University of Glasgow

Reducing the Branching in a Branch and Bound Algorithm for the Maximum Clique Problem

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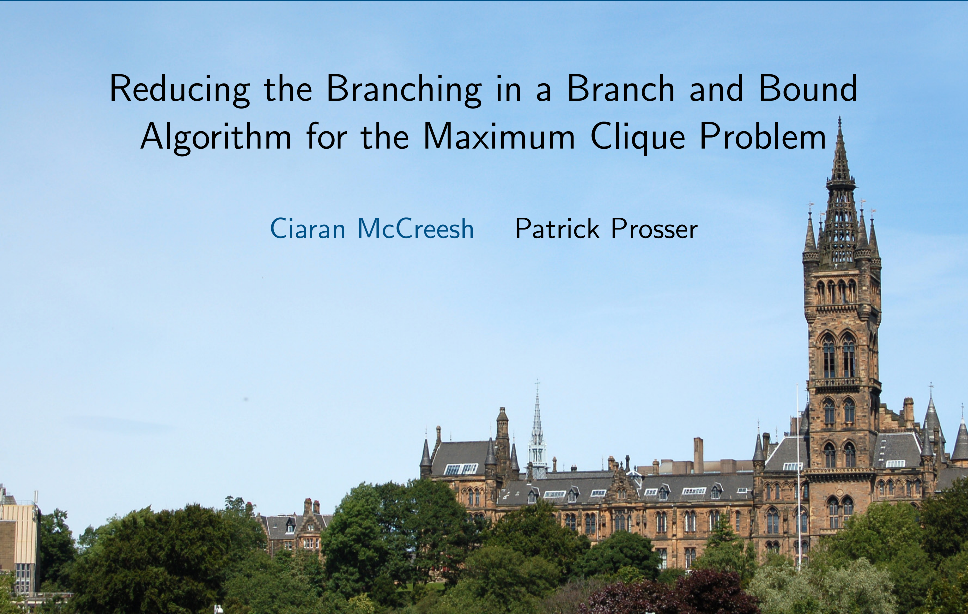
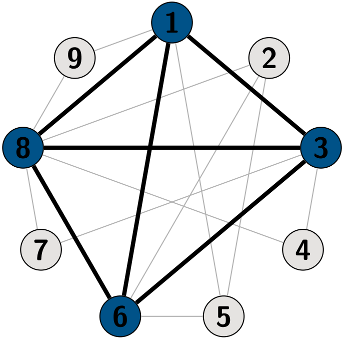
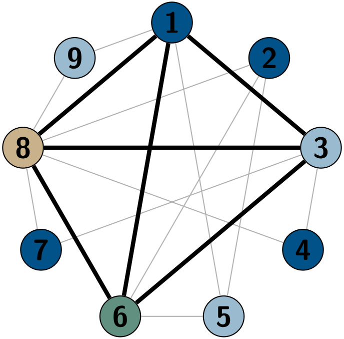


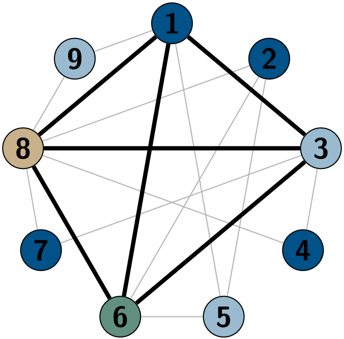
The Maximum Clique Problem



Branch and Bound



Iteration Order

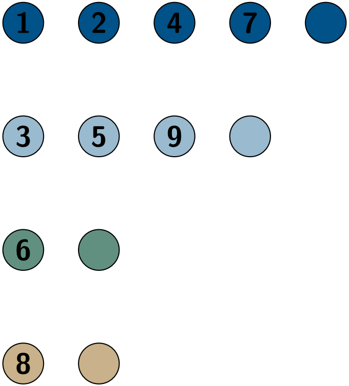


1	2	4	7	3	5	9	6	8
1	1	1	1	2	2	2	3	4

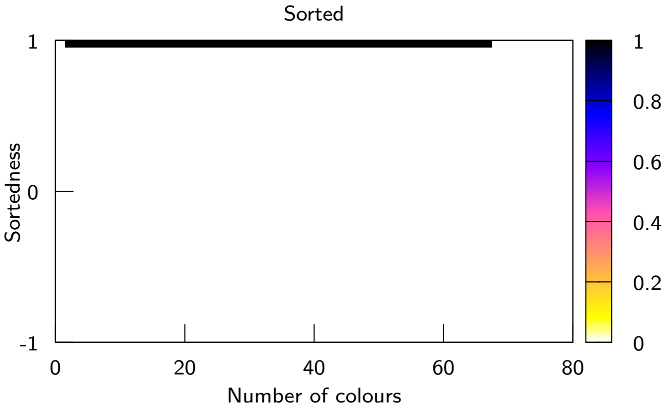
Why?

