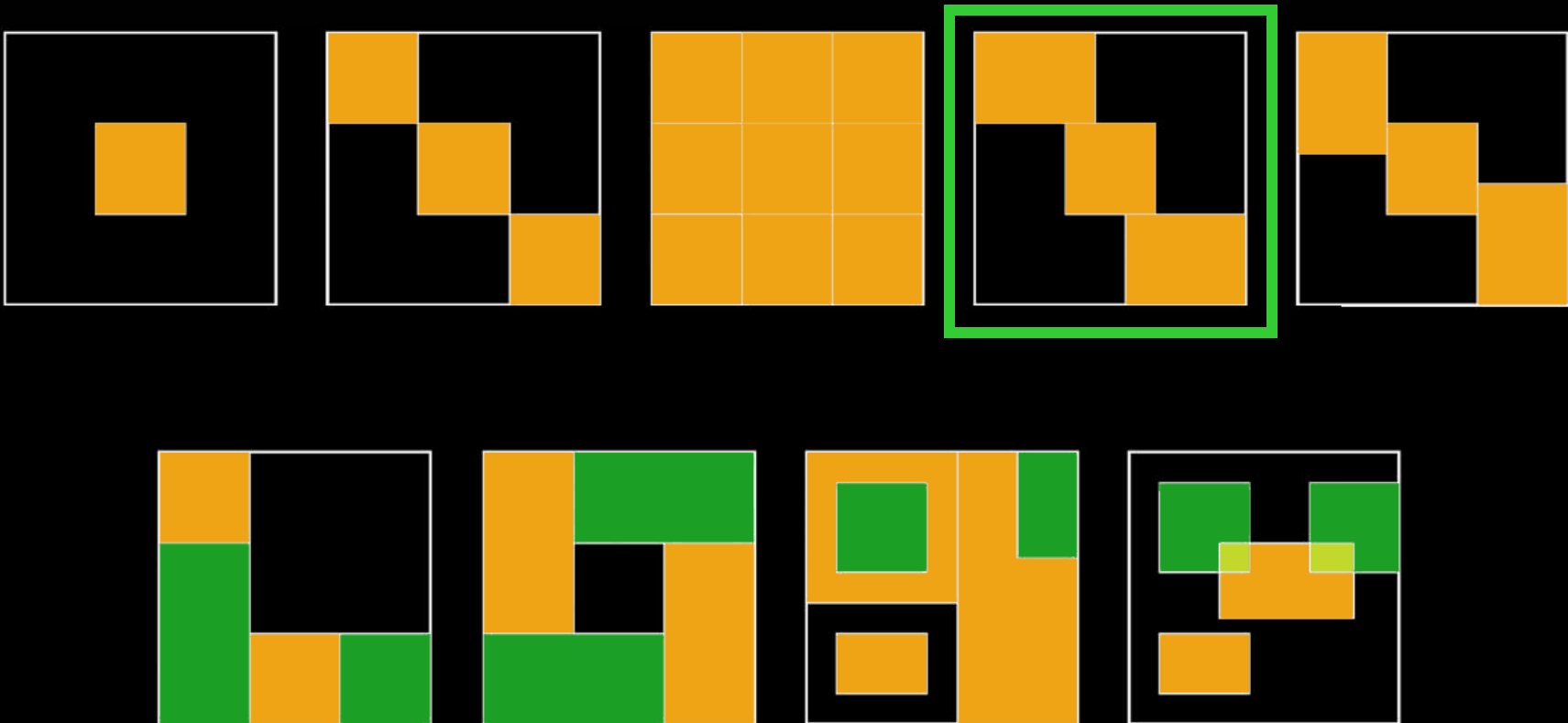
Non-overlapping checkerboard biclusters





Bicluster Structure

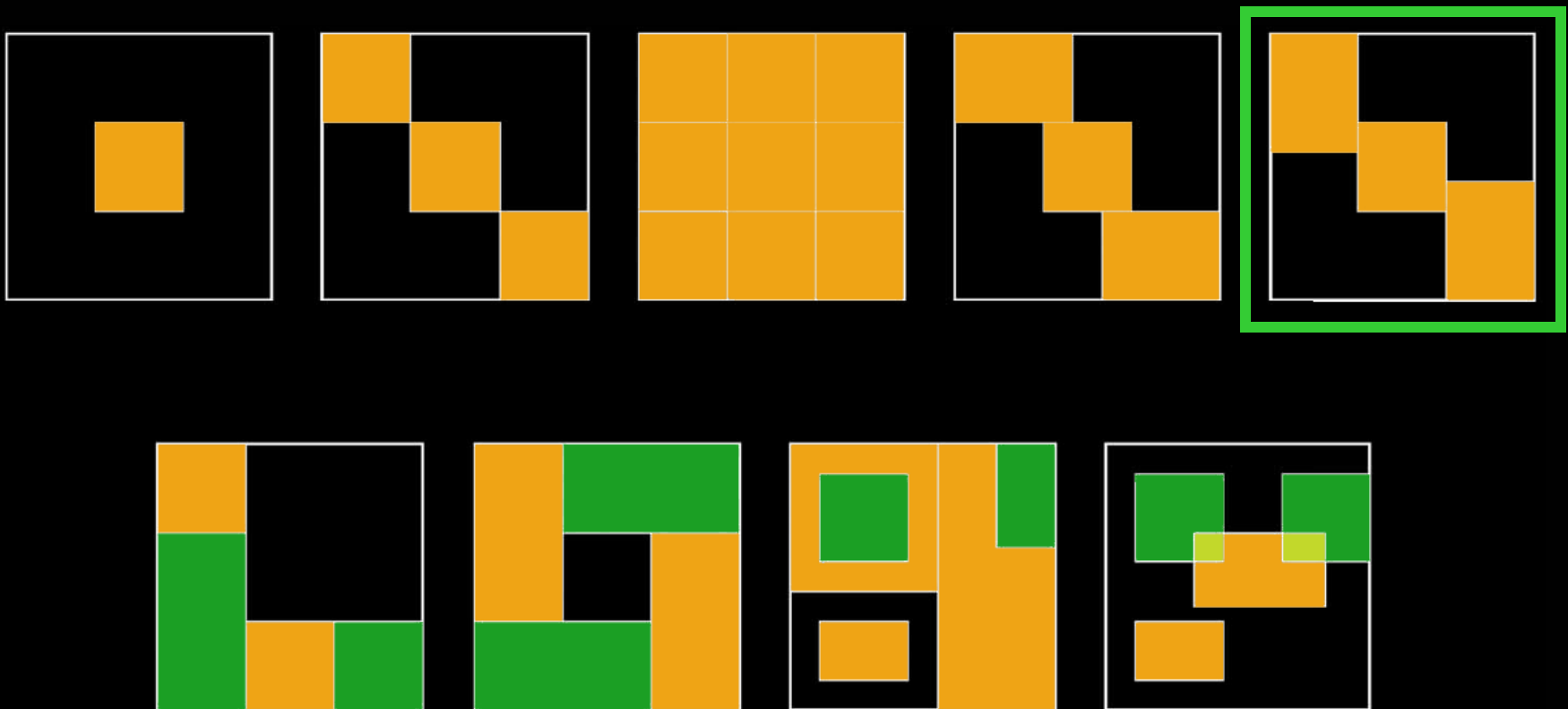
