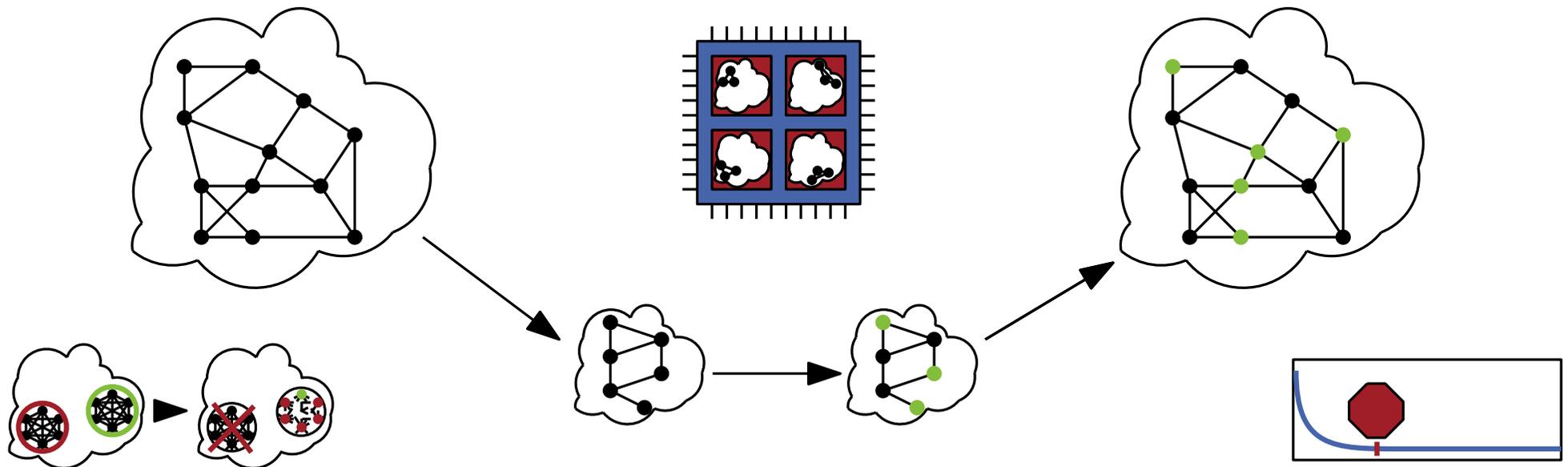


# Scalable Kernelization for Maximum Independent Sets

ALENEX 2018 · 07.01.2018

Demian Hesse, Christian Schulz, Darren Strash

INSTITUTE OF THEORETICAL INFORMATICS · ALGORITHMICS GROUP



# Huge Complex Networks

- Large networks with structure  
⇒ millions or billions of nodes

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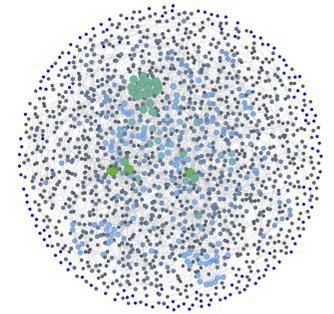
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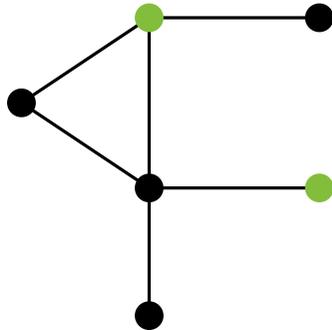
## Independent Set (IS)

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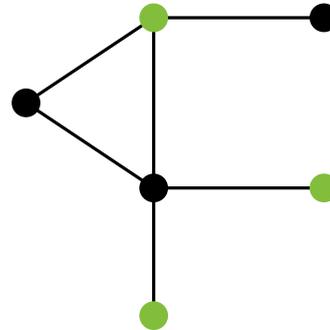
find  $I \subseteq V$  such that  $\forall u, v \in I : \{u, v\} \notin E$

- Find **Maximum** IS (MIS)  $I$ : for all IS  $I'$  of  $G$ :  $|I| \geq |I'|$

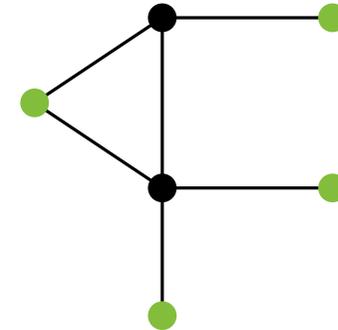
Independent Set



*Maximal* IS



*Maximum* IS



# Maximum Independent Sets

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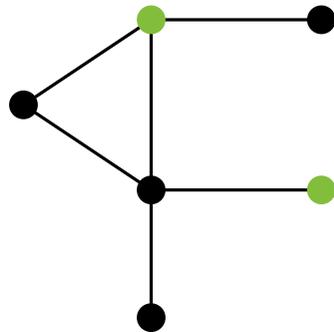
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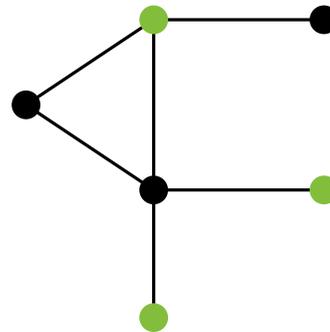
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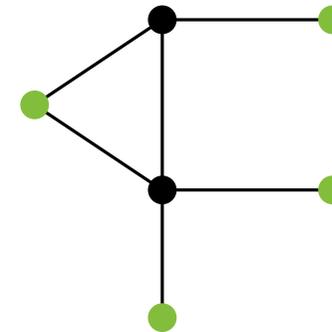
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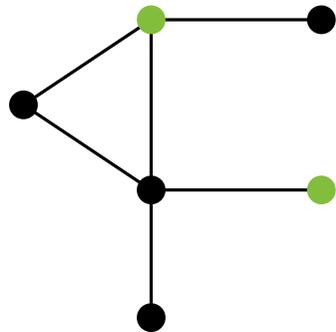
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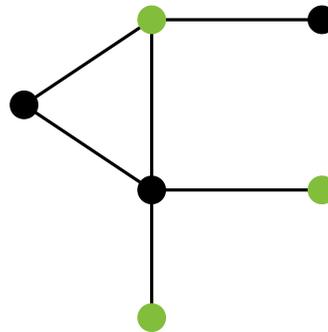
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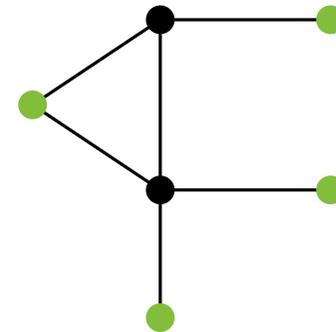
Independent Set



Maximal IS



Maximum IS

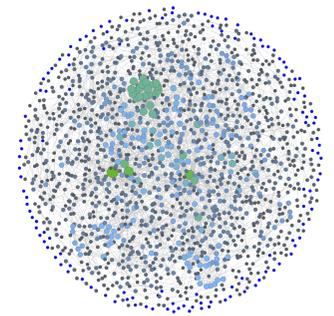


$I \subseteq V$  is a Maximum Independent Set  $\Leftrightarrow V \setminus I$  is a Minimum Vertex Cover

$I \subseteq V$  is a Maximum Independent Set of  $G = (V, E) \Leftrightarrow I$  is a Maximum Clique of  $\bar{G} = (V, \bar{E})$

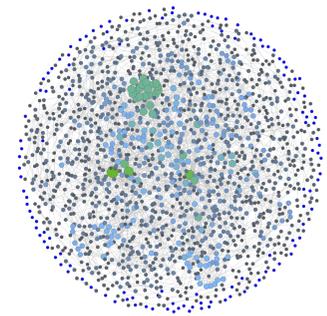
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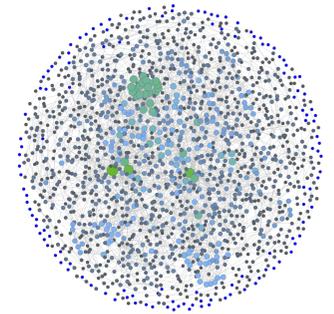
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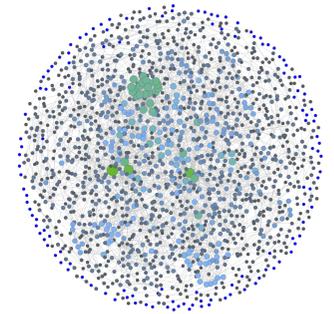
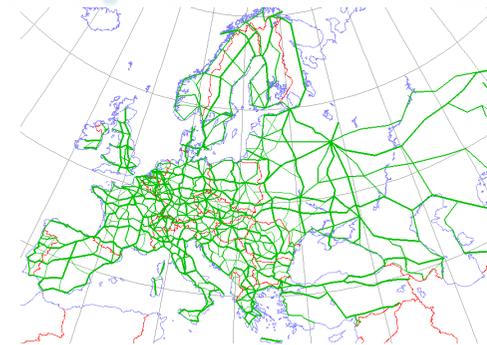
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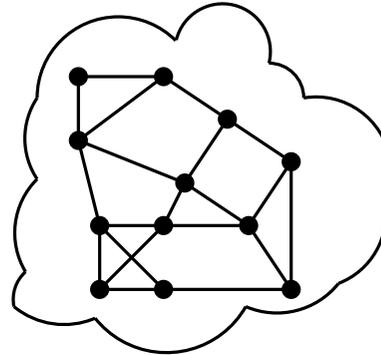
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- Biological networks (proteins and their interactions)  
**Application:** Where can we sample to find new interactions?



*Reduction Algorithm Reduce:*

- Input:  $G$
- Output:  $G'$  with  $|G'| \leq |G|$



**function** KERNELMIS( $G$ )

$G' \leftarrow \text{REDUCE}(G)$

$I' \leftarrow \text{MIS}(G')$

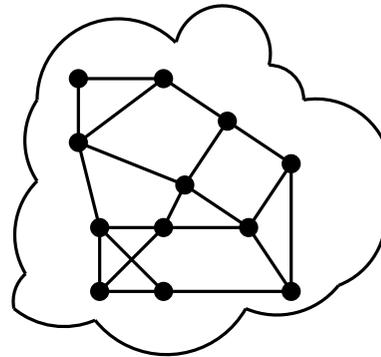
$I \leftarrow \text{REDUCE}^{-1}(G', I')$

**return**  $I$

# Kernelization

*Reduction Algorithm Reduce:*

- Input:  $G$  
- Output:  $G'$  with  $|G'| \leq |G|$



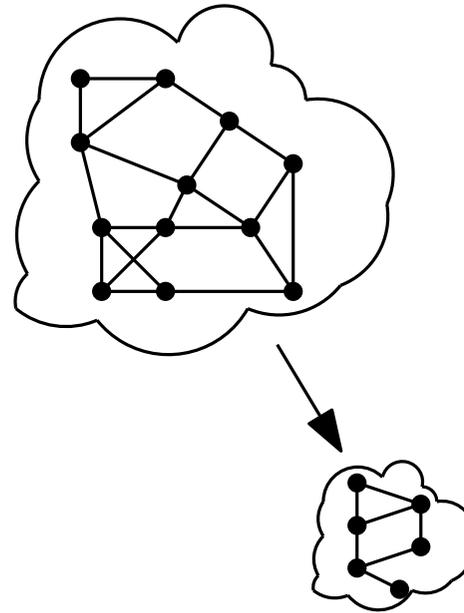
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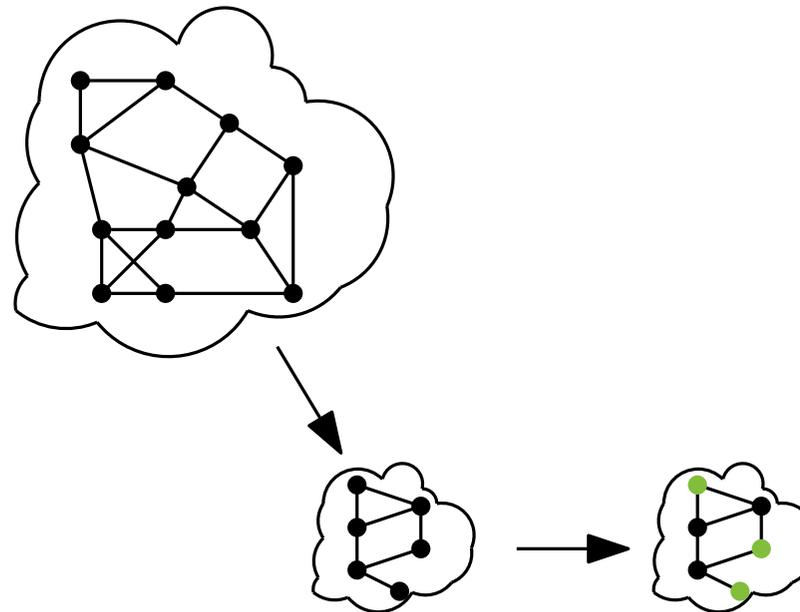


