Finding optimal tree decompositions

Tuukka Korhonen

HIIT, Department of Computer Science, University of Helsinki

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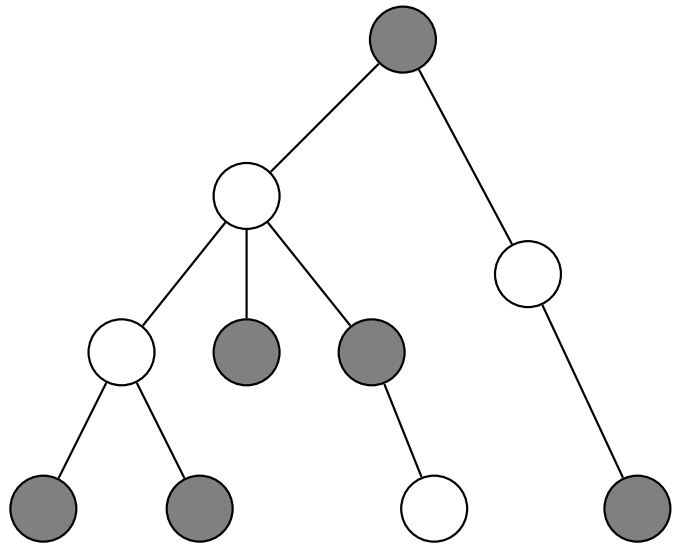
Outline

- Master's thesis on practical algorithms for finding optimal tree decompositions w.r.t. different notions of "optimal"
- Contributions
  - State-of-the-art implementations for exact computing of:
    - ★ Minimum fill-in
    - ★ Total table size
    - ★ Generalized and fractional hypertreewidth
    - ★ Maximum compatibility of multi-state phylogenetic characters
  - Papers in ACM Journal of Experimental Algorithms (2019), IJCAI 2019 and AAAI 2020
- Organization of the talk
  1. What are tree decompositions and why?
  2. Finding optimal tree decompositions

