# A Graph Modification Approach for Finding Core–Periphery Structures in Protein Interaction Networks

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# Protein Complex Identification

**Task:** Given a protein interaction network, identify its protein complexes and functional modules

#### Common assumptions:

- Complexes and functional modules are dense subnetworks
- Functional modules have no or only small overlap
- $\rightsquigarrow$  Formulation as graph clustering problem

#### **Cluster Editing**

**Input:** An undirected graph G = (V, E).

**Task:** Find a minimum-size set of edge deletions and edge insertions that converts the graph into a **cluster graph**, that is, a graph where each connected component is a clique.



### Denseness of Complexes and Functional Units **Problem:** Functional units are not necessarily dense



Nucleosome remodeling deacetylase (NuRD) complex of *M. musculus* and its interactions with transcription factors ~~ Core–periphery model of protein complexes

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[Gavin et al., Nature '06]
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Core-Periphery Structures in Protein Interaction Networks

# Core-Periphery Model

**Aim:** Uncover global **core–periphery** structure of given PPI network with dense cores and sparse peripheries.

#### Formalization:

**Split graph** = can be partitioned into clique and independent set

**Split cluster graph** = every connected component is a split graph



 $\sim \rightarrow$ 

### Split Cluster Editing

**Input:** An undirected graph G = (V, E).

**Task:** Find a minimum-size set of edge deletions and edge insertions that converts the graph into a **split cluster** graph.



# Shared Peripheries

### So far:

 Complexes and functional modules are dense subnetworks have core-periphery structure

Functional modules have no or only small overlap

Now: allow overlap but only in peripheries  $\leadsto$ 

Monopolar graph = can be partitioned into cluster graph and independent set ↔



### **Monopolar Editing**

**Input:** An undirected graph G = (V, E).

**Task:** Find a minimum-size set of edge deletions and edge insertions that converts the graph into a monopolar graph.



Problem Complexity—Split Cluster Editing



**Theorem:** (Foldes & Hammer '71) A graph is a split graph iff it does not contain an induced subgraph that is a  $2K_2$ ,  $C_4$ , or  $C_5$ .



#### Main Results:

A graph is a split cluster graph iff it does not contain an induced subgraph that is a  $C_4$ ,  $C_5$ ,  $P_5$ , necktie, or bowtie.

**Split Cluster Editing** is APX-hard and NP-hard even on graphs with maximum degree 11.

**Split Cluster Editing** can be solved in  $O(10^k \cdot m)$  time, where k is the number of necessary edge modifications.

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## Problem Complexity—Monopolar Editing



**Observation:** Monopolar graphs have **infinitely** many forbidden subgraphs (smallest and only with 5 vertices is the wheel  $W_4$  ( $\boxtimes$ )).

**Known:** Vertex-partitioning into fixed additive induced-hereditary properties is NP-hard [Farrugia, Electron. J. Combin. '04].

 $\rightsquigarrow$  **Deciding** whether a graph is monopolar is NP-hard.

# ILP formulations

- Forbidden subgraph-based
- Partition variables
- Column generation

## Forbidden subgraph-based ILP formulation for SCE

#### First try: use forbidden subgraph characterization

 $\sim \rightarrow$ 

Binary variable  $e_{uv} = 1$  if  $\{u, v\}$  is in the solution graph Define  $\bar{e}_{uv} := 1 - e_{uv}$ 

$$\begin{array}{l} \text{minimize} \quad \sum_{\{u,v\}\in E} \bar{e}_{uv} + \sum_{\{u,v\}\notin E} e_{uv} \\ \text{subject to} \\ \forall \text{ forbidden subgraph } F : \sum_{\{u,v\}\in F} \bar{e}_{uv} + \sum_{\{u,v\}\notin F} e_{uv} \geq 1 \end{array}$$

 $O(n^5)$  constraints  $\rightsquigarrow$  use row generation (lazy constraints)

## Partition variable ILP formulation for SCE

**Idea**: Fix the assignment to core and periphery before destroying the forbidden subgraphs

**Lemma:** Let G = (V, E) be a graph and  $C \cup I = V$  a partition of the vertices. Then G is a split cluster graph with **core vertices** C and **independent set vertices** I iff it does not contain an edge with both endpoints in I, nor an induced  $P_3$  with both endpoints in C.