"In procedure EXPAND(R, No), after applying NUMBER-SORT more than once, a maximum clique contains a vertex p in R such that $No[p] \geq \omega(R)$. It is generally expected that a vertex p in R such that $No[p] = Max\{No[q] | q \in R\}$ has a high probability of belonging to a maximum clique." (Tomita et al., 2007)

An Observation



Are Later Colour Classes Smaller?



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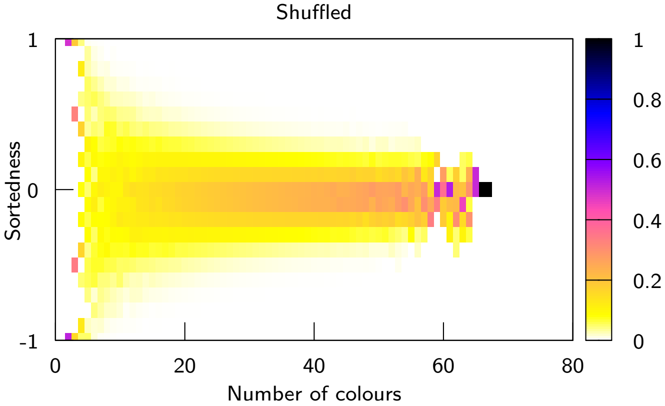
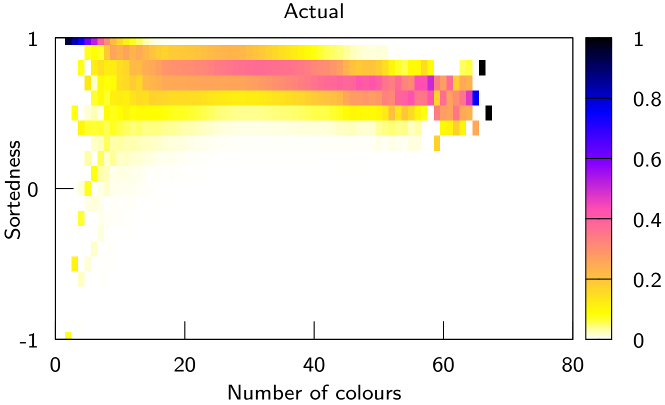
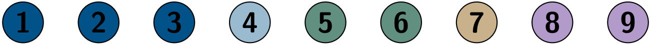