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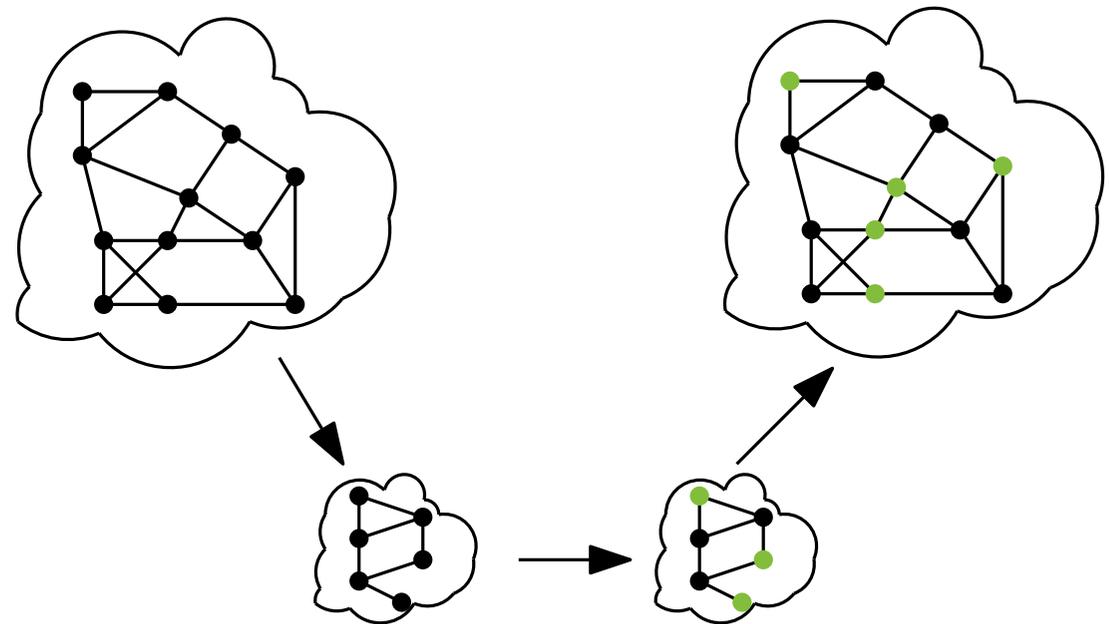


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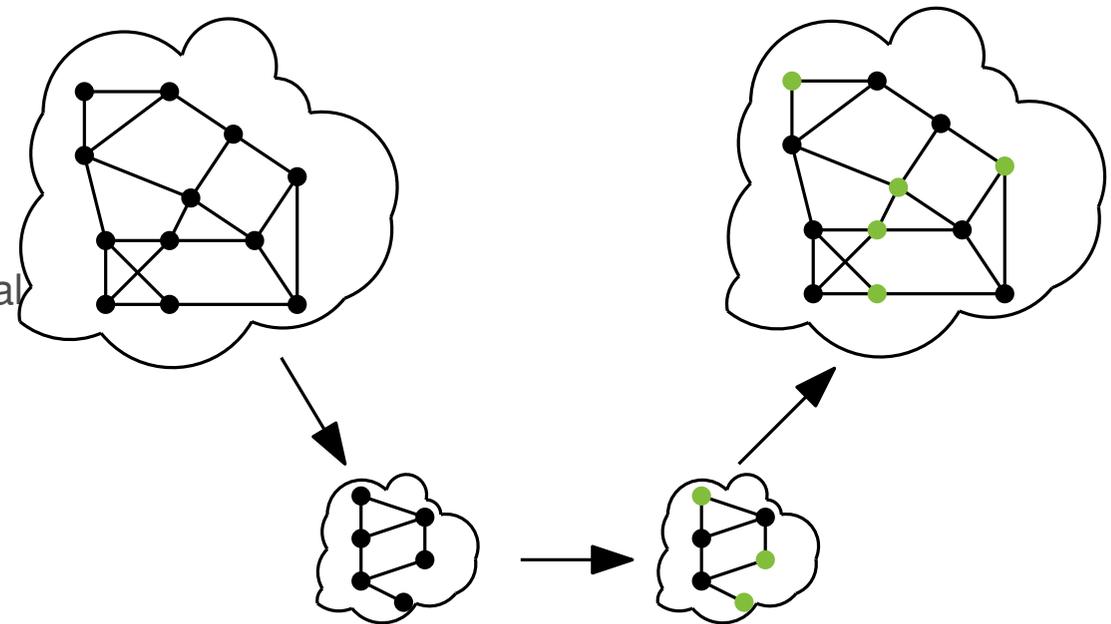


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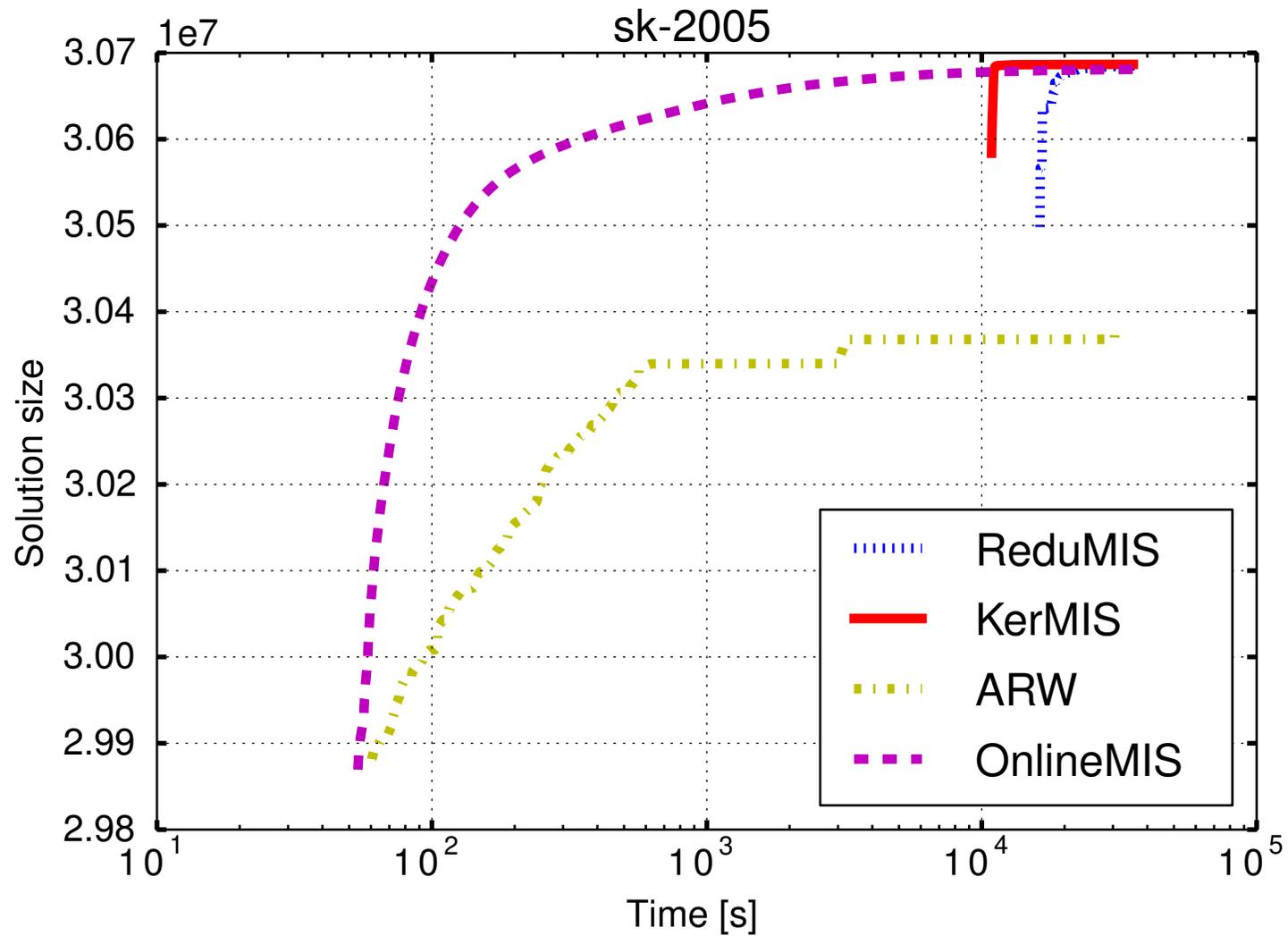
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```
function KERNELMIS( $G$ )  
   $G' \leftarrow \text{REDUCE}(G)$  ← Fast polynomial  
   $I' \leftarrow \text{MIS}(G')$  ← Slow if exact  
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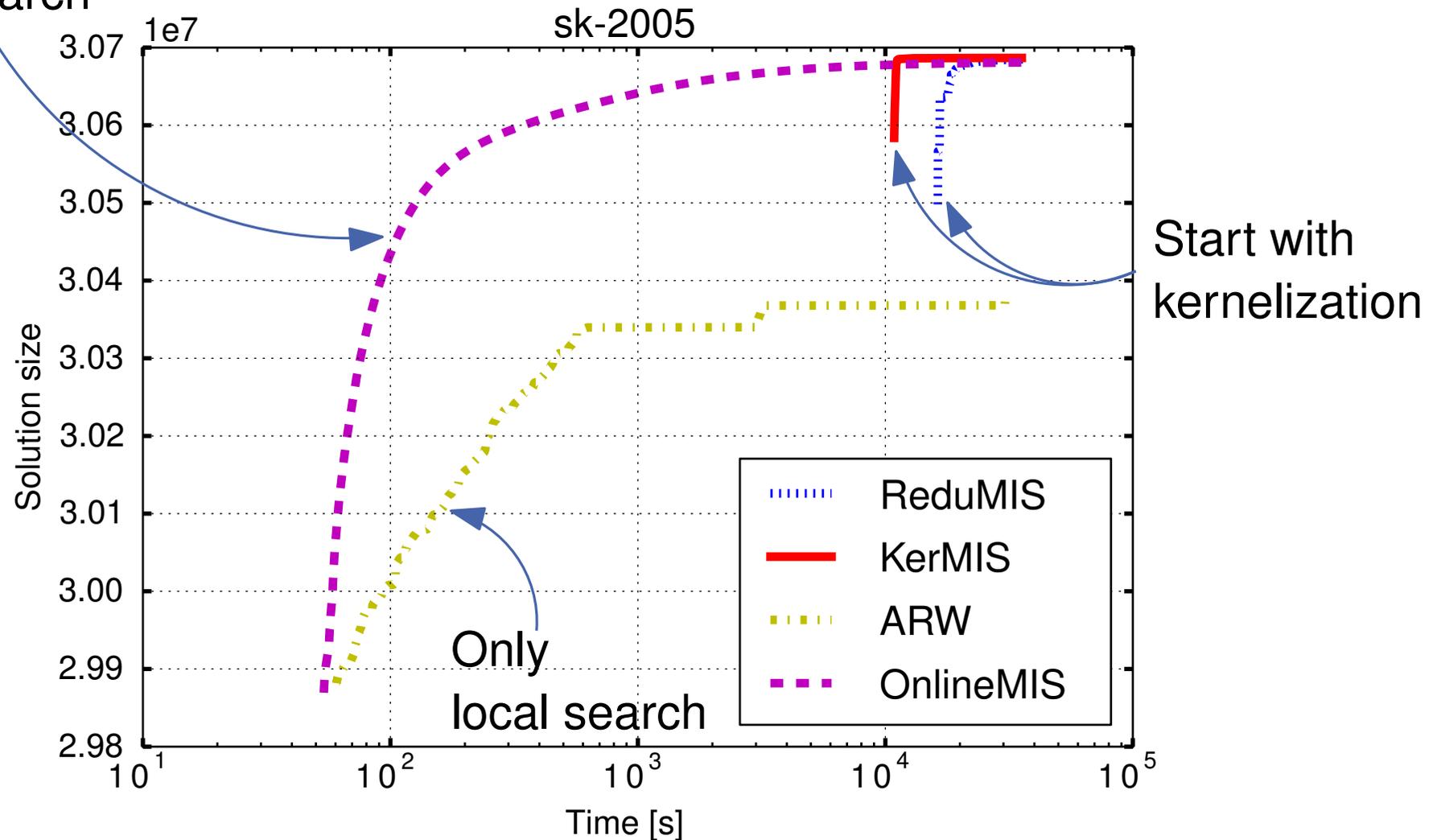