### Partition variable ILP formulation for SCE

Binary variable  $e_{uv} = 1$  if  $\{u, v\}$  is in the solution graph. Define  $\bar{e}_{uv} := 1 - e_{uv}$ 

Binary variable  $c_u = 1$  if u is a core vertex. Define  $\bar{c}_u := 1 - c_u$ .

$$\begin{array}{l} \text{minimize} \quad \sum_{\{u,v\}\in E} \bar{e}_{uv} + \sum_{\{u,v\}\notin E} e_{uv} \\ \text{subject to} \\ \forall u, v : c_u + c_v + \bar{e}_{uv} \ge 1 \\ \forall u \neq v, v \neq w > u : \bar{e}_{uv} + \bar{e}_{vw} + e_{uw} + \bar{c}_u + \bar{c}_w \ge 1 \end{array}$$

 $O(n^3)$  constraints  $\rightsquigarrow$  still use row generation (lazy constraints)

## Partition variable ILP formulation for Monopolar Editing

**Idea (again)**: Fix the assignment to core and periphery before destroying the forbidden subgraphs

**Lemma:** Let G = (V, E) be a graph and  $C \cup I = V$  a partition of the vertices. Then G is a split cluster graph with **core vertices** C and **independent set vertices** I iff it does not contain an edge with both endpoints in I, nor an induced  $P_3$  consisting only of vertices in C.



### Partition variable ILP formulation for Monopolar Editing

Binary variable  $e_{uv} = 1$  if  $\{u, v\}$  is in the solution graph. Define  $\bar{e}_{uv} := 1 - e_{uv}$ 

Binary variable  $c_u = 1$  if u is a core vertex. Define  $\bar{c}_u := 1 - c_u$ .

minimize 
$$\sum_{\{u,v\}\in E} \bar{e}_{uv} + \sum_{\{u,v\}\notin E} e_{uv}$$

subject to

 $\begin{aligned} \forall u, v : c_u + c_v + \bar{e}_{uv} \geq 1 \\ \forall u \neq v, v \neq w > u : \bar{e}_{uv} + \bar{e}_{vw} + e_{uw} + \bar{c}_u + \bar{c}_v + \bar{c}_w \geq 1 \end{aligned}$ 

 $O(n^3)$  constraints  $\rightsquigarrow$  still use row generation (lazy constraints)

## Column generation for Split Cluster Editing

Binary variables  $z_C = 1$  if cluster  $C \in 2^V$  is part of the solution.

$$\begin{array}{ll} \text{maximize} & \displaystyle\sum_{C\in 2^V} c_C z_C, \\ \text{s. t.} & \displaystyle\sum_{C\in 2^V \mid u\in C} z_C = 1 \quad \forall u\in V, \end{array}$$

where  $c_C$  is the "value" of the cluster (number of edges of G[C] minus the *splittance* of G[C], that is, the number of edge insertions and deletions to make it a split graph).

Problem: Exponentially many variables.

**Idea:** Successively add only those variables ("columns") that are "needed", that is, their introduction improves the objective.

## Column Generation: Auxiliary problem

**Lemma:** For the relaxation of the ILP, the objective function change from adding a cluster C is

$$c_C - \sum_{u \in C} \lambda_u$$

where  $\lambda_u$  is the shadow price associated with the constraint of vertex u.

 $\rightsquigarrow$  need to find a cluster that maximizes cluster value minus vertex weights.

Idea: Use an ILP.