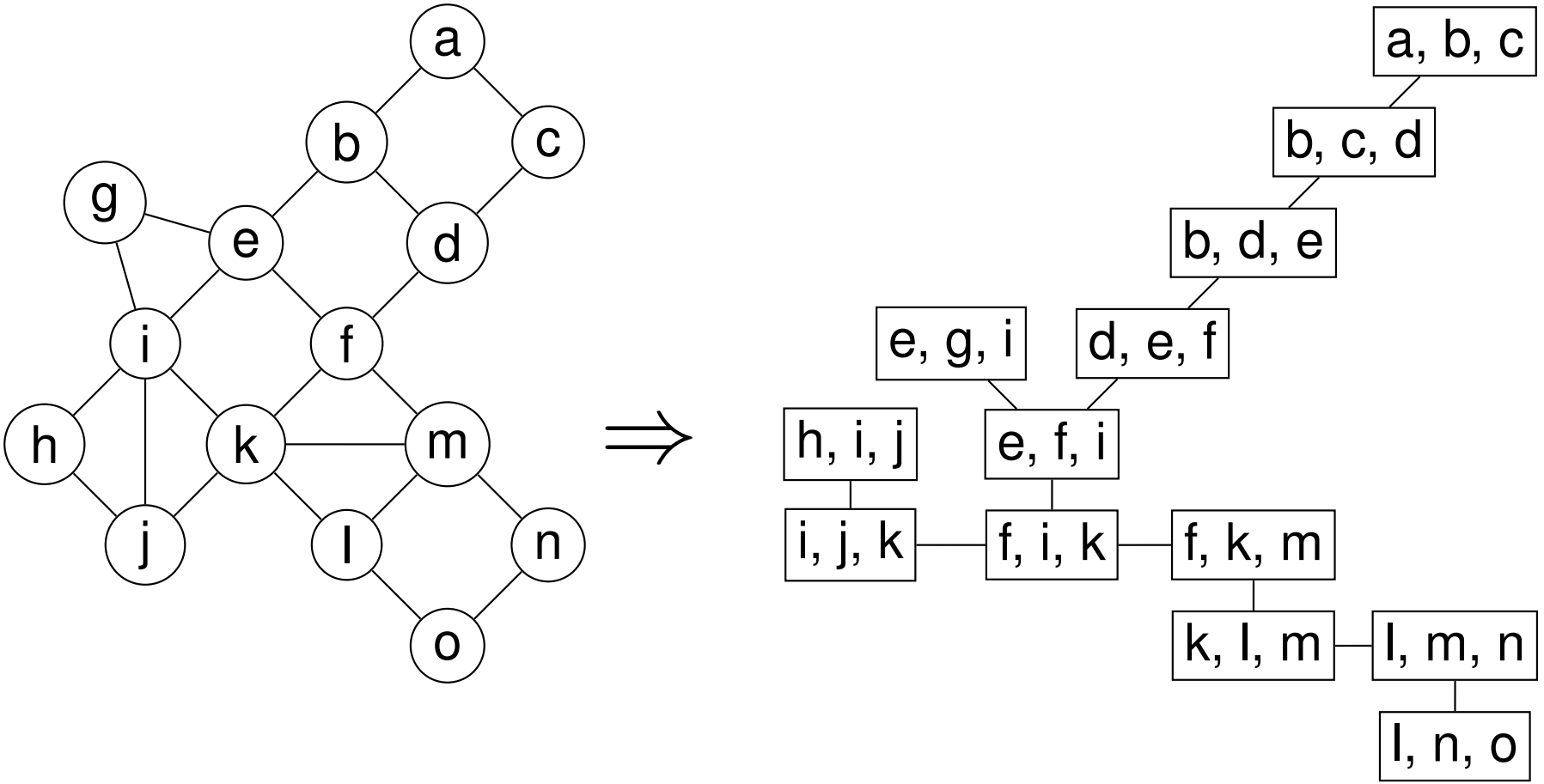
Motivation

- Hard problems are easy when data has special structure
- Example: Maximum independent set
  - Find the largest set of vertices with no edges in between
  - NP-hard in graphs in general
  - Linear-time in trees



Tree decompositions

- What if the graph is not a tree, but almost?
- Tree decomposition with low treewidth



Applications

- Theory: Huge number of problems become easy when underlying graph has low treewidth
  - $O(n)$ algorithms for constant treewidth
- Successful applications in practice:
  - Probabilistic inference
  - Solving quantified Boolean formulas
  - Compiler optimization

Beyond treewidth

- Different problems require different kinds of tree decompositions
- In constraint solving:
  - Generalized hypertreewidth
  - Fractional hypertreewidth
- Motivated by sparse matrix computations (linear programming):
  - Minimum fill-in
- Motivated by probabilistic inference (junction tree algorithm):
  - Total table size
- Problems in phylogenetics formulated with tree decompositions:
  - Perfect phylogeny
  - Maximum compatibility of phylogenetic characters

Part 2

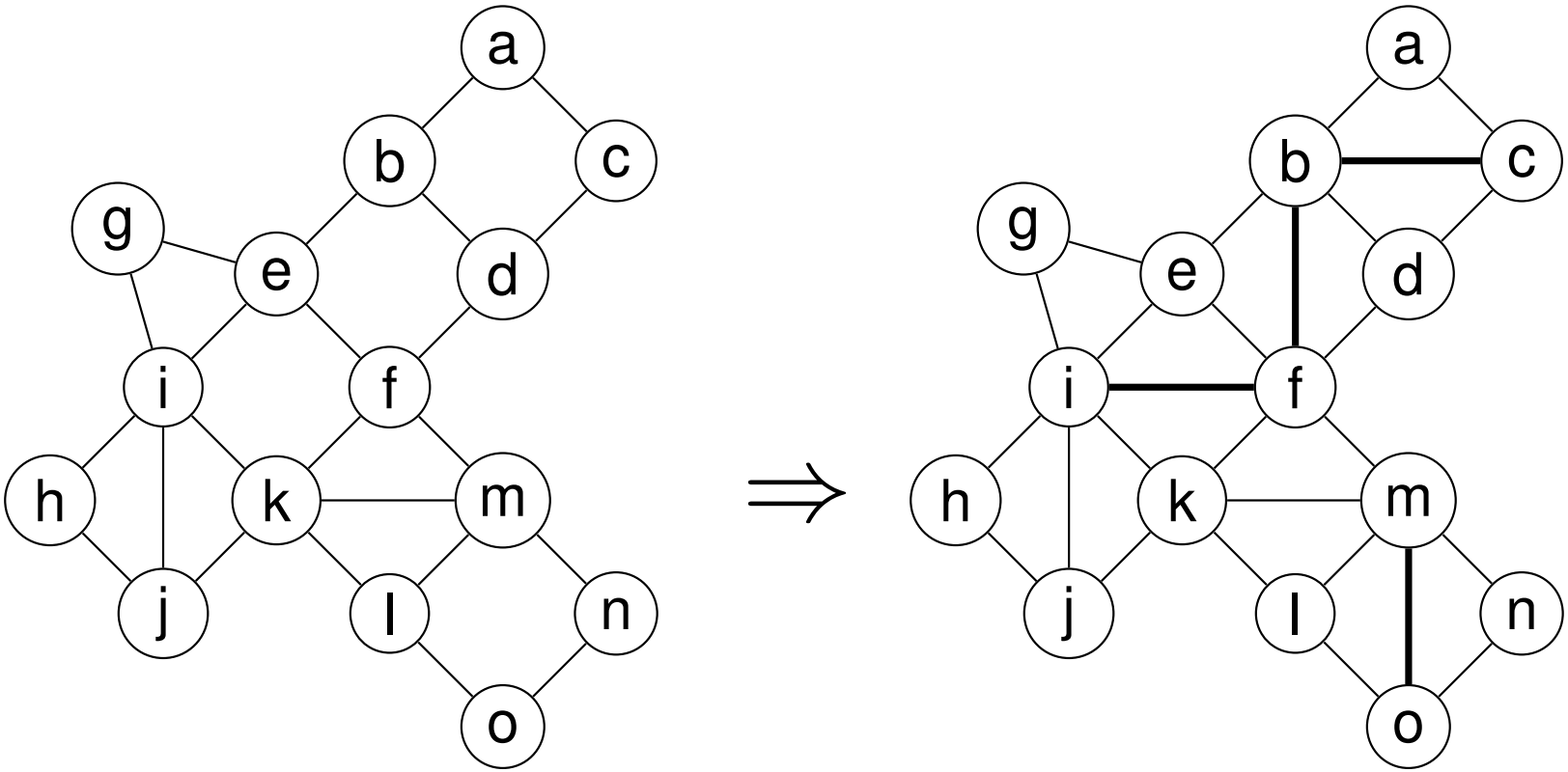
Optimal tree decompositions w.r.t. treewidth and all other parameters of the previous slide can be computed with **Bouchitté–Todinca algorithm**