# Motivation



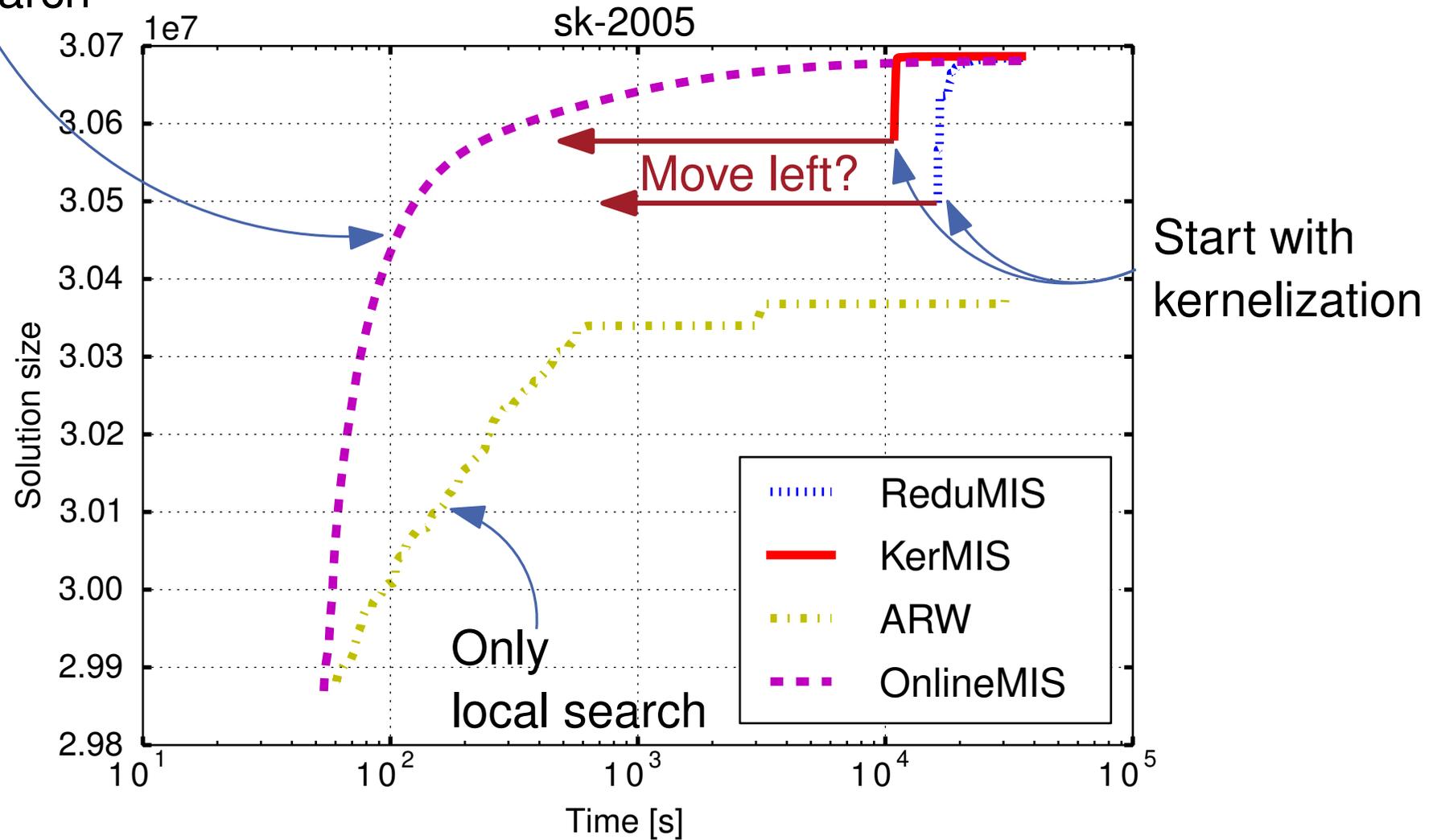
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Reductions during  
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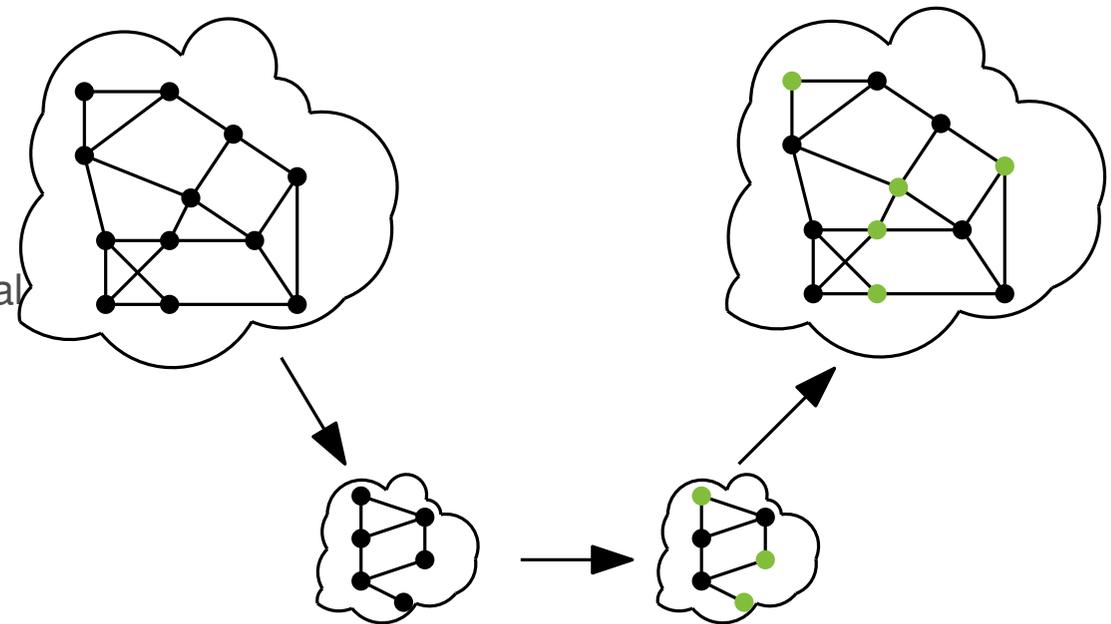


# Kernelization: Reduction Rules

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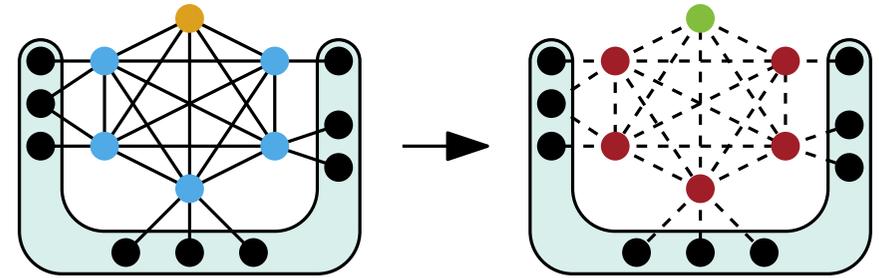
$I' \leftarrow$  MIS( $G'$ )

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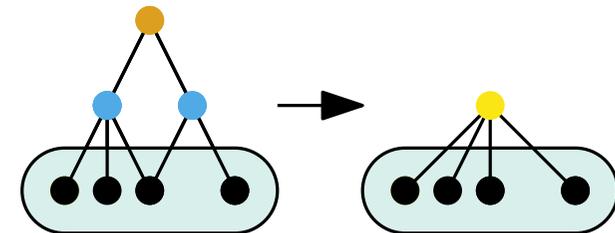
**return**  $I$

Fast  
polynomial

Slow  
if exact



■ Isolated Clique Reduction



■ Degree 2 Vertex Folding

■ Twin Reduction

■ Unconfined and Diamond Reduction

■ LP via Maximum Bipartite Matching

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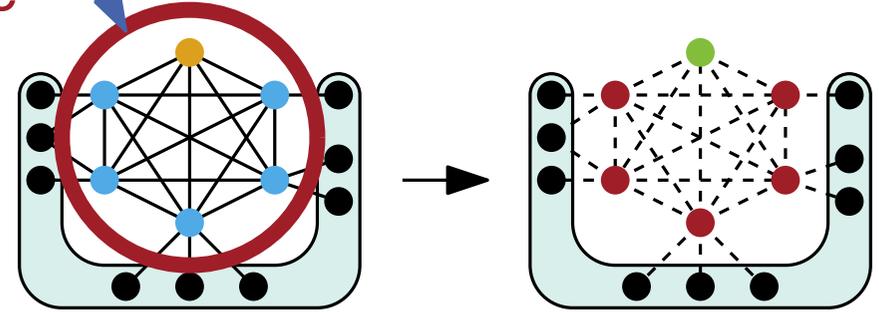
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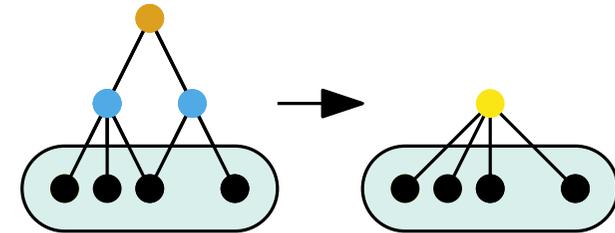
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Clique



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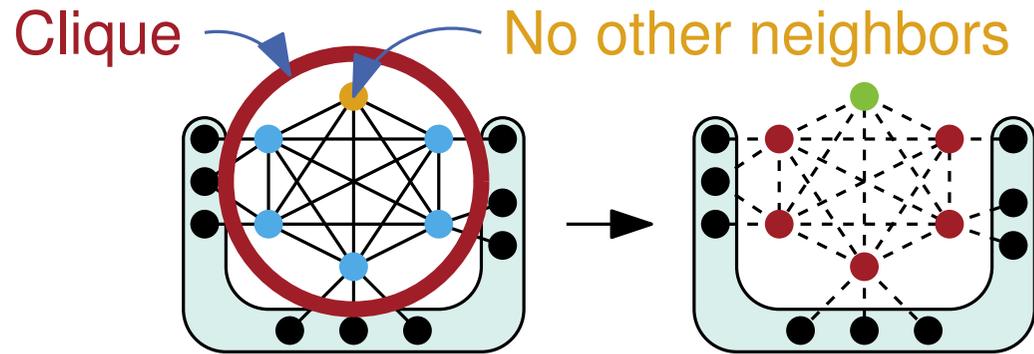
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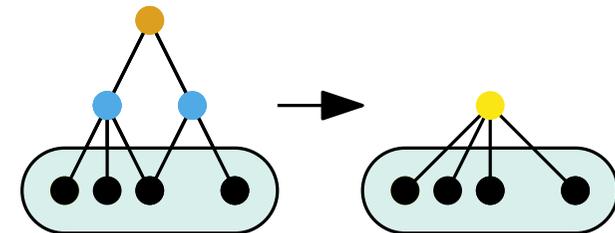
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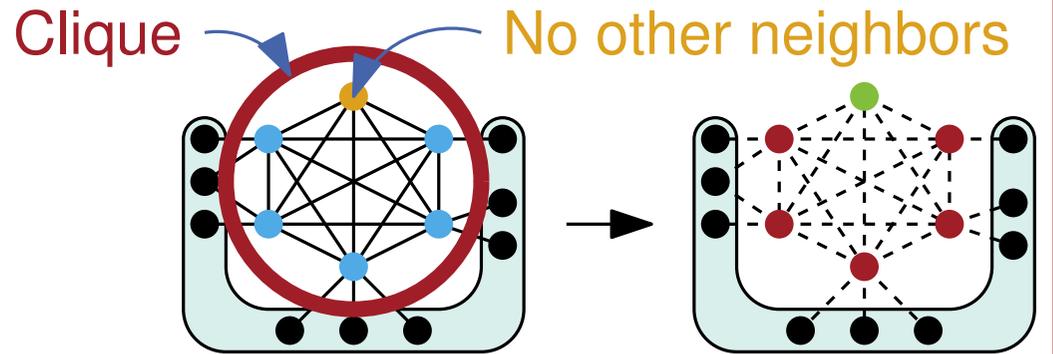
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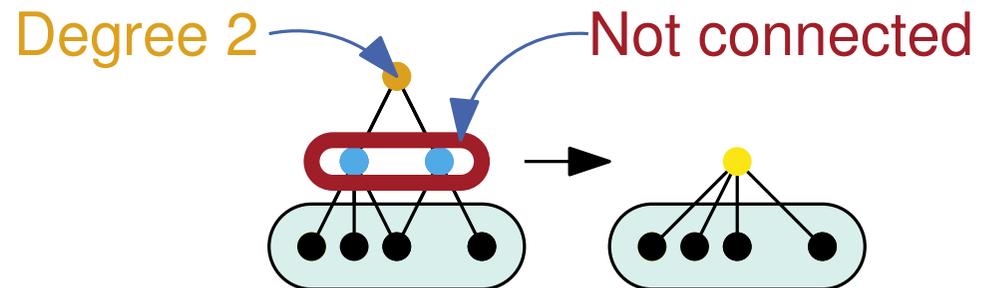
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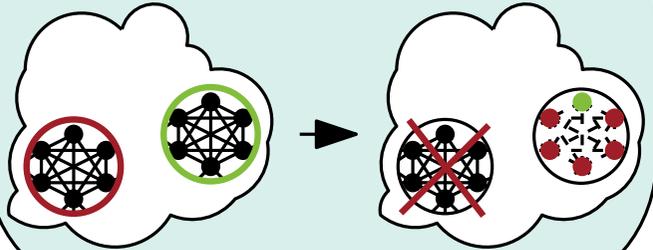
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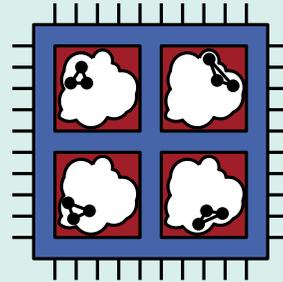
- Degree 2 Vertex Folding
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- Unconfined and Diamond Reduction
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# Contribution