Exclusive-rows biclusters





Bicluster Structure

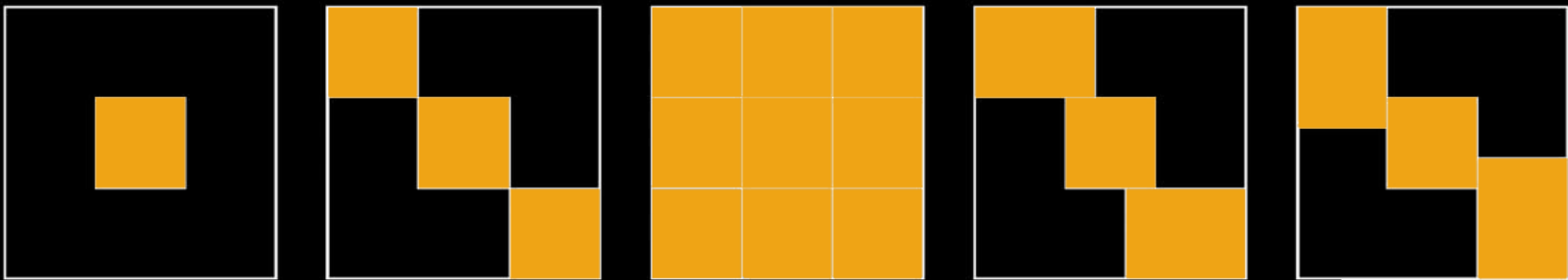