BT algorithm – History

- New algorithm for treewidth and minimum fill-in using *potential maximal cliques* [Bouchitté and Todinca, 2001]
- Many theoretical results based on potential maximal cliques [Fomin et al., 2008; Fomin and Villanger, 2013]
- Best implementations in PACE 2017 challenge for treewidth and minimum fill-in use potential maximal cliques [Dell et al., 2017]
- Potential maximal cliques yield state-of-the-art practical algorithms in many more related problems [Korhonen et al., 2019b; Korhonen and Järvisalo, 2020]

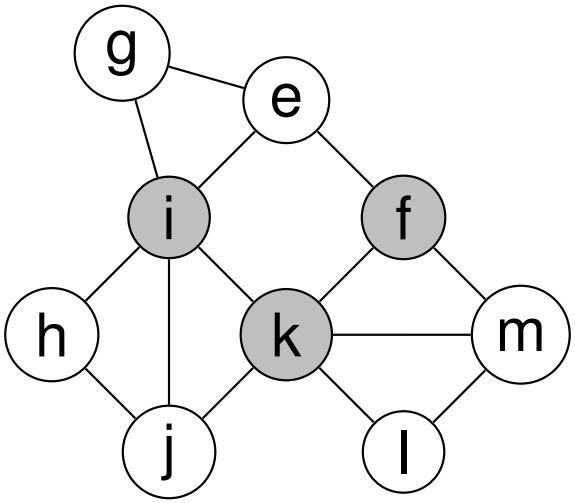
Triangulations of graphs

- Finding optimal tree decompositions is equivalent to finding optimal *triangulations* of graphs
- Triangulation: Add edges so that graph becomes *chordal*
- Chordal: All cycles of length ≥ 4 have a chord



Potential maximal cliques

- Potential maximal cliques are building blocks of triangulations
- A vertex set is a potential maximal clique if it is a maximal clique in some minimal triangulation
- Highly related to minimal separators
  - $O(|\Delta|^2 n^2 m)$ algorithm to list all potential maximal cliques, where Δ is the set of minimal separators