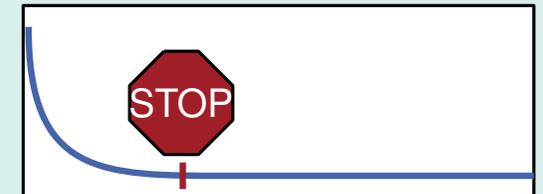
## Dependency Checking



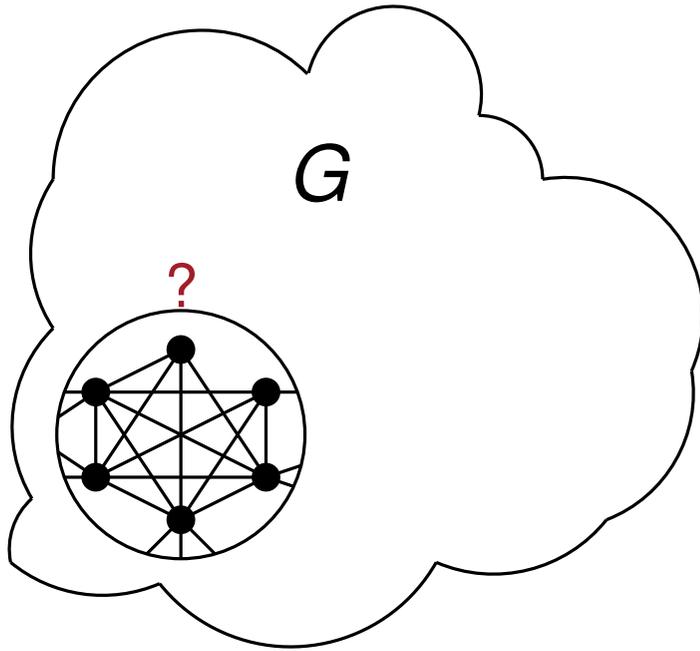
## Parallelization



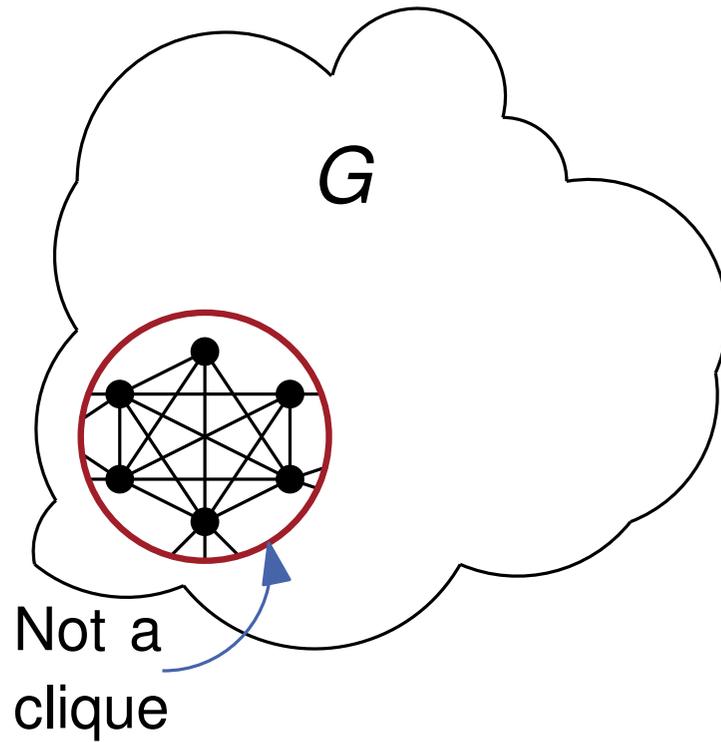
## Reduction Tracking



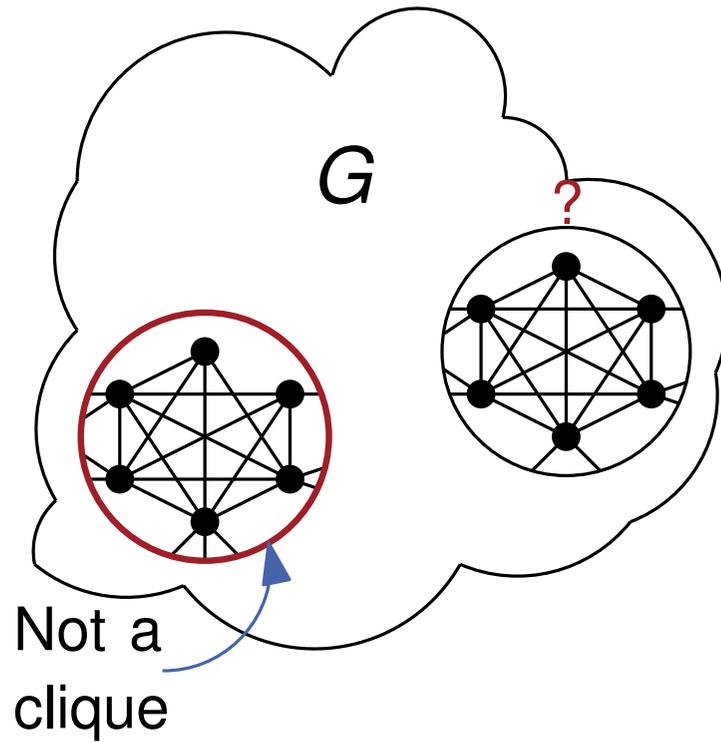
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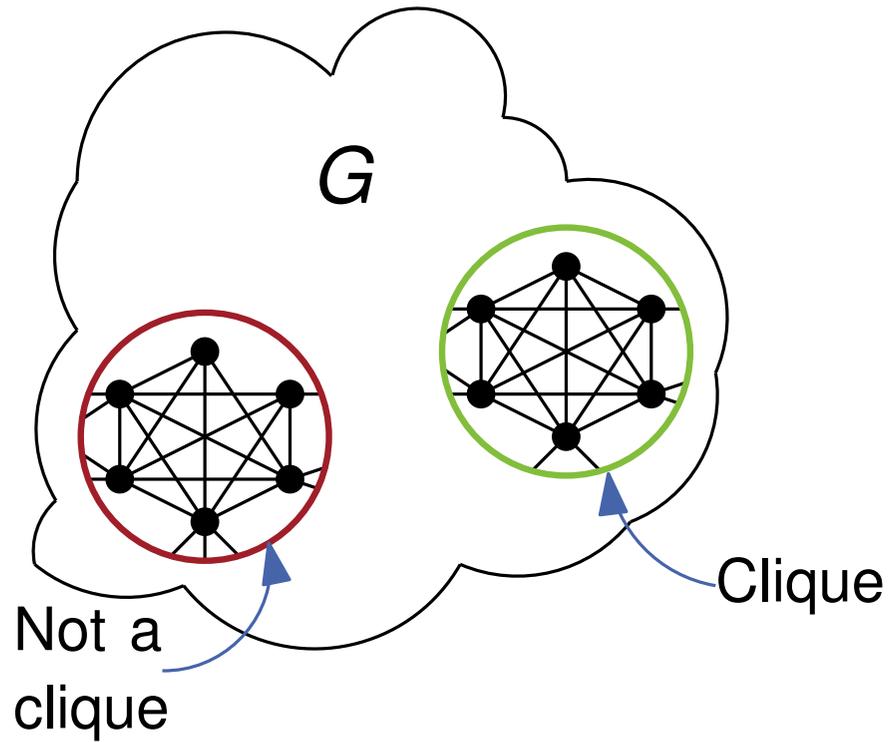
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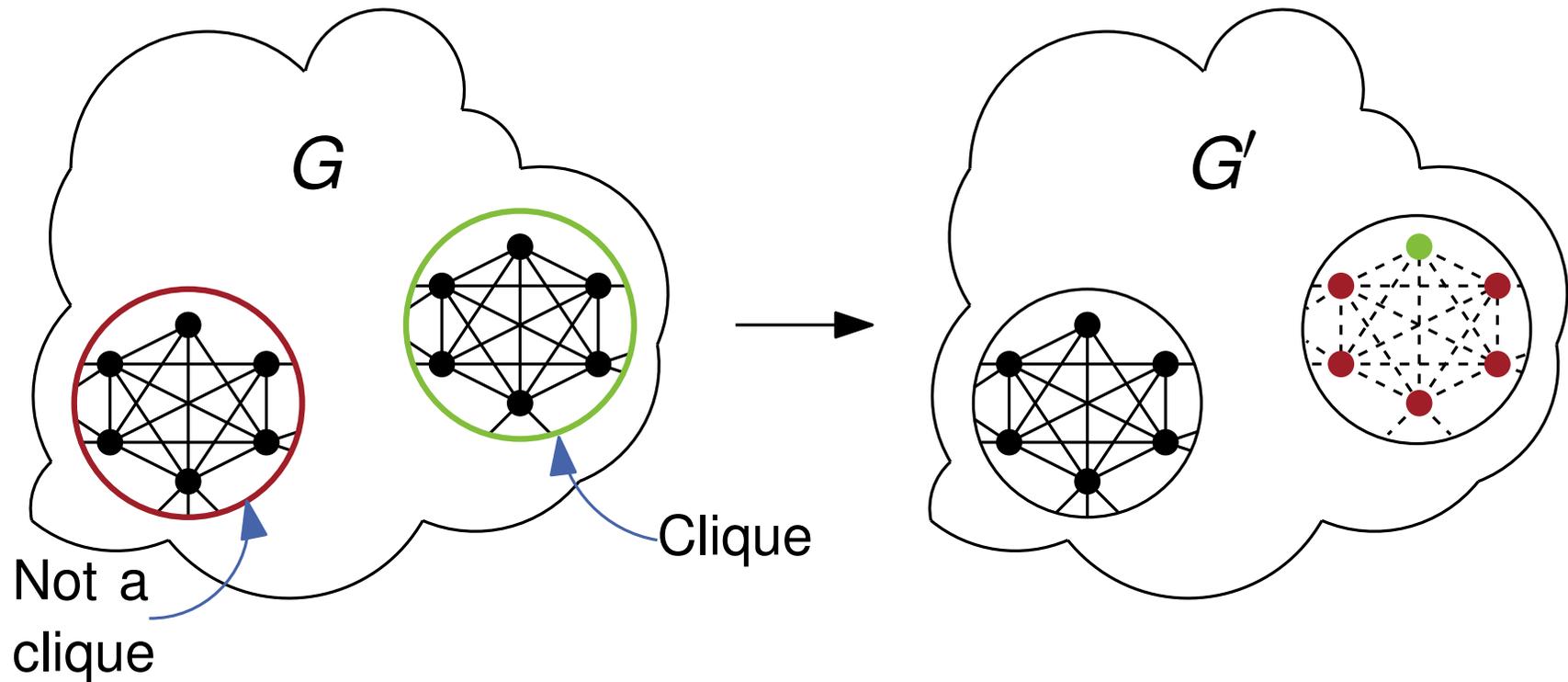
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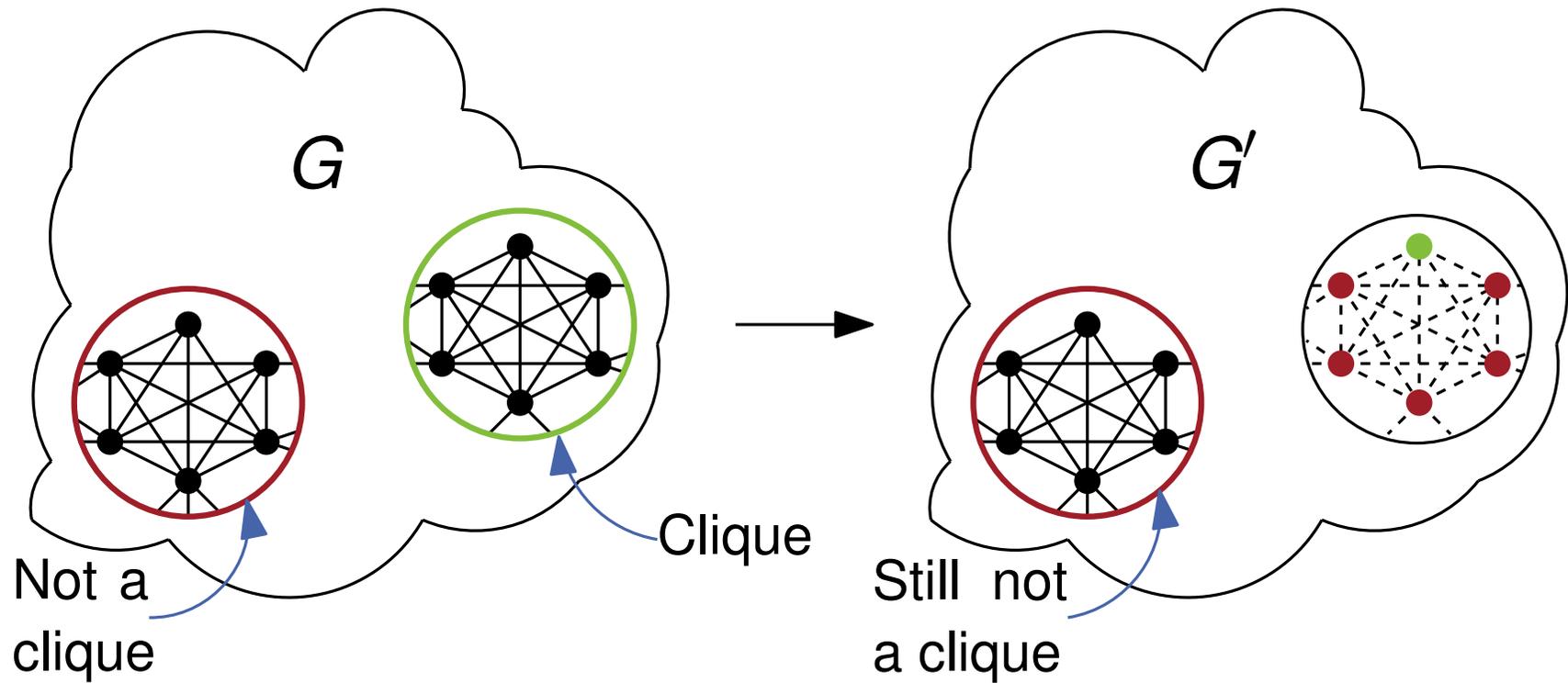
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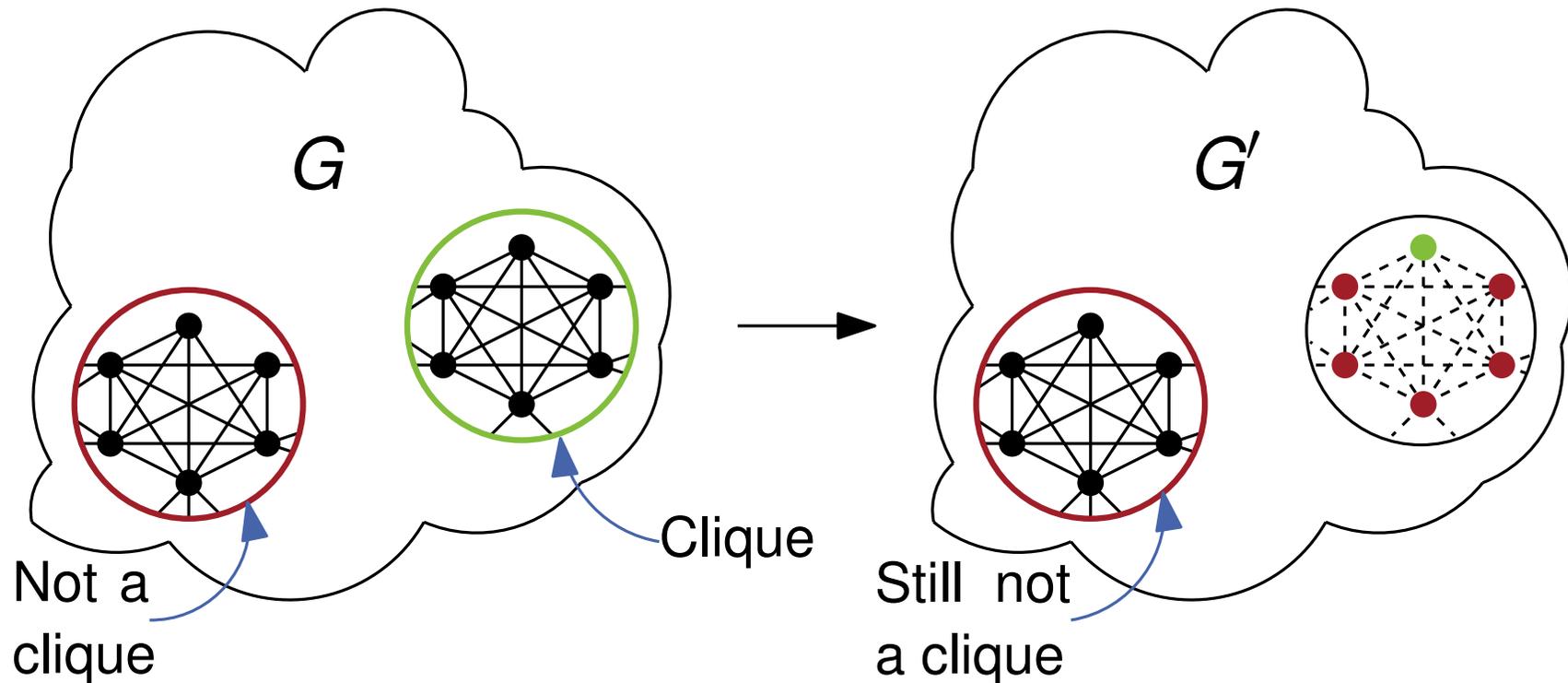
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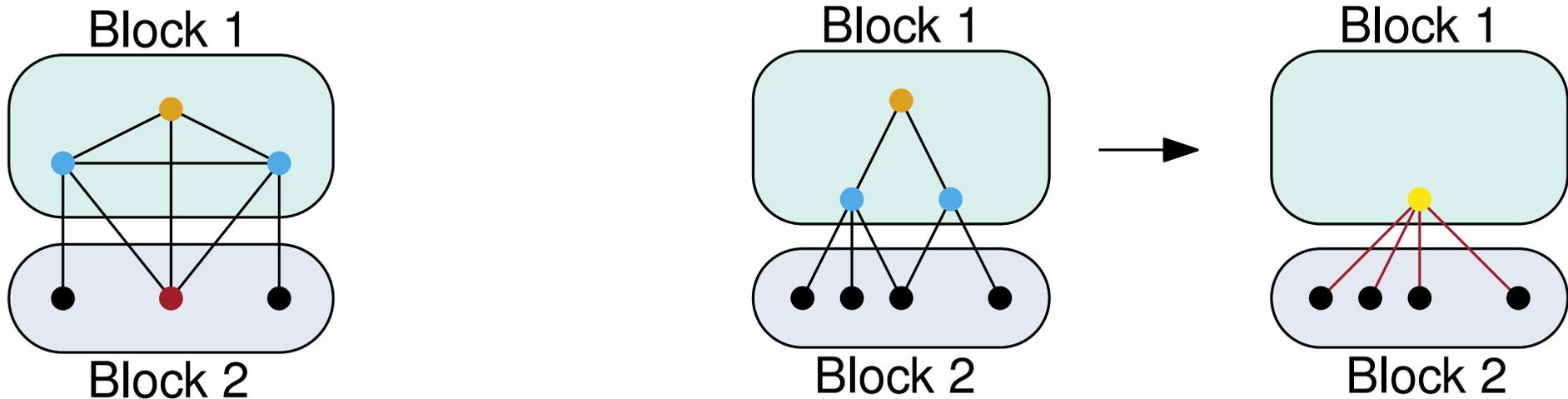