Exclusive-columns biclusters





Bicluster Structure

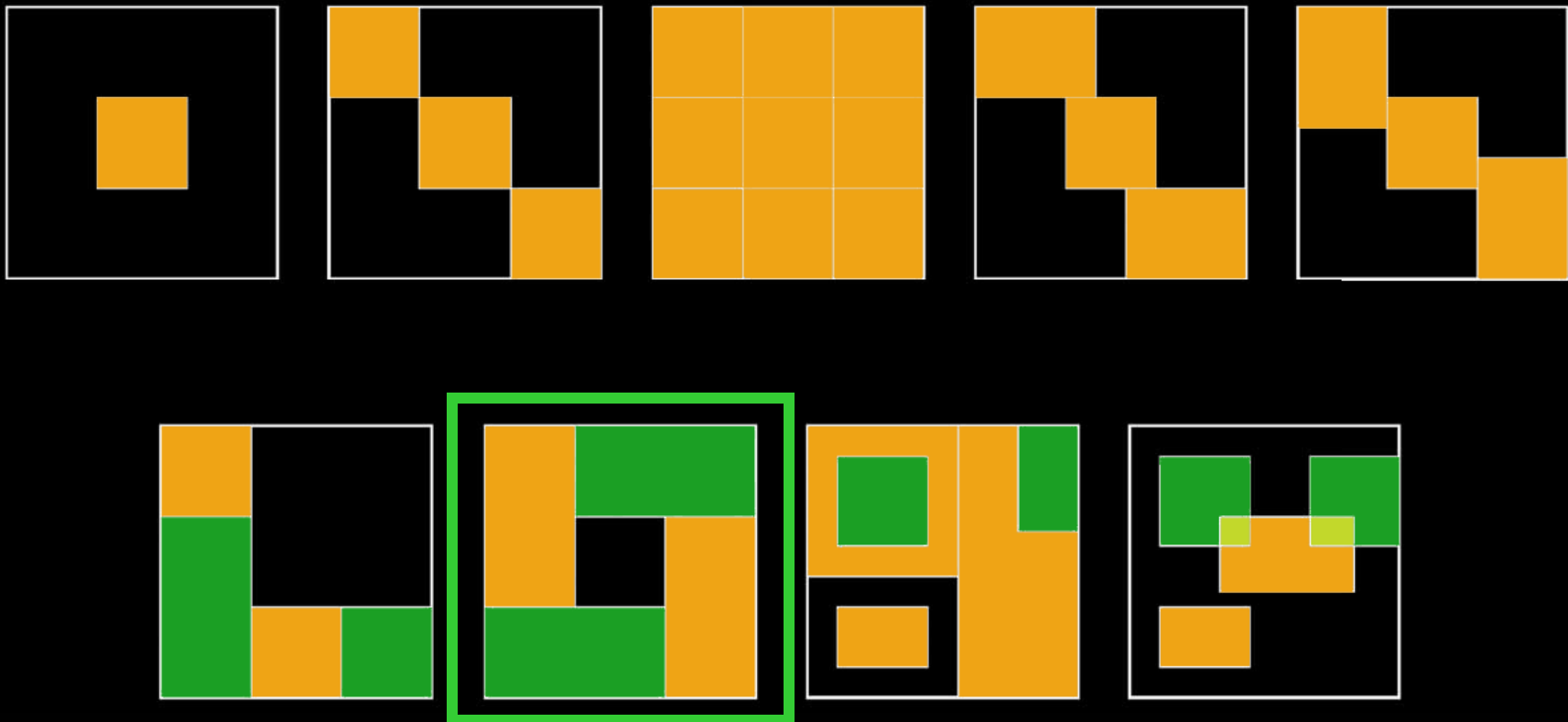
Non-overlapping tree structured biclusters