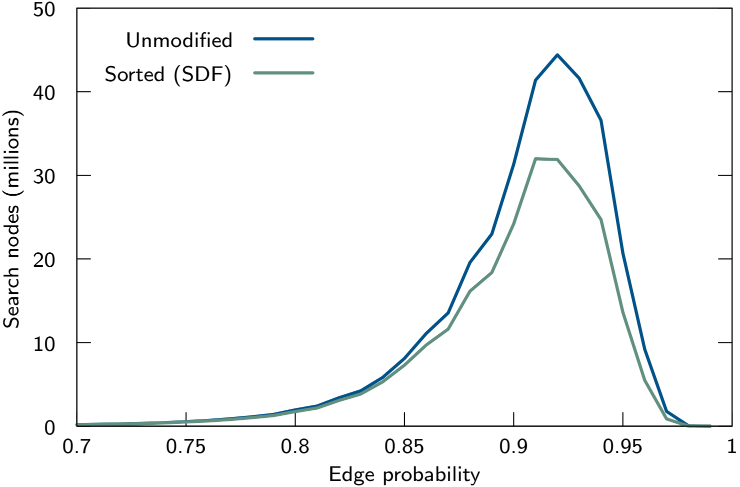
Later Colour Classes are Smaller



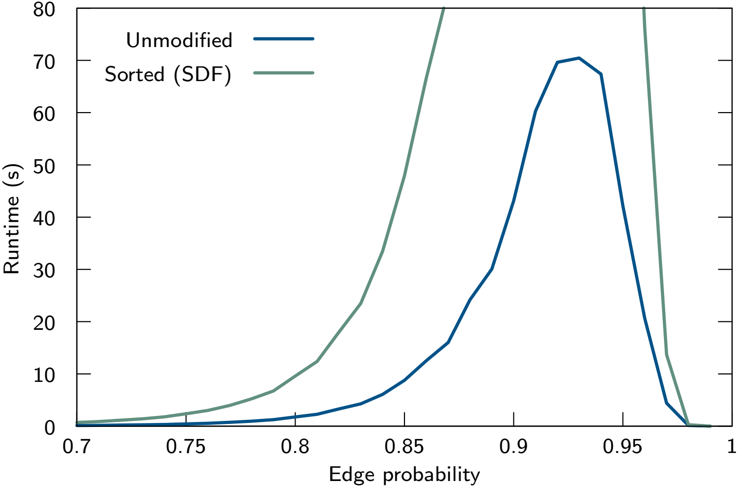
Later Singletons have More Filtering Power



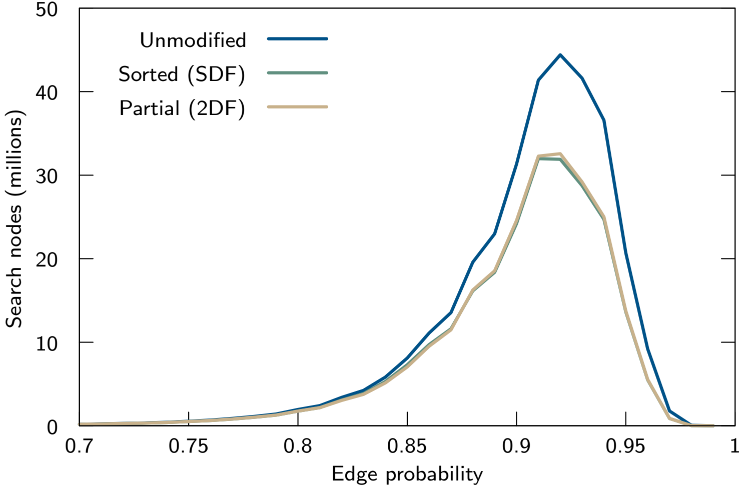
Smallest Domain First (SDF)



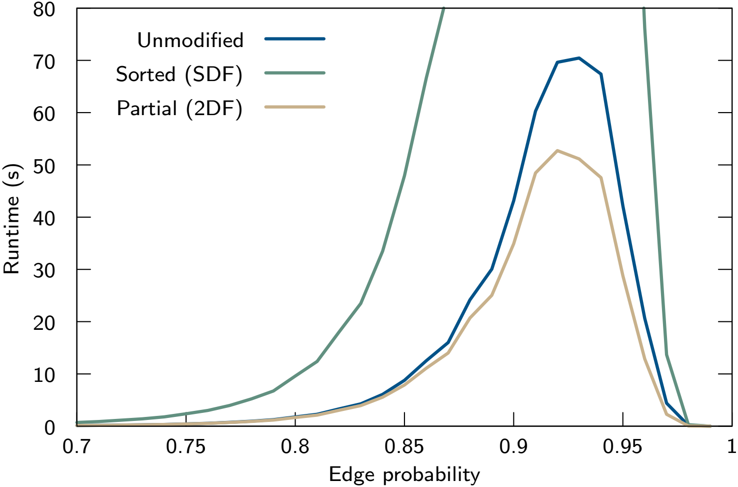
SDF is Expensive



Domains of Size 2 First (2DF)



2DF is Cheap



Unmodified
Sorted (SDF)
Partial (2DF)
Runtime (s)
0
10
20
30
40
50
60
70
80
0.7
0.75
0.8
0.85
0.9
0.95
1
Edge probability

Standard Benchmark Instances

- Modest improvements to both search space size and node counts in 39 out of 50 medium-sized DIMACS instances, minimal effect in 10 more, and a large slowdown in 1.
- Improvements of 10% to 25% for the smallest ten BHOSLIB instances.
- A full sort is typically slightly better for the search space size, but around five times as expensive.

But more importantly. . .

- By rephrasing these algorithms using language and techniques from CP, we now understand more about why they work, and what we should be preserving when making changes.

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