No reduction in  $G$  and  $N_G(v) = N_{G'}(v) \Rightarrow$  No reduction in  $G'$

- |                             |   |                        |   |
|-----------------------------|---|------------------------|---|
| ■ Isolated Clique Reduction | ✓ | ■ Unconfined Reduction | ✗ |
| ■ Degree 2 Fold Reduction   | ✓ | ■ Diamond Reduction    | ✗ |
| ■ Twin Reduction            | ✓ | ■ LP Reduction         | ✗ |

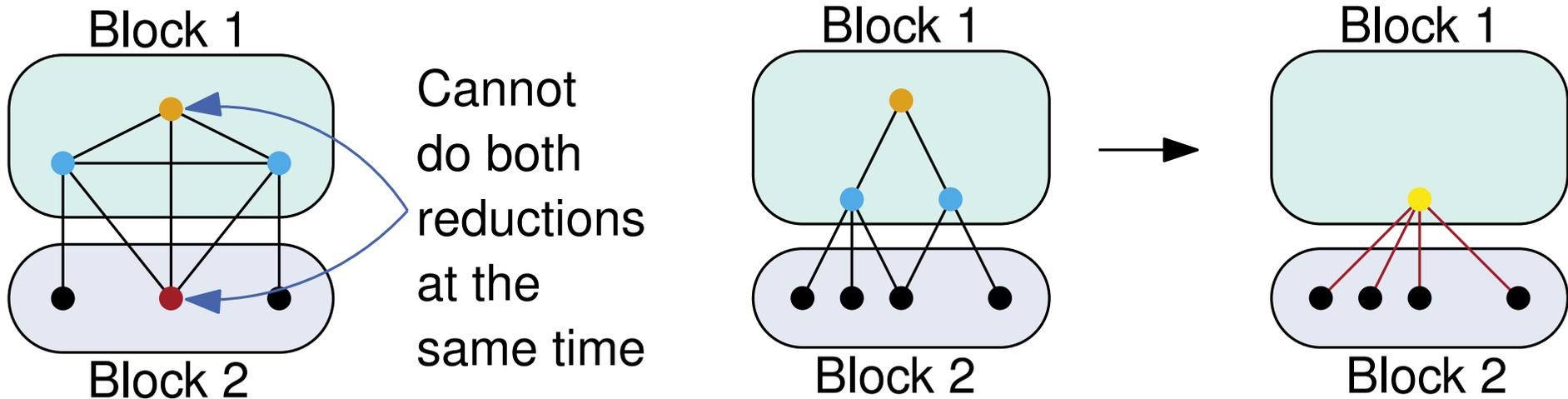
# Parallelization by Graph Partitioning

- Idea: Partition graph into blocks and reduce them separately
- Boundaries problematic