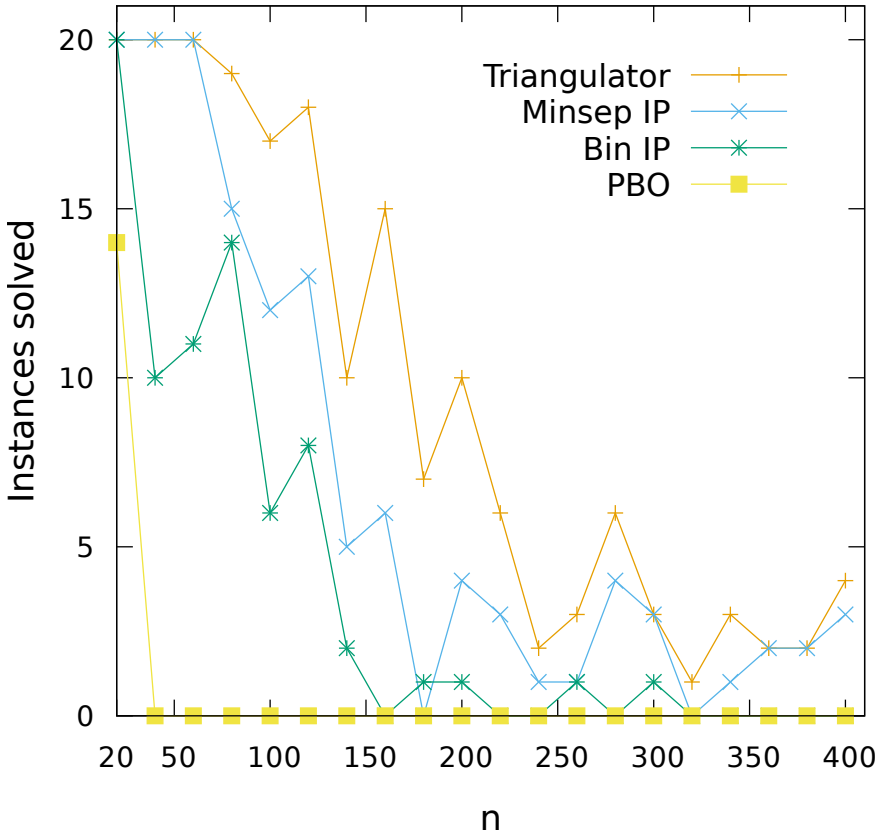
For example $\{i, k\}$, $\{k, f\}$ and $\{i, f\}$ are minimal separators and $\{i, f, k\}$ is a potential maximal clique.

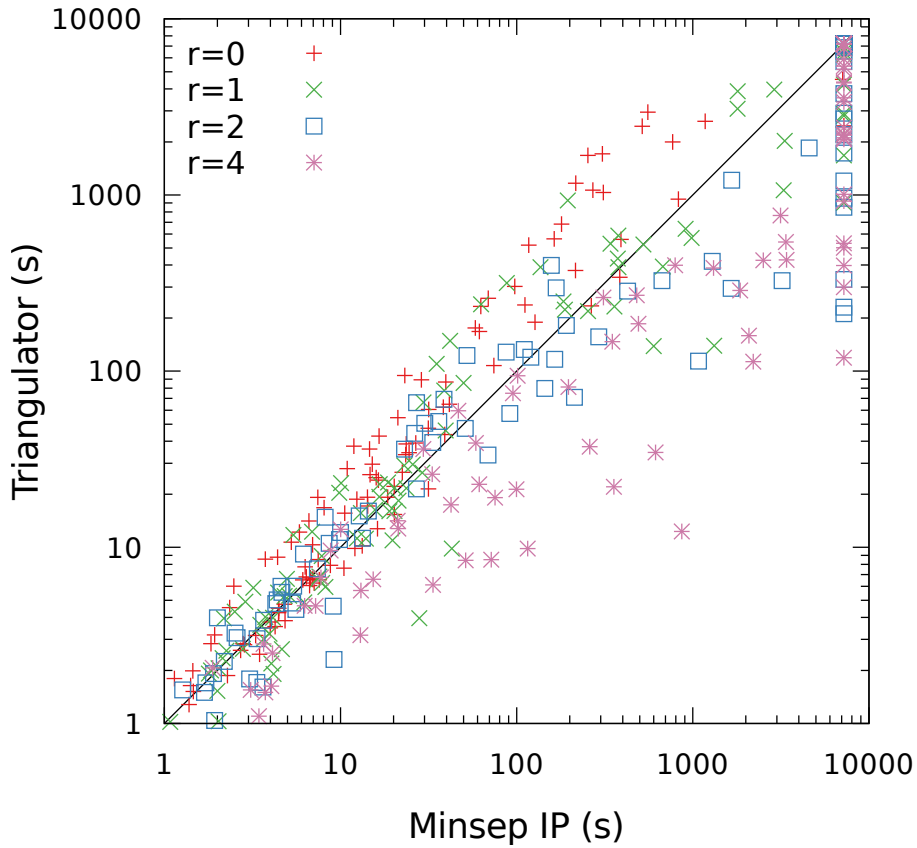
BT algorithm

- Given the potential maximal cliques Π, an optimal minimal triangulation can be found in $O(|\Pi|n^3)$ time
- BT algorithm:
  1. Enumerate potential maximal cliques
  2. Dynamic programming over potential maximal cliques to find an optimal triangulation
- In practice, phase 1 is the running time bottleneck