## ILP tuning tricks

- Warm start with heuristic solution
- MIP emphasis: balance between proving optimality and finding better solutions
- Cutting planes for  $P_5$ : for all distinct  $u, v, w, x, y \in V$ :

$$ar{e}_{uv}+ar{e}_{vw}+ar{e}_{wx}+ar{e}_{xy}+rac{1}{2}e_{uw}+e_{vx}+rac{1}{2}e_{wy}+rac{1}{2}e_{xu}+rac{1}{2}e_{yv}\geq 1.$$

(for monopolar,  $W_4$ )

## Heuristics

- Forbidden subgraph-based
- Simulated annealing

Forbidden subgraph heuristic for Split Cluster Editing

#### Idea

Edit an edge that destroys many forbidden subgraphs.

### Problems

- Slow
- Can get caught in loops
- Not very good results

# Simulated Annealing heuristic for Split Cluster Editing

### Simulated Annealing

- Start with a clustering where each vertex is a singleton.
- Randomly move a vertex to a cluster that contains one of its neighbors.
- Accept if this improves the objective k; otherwise, accept with small probability that decreases over time.

To evaluate the objective, we can use the following theorem:

## Theorem (Hammer & Simeone '81)

The minimum number of edits to make a graph a split graph can be found in linear time.

### Data reduction

We didn't find any useful data reduction rules. However, we have two rules that allow to fix the value of variables in the ILP:

#### Rule 1

If there is a degree-one vertex u whose neighbor has degree larger than one, then label u as periphery ( $c_u = 0$ ).

#### Rule 2

If there is an edge  $\{u, v\}$  between two vertices labeled as periphery, then this edge cannot be present in the solution  $(e_{uv} = 0)$ .

## Experimental Setup

Data: three yeast protein interaction subnetworks



#### **Comparison with:**

- Core-periphery enumeration algorithm [Luo et al., BMC Bioinformatics '09]
- **SCAN** clustering algorithm [Xu et al., KDD '07]

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# Experimental Results (I)

#### **Objective value:**

	п	т	k <sub>SCE</sub>	k <sub>ME</sub>
cell cycle	196 215	797 786	321 273	126 106
translation	188	2352	308	240

Results for Simulated Annealing; confirmed as optimal by ILP in green.

# Experimental Results (II)

#### GO-term coherence & cluster number:

	transcription						
	K	р	k	Ct	C <sub>c</sub>	Сp	
SCE	13	112	273	0.54	0.54	0.57	
ME	26	78	106	0.55	0.61	0.54	
SCAN	26	58	—	0.53	0.51	0.47	
Luo	12	125	—	0.40	0.52	0.38	

- K = number of clusters
- p = size of periphery
- $c_t$  = average cluster coherence
- $c_c$  = average core coherence
- $c_p$  = average periphery coherence

# Experimental Results (III)

#### Overlap test with known protein complexes (CYC2008):

Hypothesis for perfect recovery:

- Core contains only complex proteins
- Complex is contained completely in cluster

	transcription				
	D	core%	comp <sub>%</sub>		
SCE	7 / 11	89	100		
ME	$11 \ / \ 11$	100	100		
SCAN	8 / 11	84	100		
Luo	6 / 11	87	100		

D : number of detected clusters

 $\mathsf{core}_\%$  : median percentage of core proteins in complex  $\mathsf{comp}_\%$  : median percentage of complex proteins in cluster

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# Conclusion

#### **Results:**

- Two new concrete graph-theoretic models for uncovering global core-periphery structure of PPI networks
- Useful ILP formulations based on core/periphery-assignment
- Simulated Annealing heuristic performs well
- Monopolar Editing gives best biological results

#### Outlook:

- Algorithmic improvements (goal: good results for complete interactome)
- Incorporate interaction confidence scores
- Further combinatorial core-periphery models
- Find further approaches to exploit/evaluate predictions by Monopolar Editing