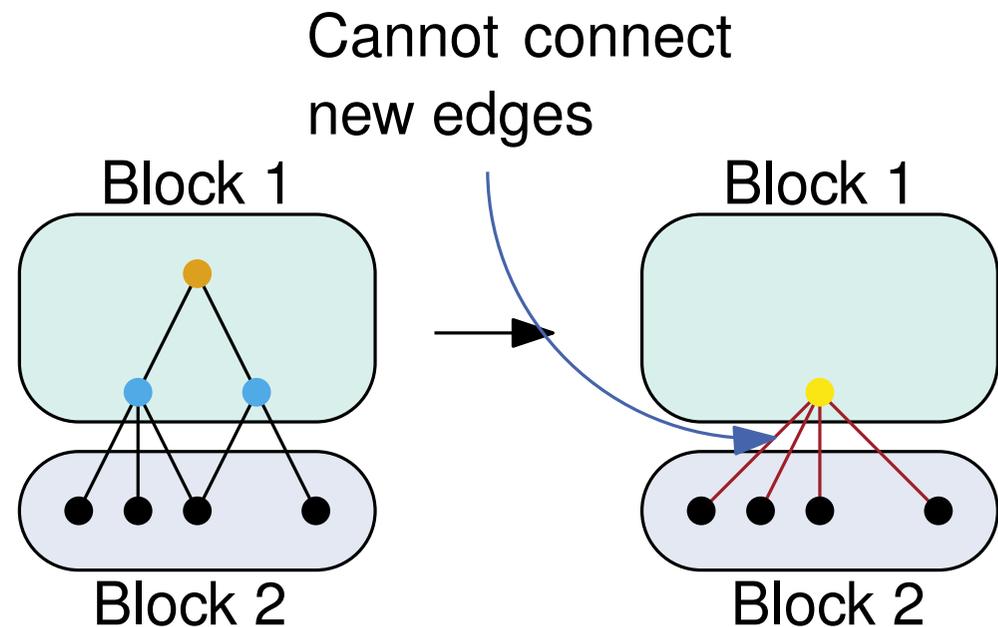
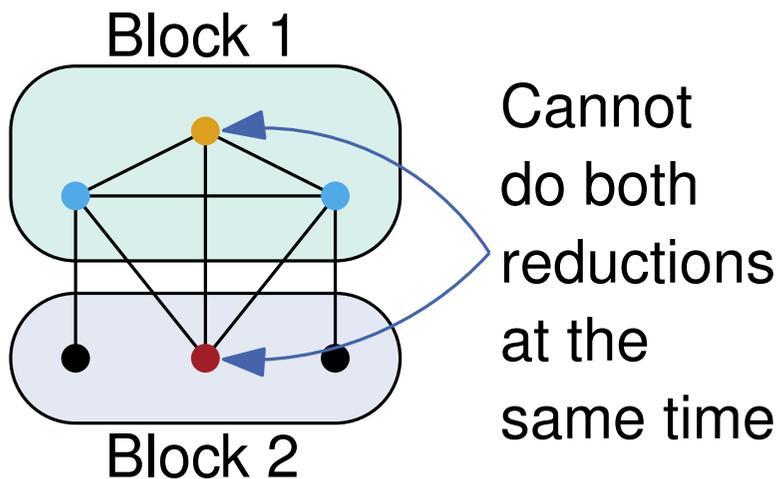
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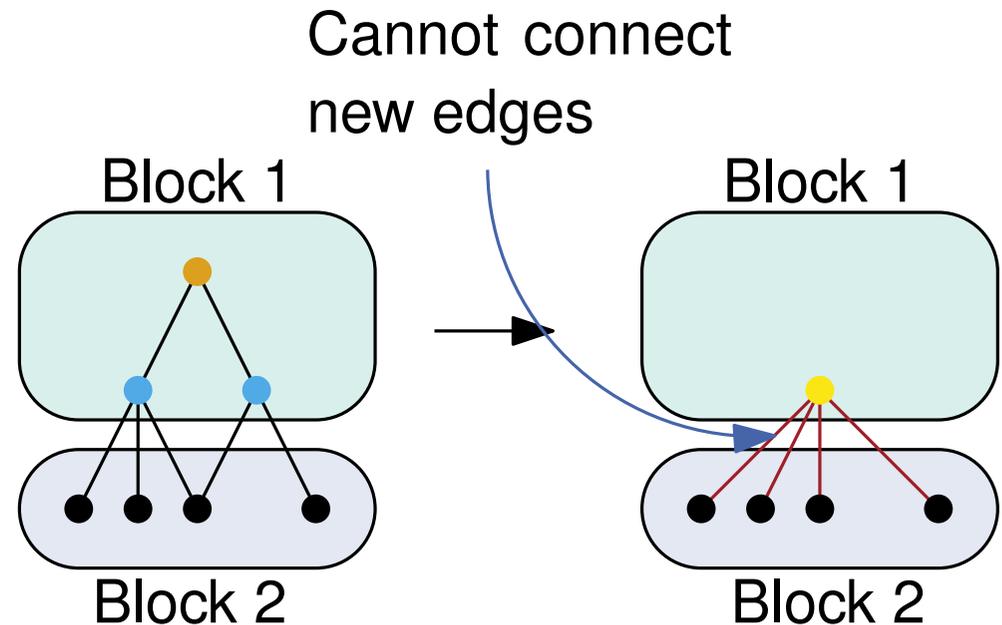
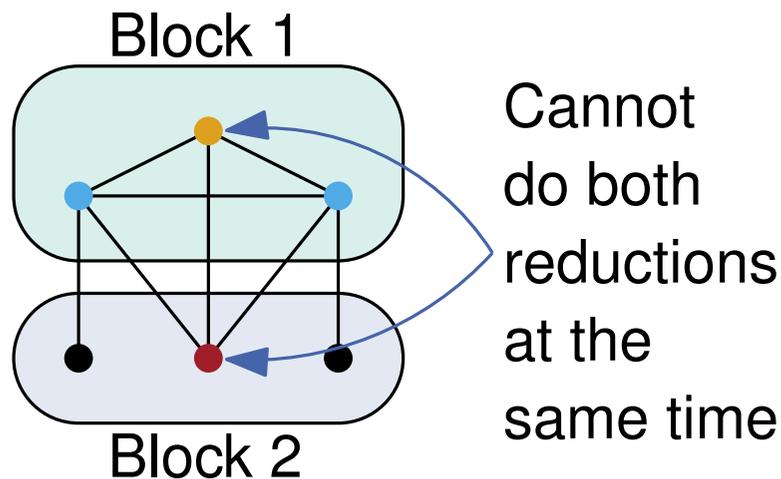
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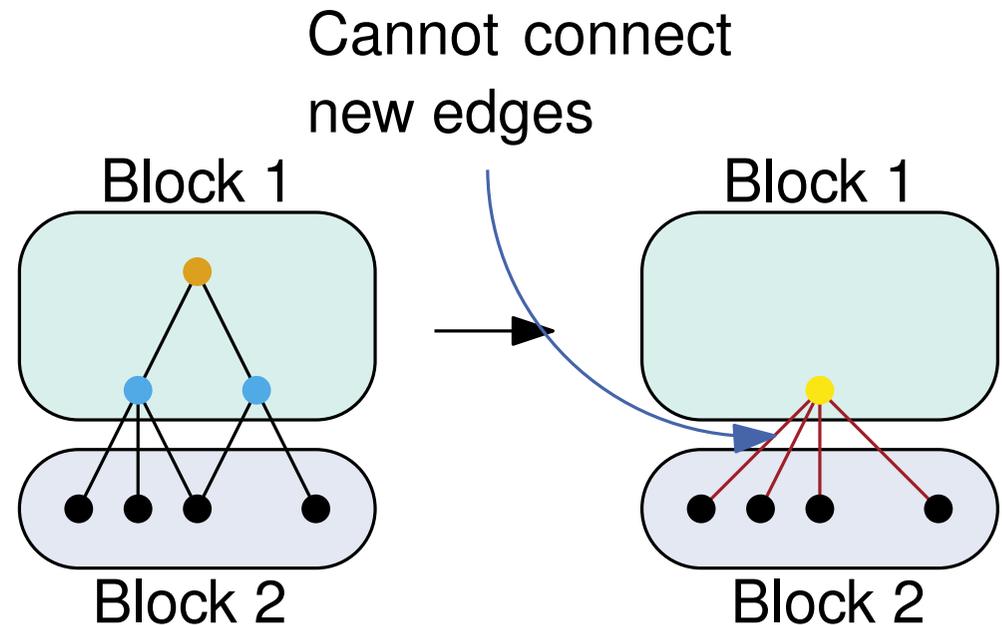
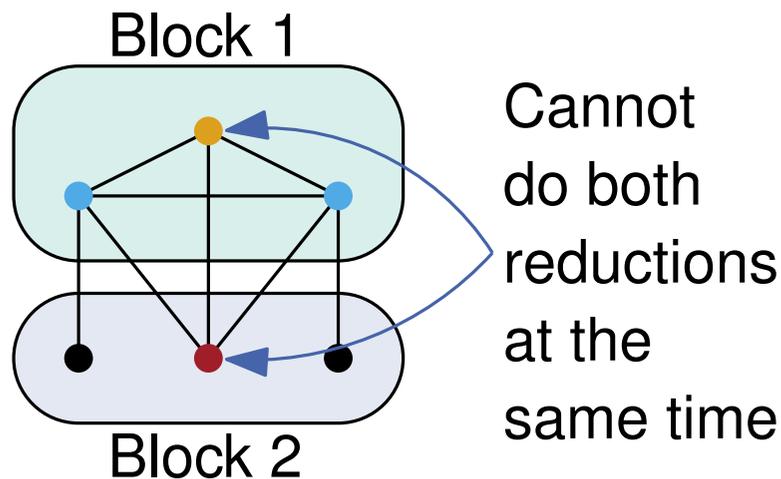
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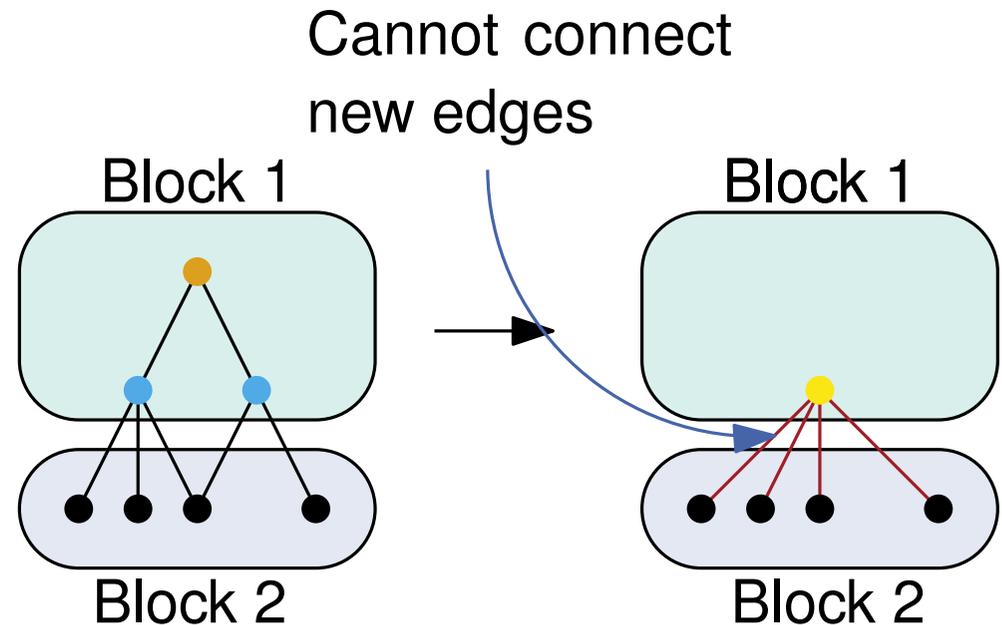
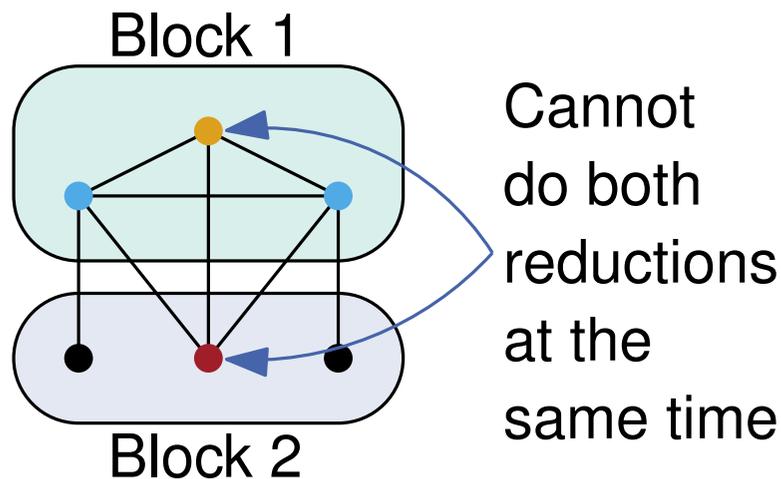
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⇒ ParHIP (part of KaHIP) finds small cuts in parallel [Meyerhenke et al., TPDS'17]

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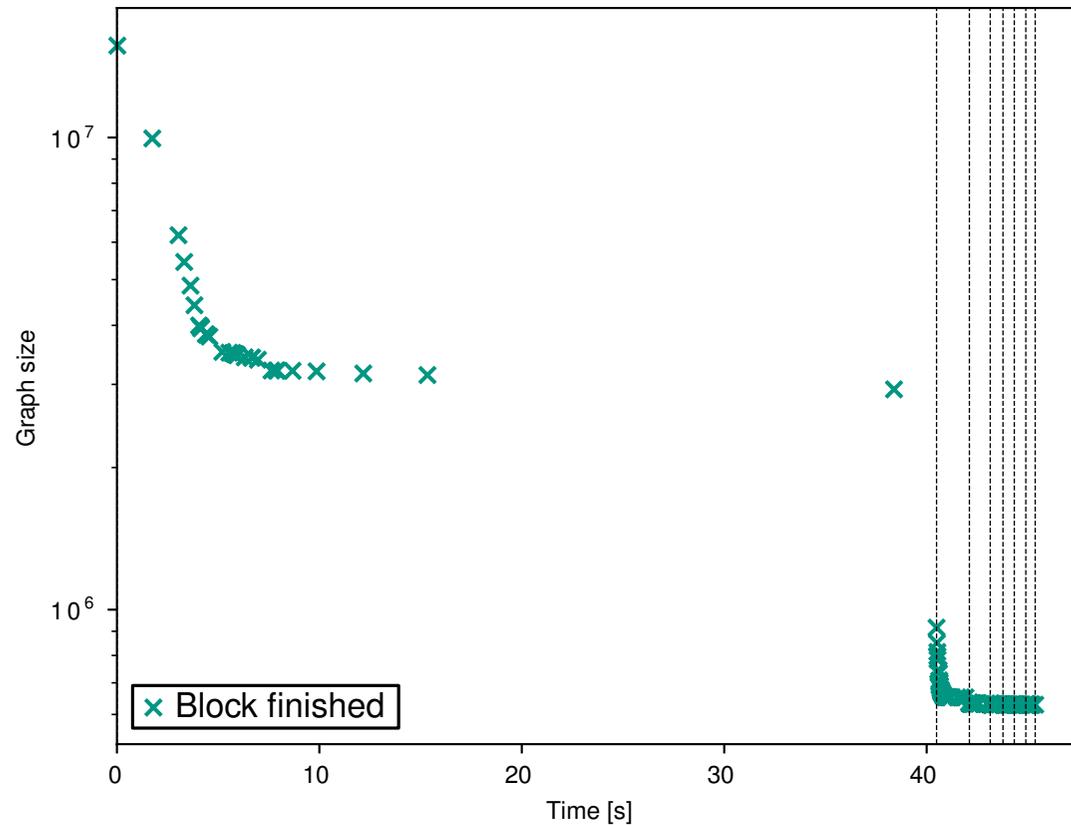
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- We want few edges between blocks (small cut)
- ⇒ ParHIP (part of KaHIP) finds small cuts in parallel [Meyerhenke et al., TPDS'17]
- Parallelize LP reduction with parallel maximum bipartite matching [Azad et al., TPDS'17]