Experimental results

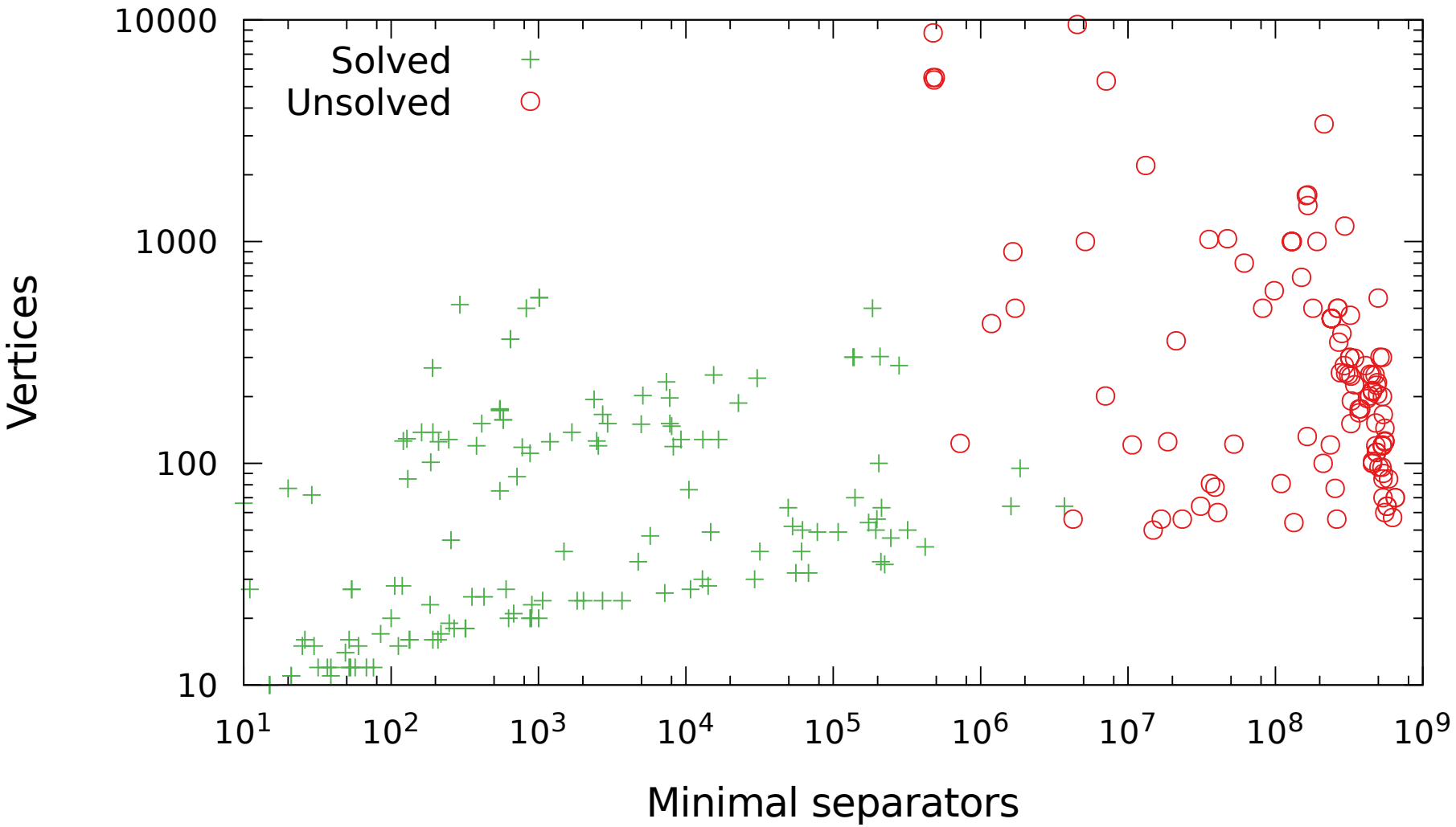
Comparison to other algorithms on Maximum compatibility problem of phylogenetic characters





Experimental results

How large instances can we solve? (Minimum fill-in)



The end

Thank you for your attention!

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