Bicluster Structure

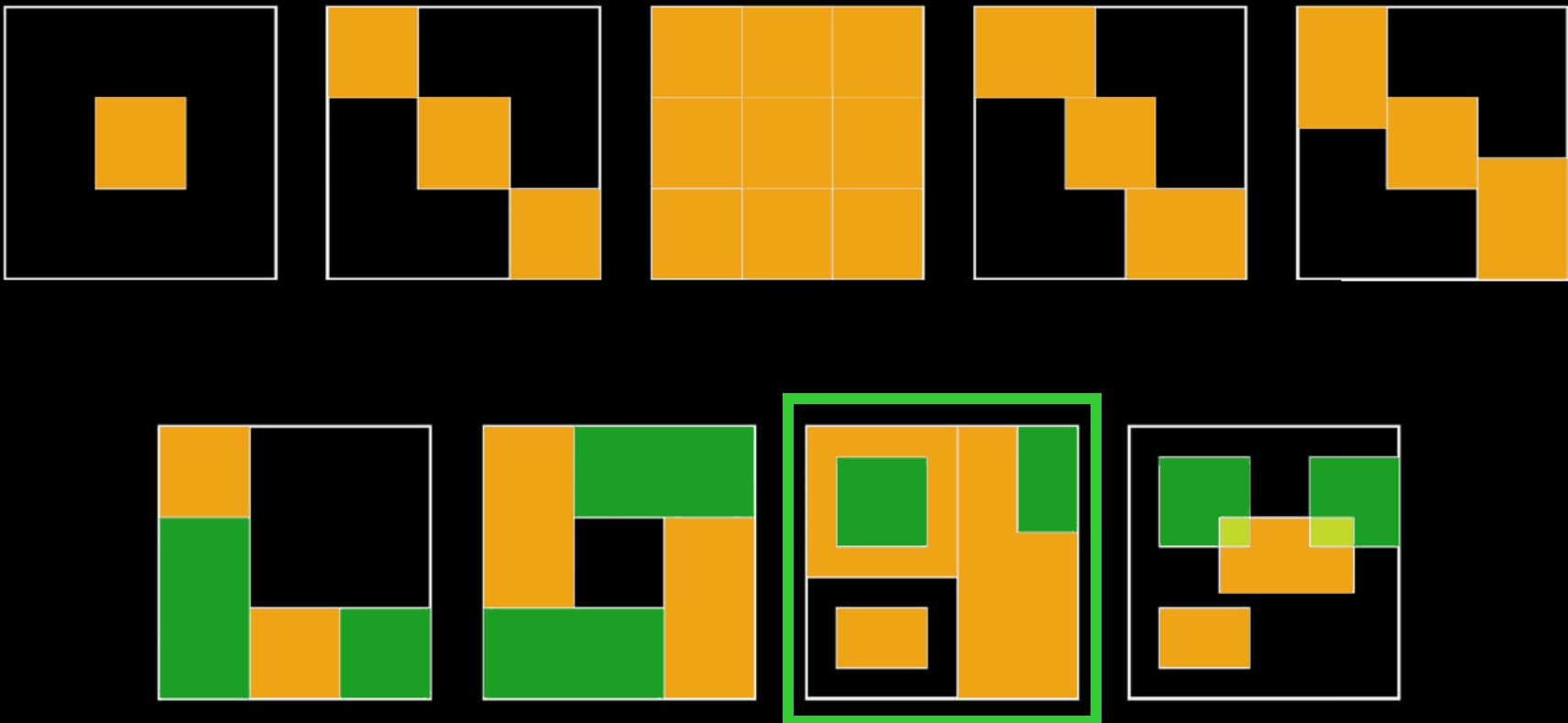
Non-overlapping non-exclusive biclusters