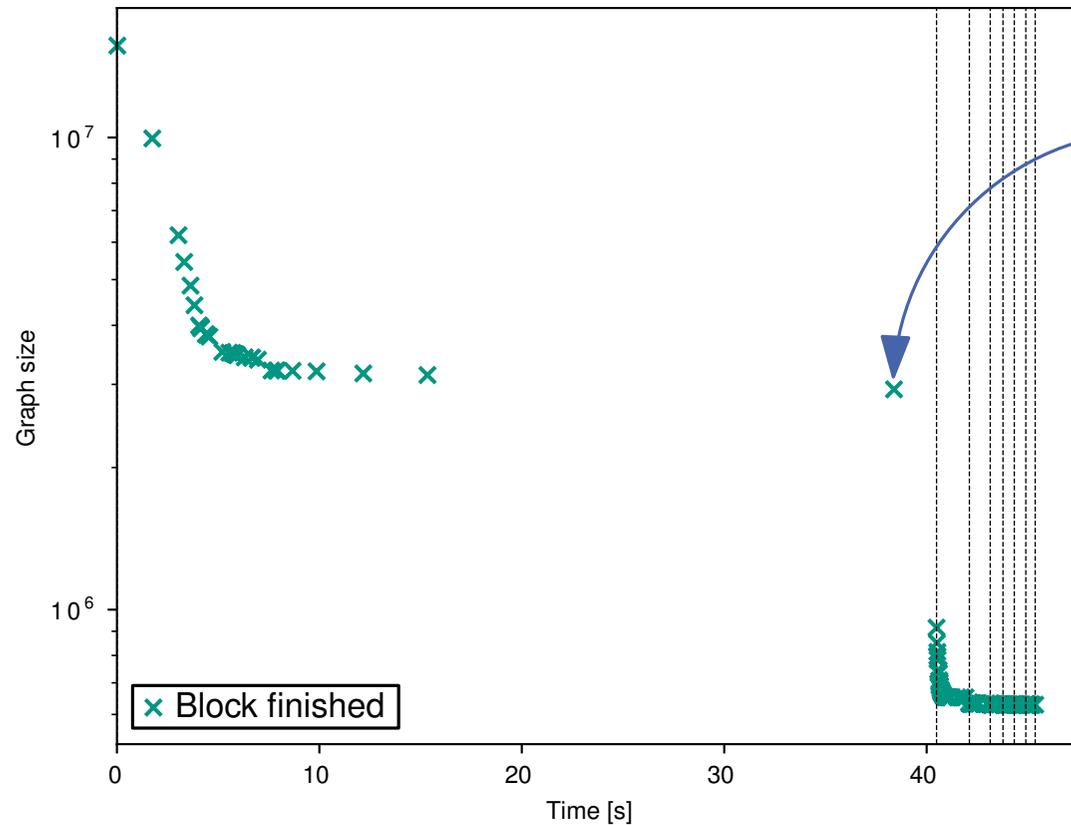
# Reduction Tracking

- Some blocks take significantly longer than others
- Few changes after a while



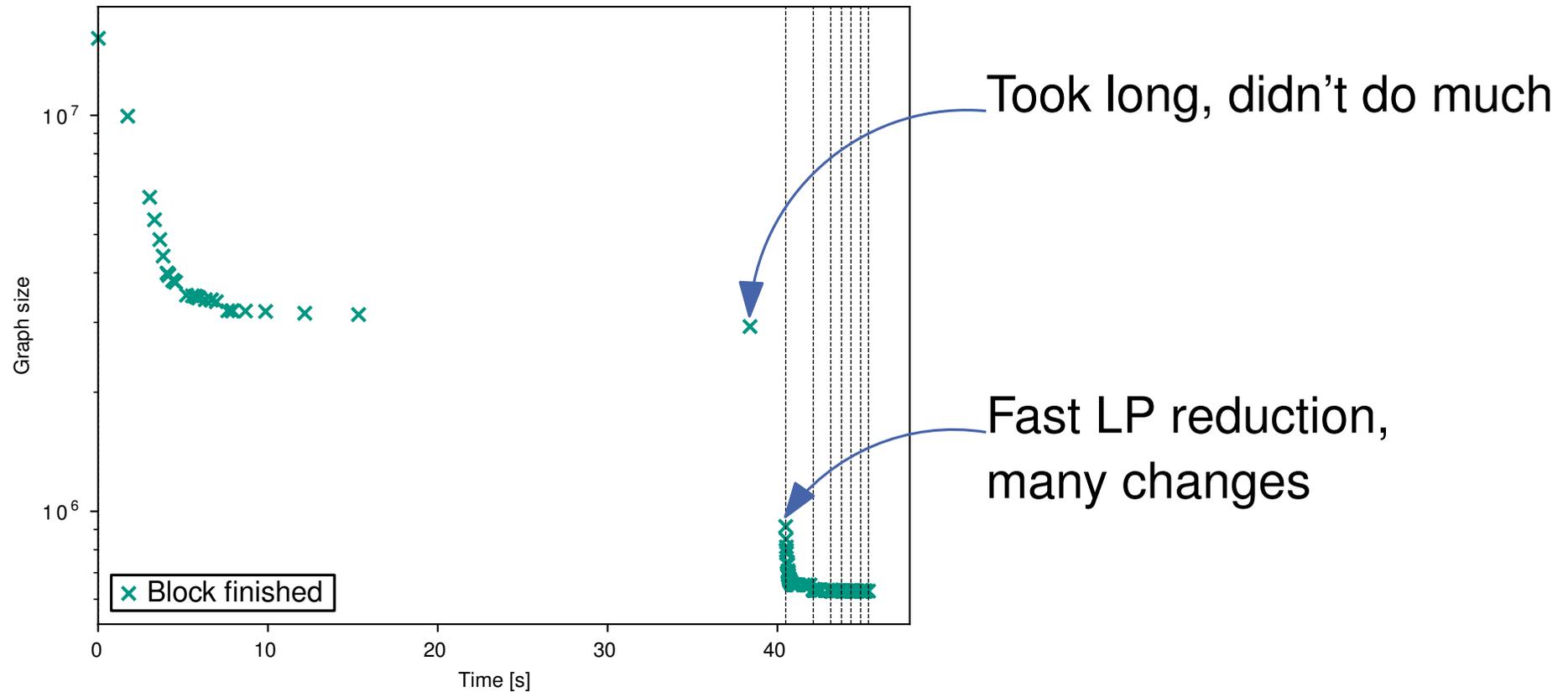
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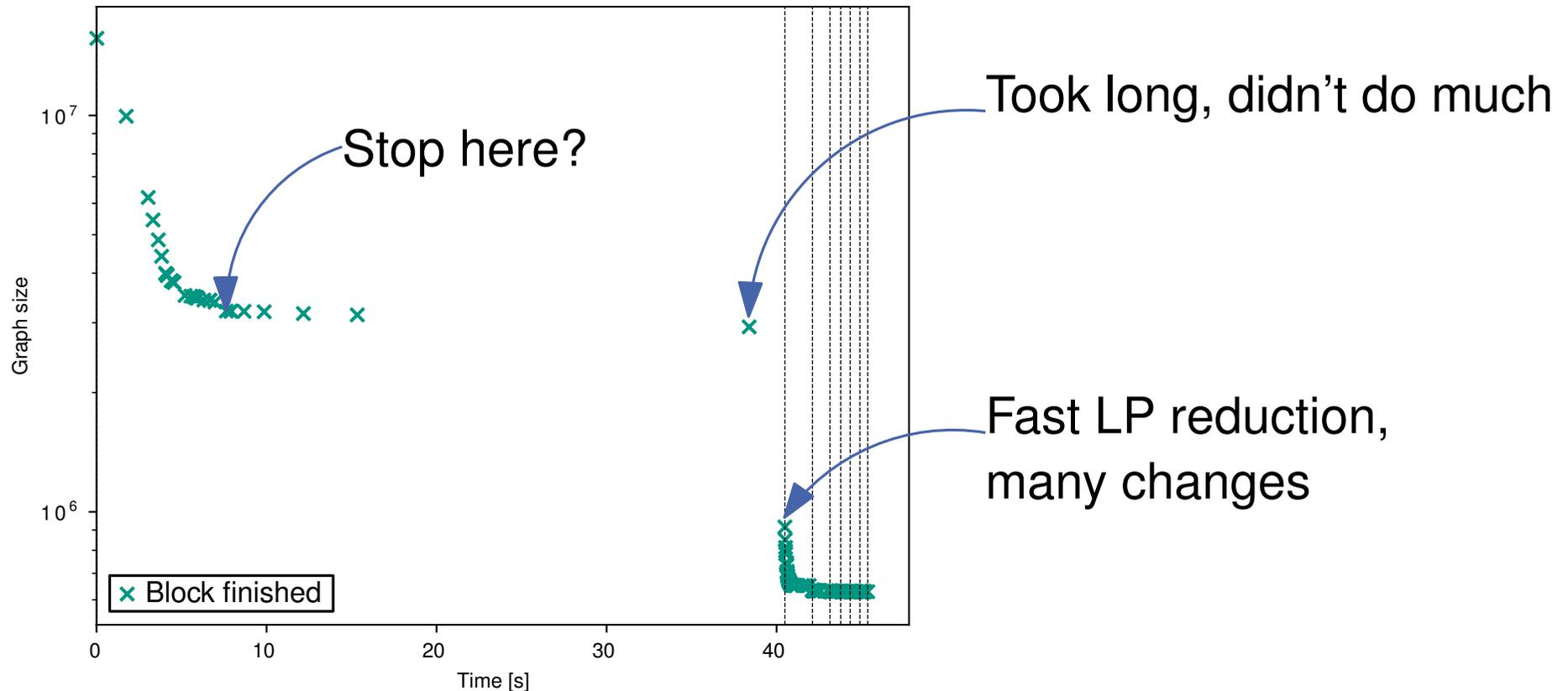
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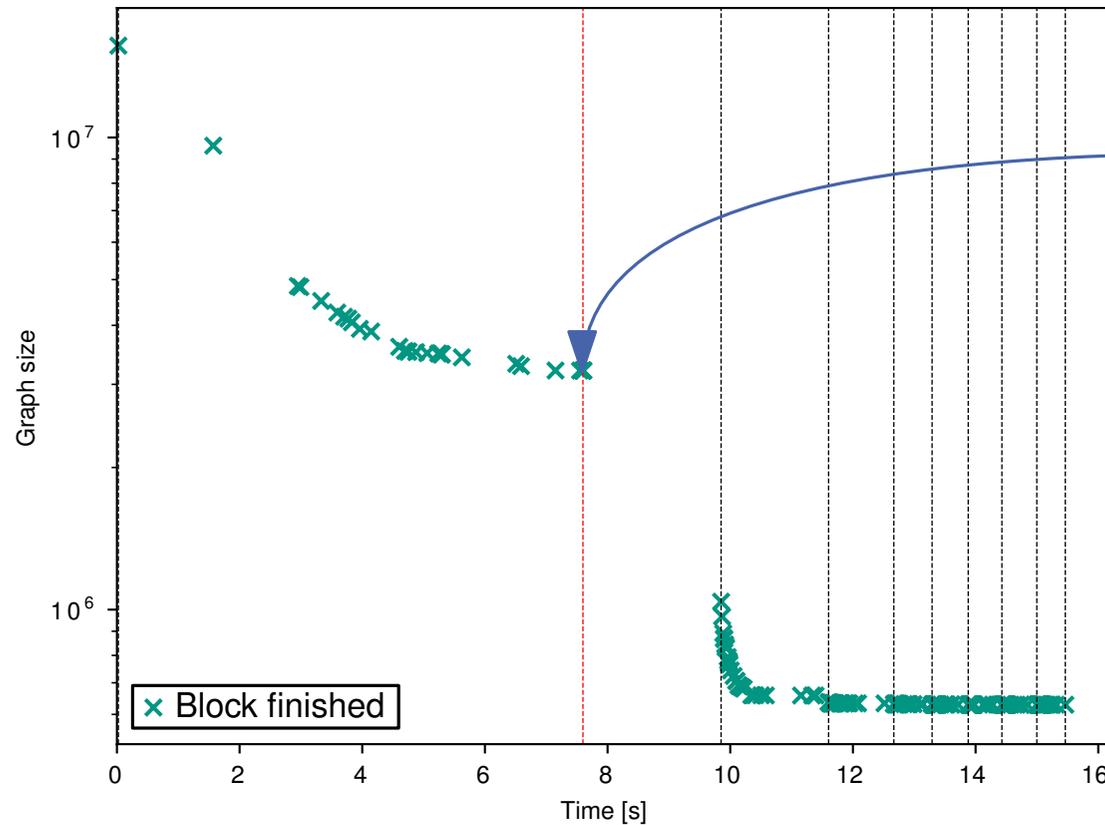
# Reduction Tracking

- Some blocks take significantly longer than others
- Few changes after a while



- Start sampling graph size after first block finishes
- Stop if  $\frac{\text{size}_j - \text{size}_{j-1}}{\text{time}_j - \text{time}_{j-1}}$  much smaller than  $\frac{\text{size}_j - \text{size}_1}{\text{time}_j - \text{time}_1}$

# Reduction Tracking: Results



Stop "local" reductions  
Start LP reduction

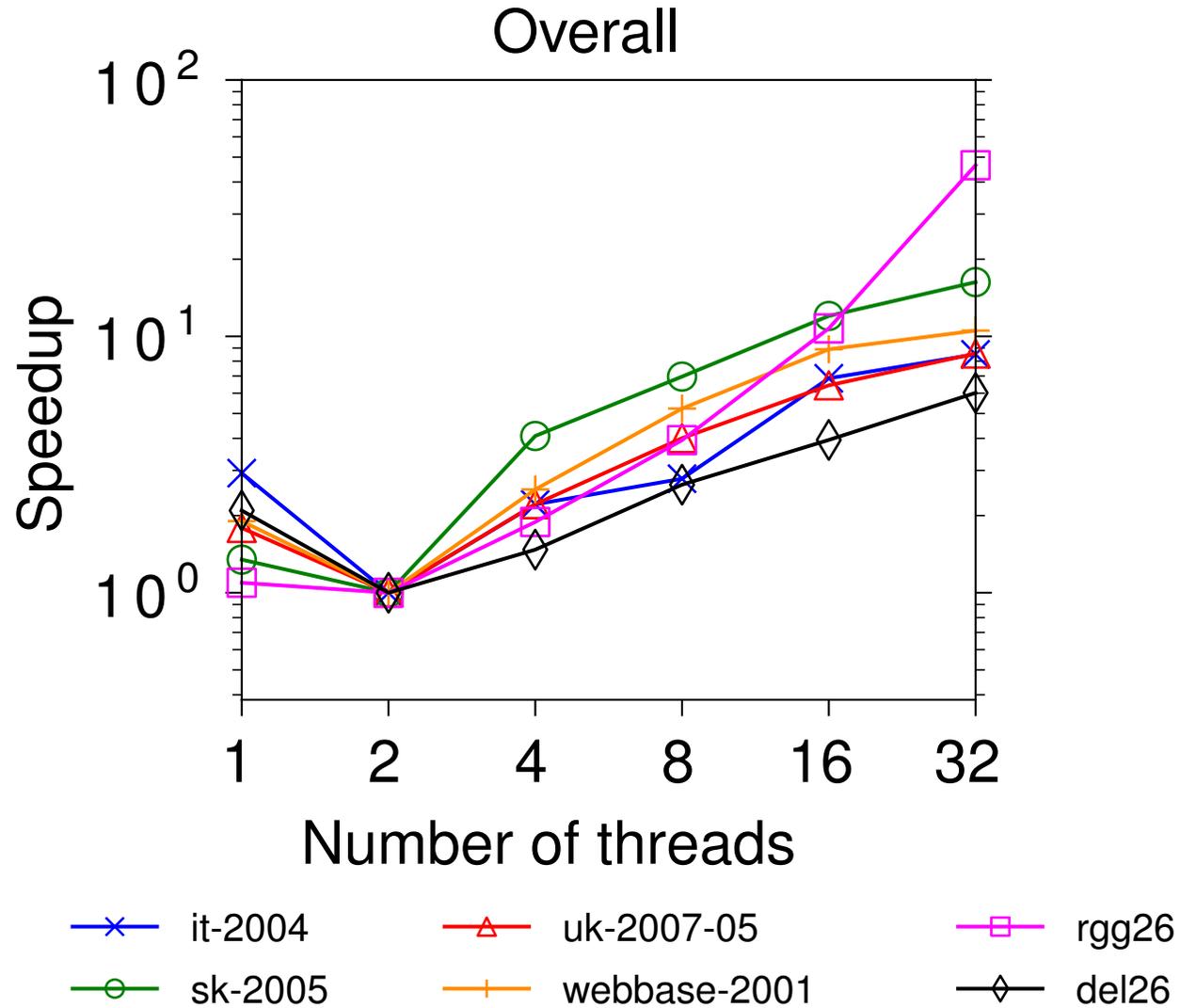
- Different input graphs with  $>10M$  vertices
  - Real world: Web graphs, road networks
  - Synthetic: RGG, RHG, Delaunay triangulations
  
- Comparison with state of the art (sequential) algorithms:
  - VCSolver [Akiba and Iwata, TCS'16]: Slow but small kernels
  - LinearTime and NearLinear [Chang et al., MOD'17]: Fast but large kernels
    - We use LinearTime as preprocessing step

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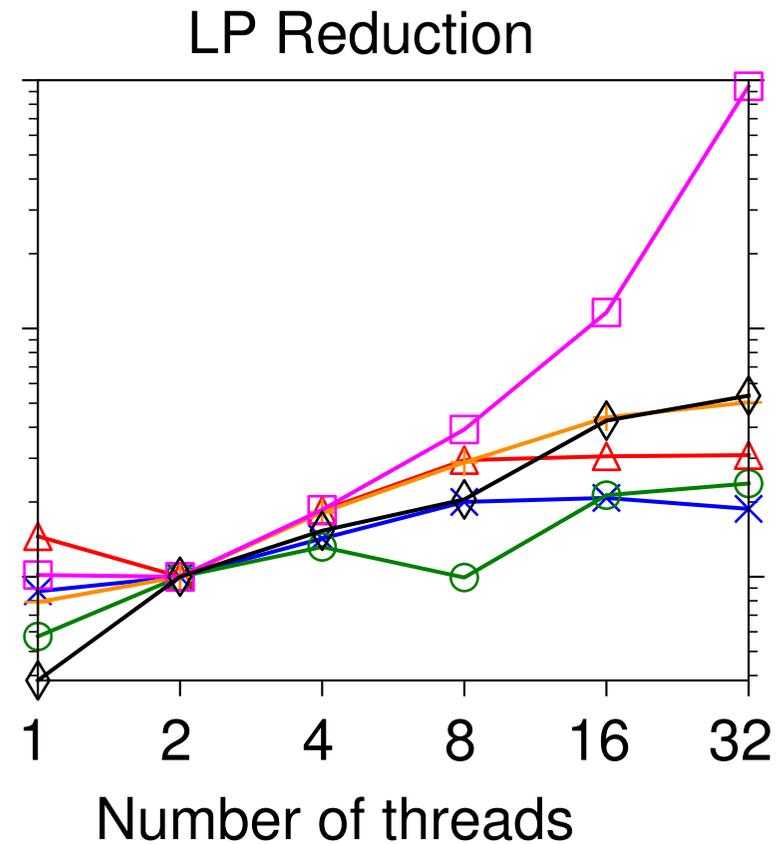
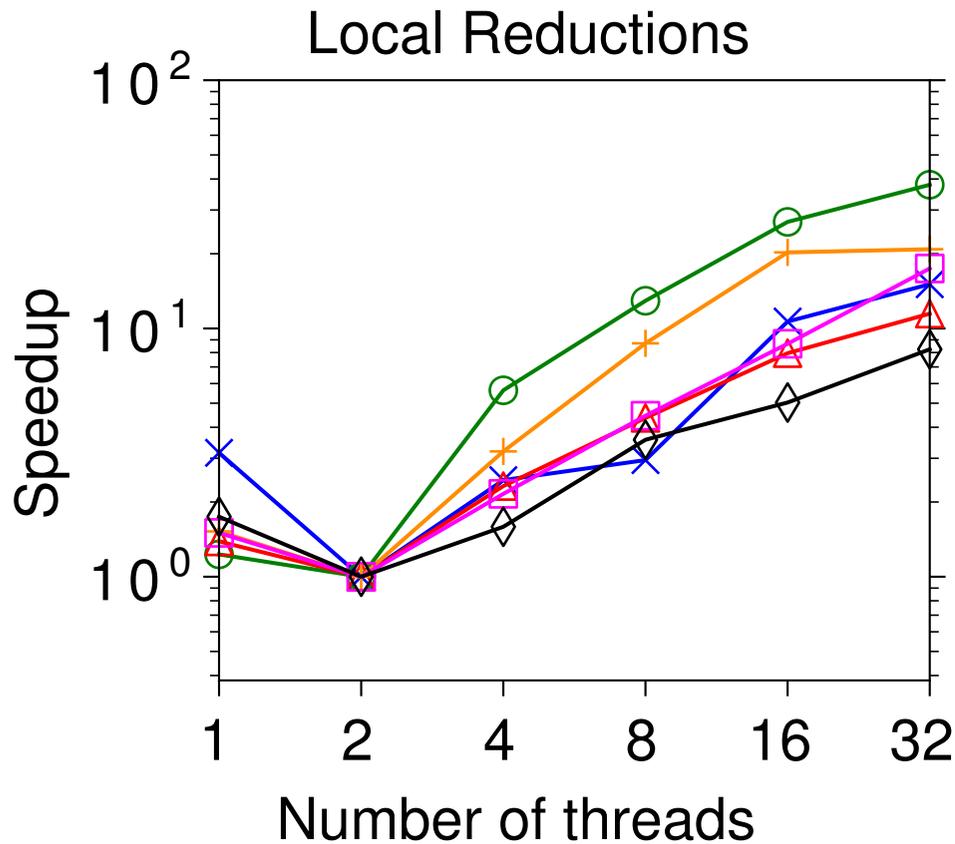


# Speedup Relative to 2 Threads



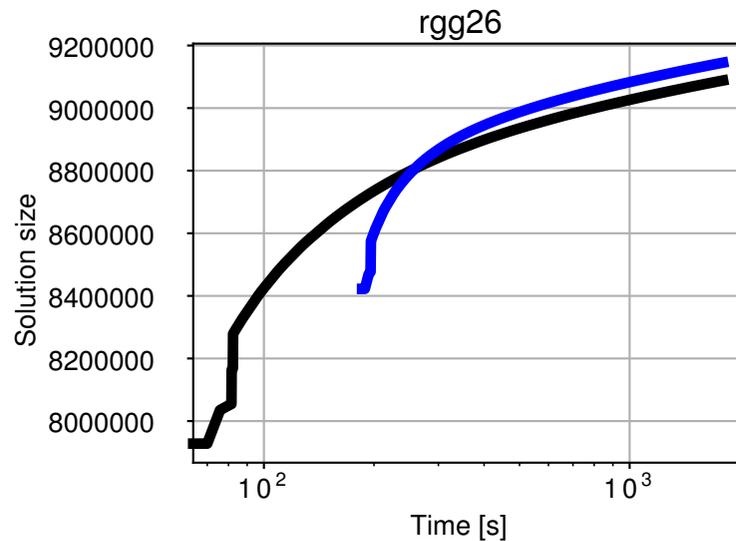
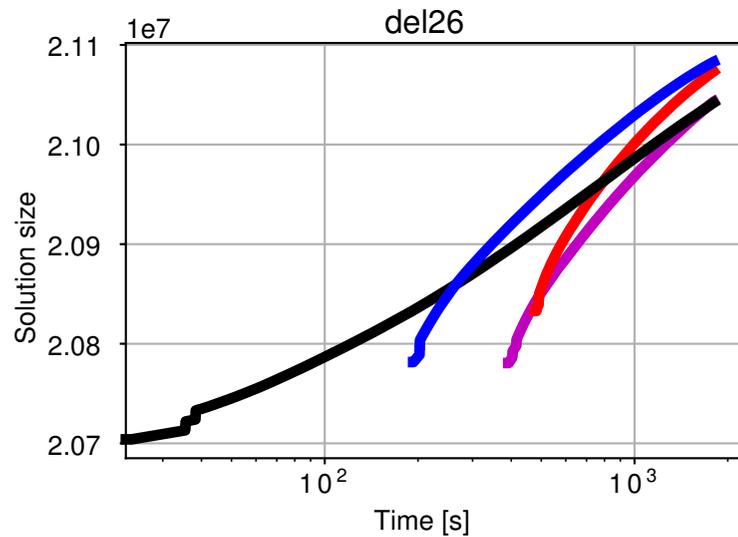
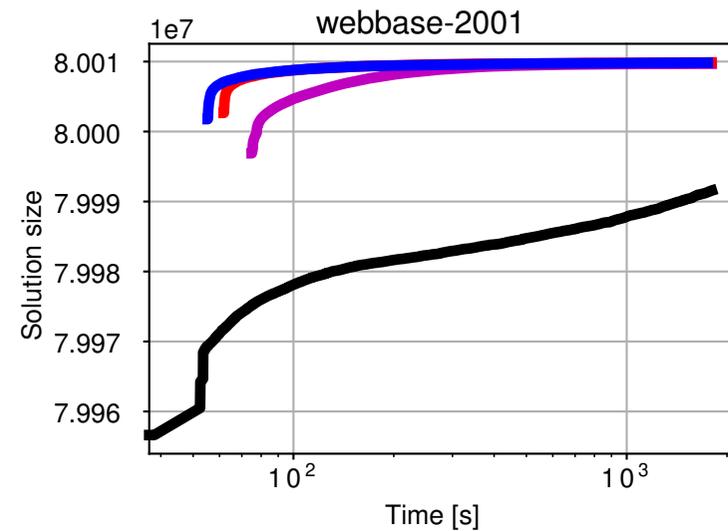
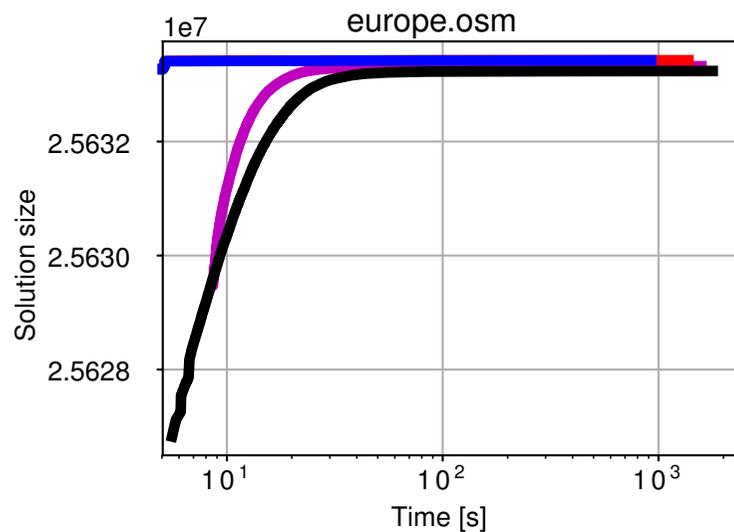
2 x Intel Xeon E5-2683 v4 processors (16 cores each), 512 GB Memory

# Speedup Relative to 2 Threads



2 x Intel Xeon E5-2683 v4 processors (16 cores each), 512 GB Memory

# Using the Kernel for Local Search



— NearLinear    
 — ParFastKer + NearLinear    
 — LinearTime    
 — ParFastKer + LinearTime

2 x Intel Xeon E5-2683 v4 processors (16 cores each), 512 GB Memory

# Conclusion

- Orders of magnitude smaller than fast methods
- Orders of magnitude faster than algorithms with similar-sized kernels
- Local search shows: Small kernels matter!
  - We find *larger* independent sets *faster*

## Future Work

- Distributed memory
- Use faster parallel partitioning
- What about other MIS algorithms that use kernelization?
- Other problems that use kernelization
  - e.g., undirected feedback vertex set, graph coloring problems