Bicluster Structure

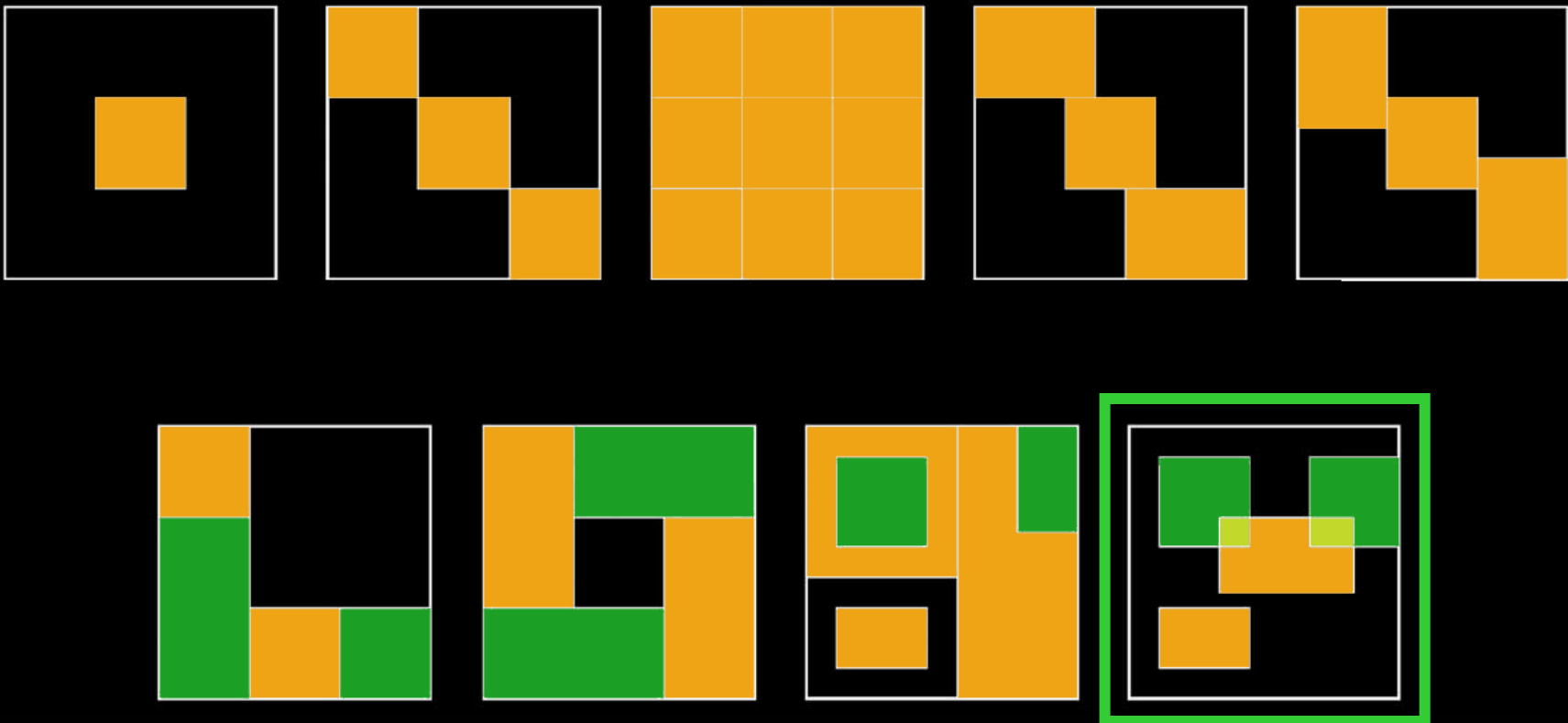
Overlapping hierarchically-structured biclusters





Bicluster Structure

Arbitrary overlapping biclusters





Ordering an Algorithm

- Biclust^{er} Type
- Biclust^{er} Structure
- Algorithmic Approach





Algorithmic Approaches

- Iterative row and column clustering combo
- Divide and conquer
- Greedy iterative search
- Exhaustive bicluster enumeration
- Distribution parameter identification



Iterative Row and Column

- Coupled Two-Way Clustering (CTWC)
 - Keep sets of row and column clusters
 - Start with all rows and all columns
 - Hierarchically cluster based on pairs of row/column clusters
 - Identify new “stable” row/column clusters
 - Repeat until a desired resolution



Iterative Row and Column

- Interrelated Two-Way Clustering (ITWC)
 - Cluster the rows into K groups
 - Cluster columns into two groups based on each row group
 - Combine row and column clusterings
 - Identify row/column cluster pairs that are very different from each other
 - Keep the best $1/3$ rows in the heterogeneous pairs
 - Repeat



Divide and Conquer

- Block Clustering (Hartigan)
 - Sort by row or column mean
 - Find best row or column split to reduce “within block” variance
 - Continue, alternating row or column splits
 - Stop when arrive at desired K blocks
- Very fast, but likely to miss good biclusters due to early splits



Greedy Iterative Search

- δ -biclusters (Cheung & Church)
 - Find biclusters with mean squared residue $< \delta$
 - Iterative procedure
 - Remove the row/col that reduces H the most
 - Add rows/cols that do not increase H
 - Stop when $H < \delta$
 - Mask bicluster with random values
 - Repeat to find next bicluster



Exhaustive Biclusters Enumeration

- Statistical-Algorithmic Method for Biclusters Analysis (SAMBA, Tanay et al.)
 - Conversion to bipartite graph
 - Equivalent to selection of heaviest subgraphs
 - Assumes rows have d -bounded degree
 - Report the K heaviest bicliques



Distribution Parameter Identification

- Plaid Model (Lazzeroni and Owen)
 - Given $K-1$ biclusters, select the K th bicluster that minimizes sum of squared errors

$$Q = \frac{1}{2} \sum_{i=1}^n \sum_{j=1}^m (Z_{ij} - \theta_{ijK} \rho_{iK} \kappa_{jK})^2$$

$$Z_{ij} = a_{ij} - \theta_{ij0} - \sum_{k=1}^{K-1} \theta_{ijk} \rho_{ik} \kappa_{jk}$$

- Sort of like EM, determine θ from ρ and κ , then ρ from θ and κ , then κ from θ and ρ
- “Fuzzy” membership until end ($\rho, \kappa \in [0,1]$)



Ordering an Algorithm

- Biclusters Type
- Biclusters Structure
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Comparison of Biclustering Algorithms

		Type	Structure	Discovery	Approach
<i>Block Clustering</i>	[24]	Constant	4(f)	One Set at a Time	Div-and-Conq
<i>δ-biclusters</i>	[10]	Coherent Values	4(i)	One at a Time	Greedy
<i>FLOC</i>	[50]	Coherent Values	4(i)	Simultaneous	Greedy
<i>FLOC</i>	[51]	Coherent Values	4(i)	Simultaneous	Greedy
<i>pClusters</i>	[48]	Coherent Values	4(g)	Simultaneous	Exh-Enum
<i>Plaid Models</i>	[34]	Coherent Values	4(i)	One at a Time	Dist-Ident
<i>PRMs</i>	[41]	Constant Columns	4(b)	Simultaneous	Dist-Ident
<i>PRMs</i>	[40]	Coherent Values	4(i)	Simultaneous	Dist-Ident
<i>CTWC</i>	[21]	Coherent Values	4(i)	One Set at a Time	Clust-Comb
<i>ITWC</i>	[45]	Coherent Values	4(d)/4(e)	One Set at a Time	Clust-Comb
<i>DCC</i>	[8]	Coherent Values	4(b)/4(c)	Simultaneous	Clust-Comb
<i>δ-Patterns</i>	[9]	Constant Rows	4(i)	Simultaneous	Greedy
<i>Spectral</i>	[32]	Coherent Values	4(c)	Simultaneous	Greedy
<i>Gibbs</i>	[42]	Constant Columns	4(d)/4(c)	One at a Time	Dist-Ident
<i>OPSMs</i>	[6]	Coherent Evolution	4(a)/4(i)	One at a Time	Greedy
<i>SAMBA</i>	[44]	Coherent Evolution	4(i)	Simultaneous	Exh-Enum
<i>xMOTIFs</i>	[37]	Coherent Evolution	4(a)/4(i)	Simultaneous	Greedy
<i>OP-Clusters</i>	[35]	Coherent Evolution	4(i)	Simultaneous	Exh-Enum
<i>Co-Clusters</i>	[11]	Constant/Coherent Values	4(i)	Simultaneous	Greedy



Other Applications

- Information Retrieval
 - Targeted marketing
 - Text mining
- Dimensionality Reduction
 - automatic subspace clustering
- Electoral Data Analysis
- much more...



Conclusions

- Biclustering is useful for BioInformatics and many other research areas
- NP-Complete
- Choice of bicluster type and structure with an algorithmic approach → Algorithm