Computing the Flip Distance of Triangulations

Bachelor-Kolloquium

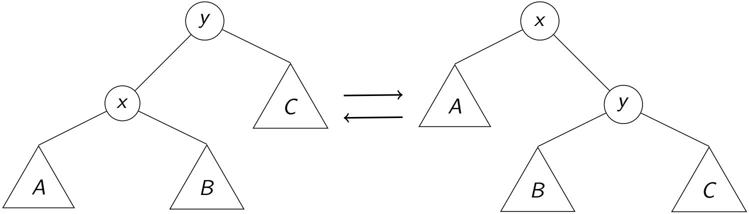
Fabian Lipp

July 5, 2012

Contents

Motivation of the Problem

- Let T_1, T_2 be binary search trees
- Operations: Left rotation, right rotation



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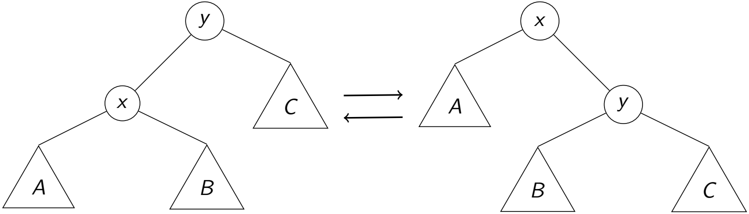

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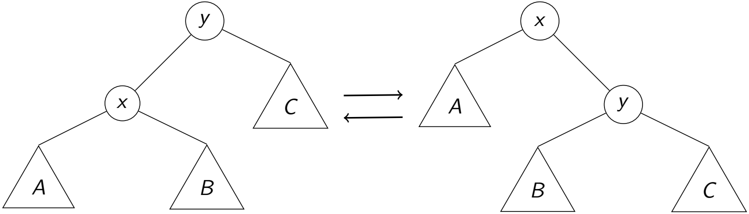

- Task: Find a shortest sequence of rotations that lead from T_1 to T_2
- There is no polynomial-time algorithm known for this problem, but NP-hardness is not proven

Transformation of the Problem

Represent a binary tree with $n-2$ nodes as a triangulation of a polygon with n corners

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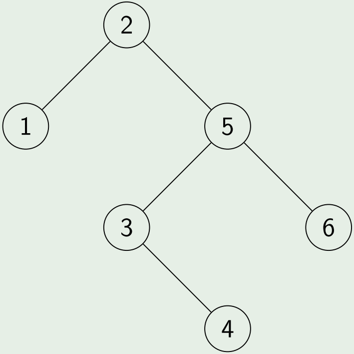

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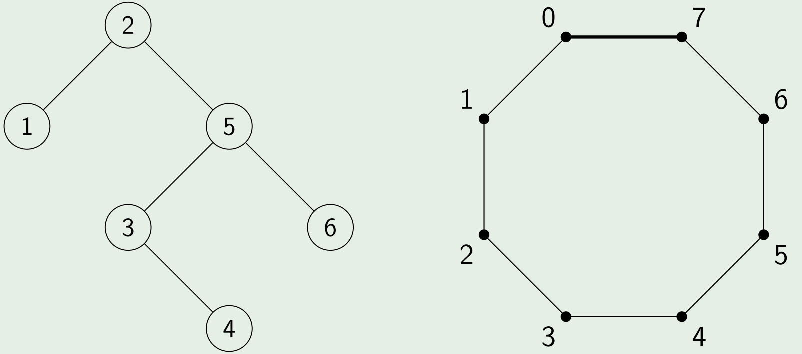

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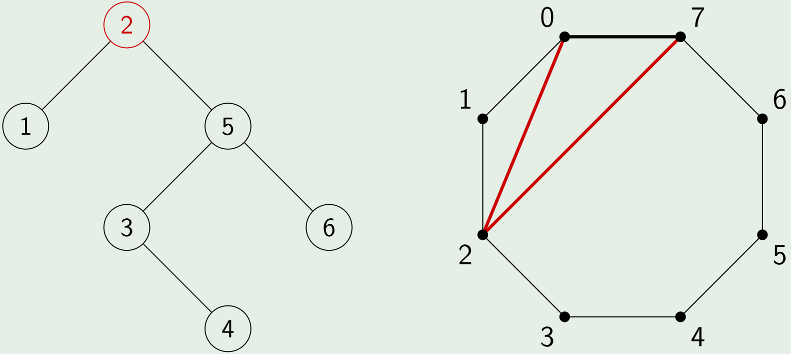

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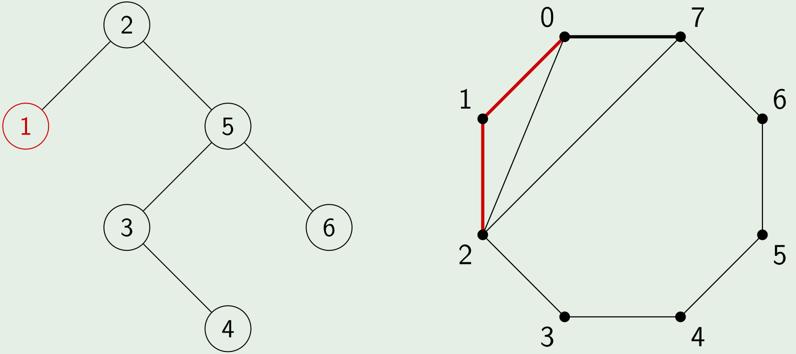

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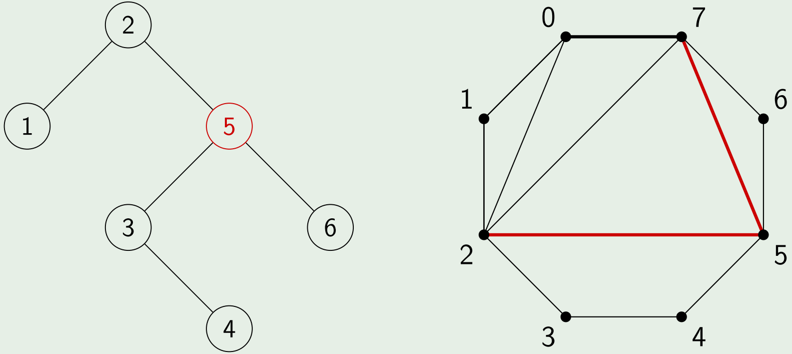

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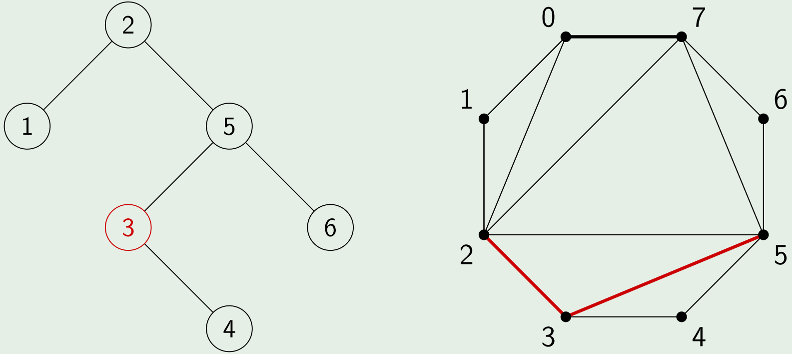

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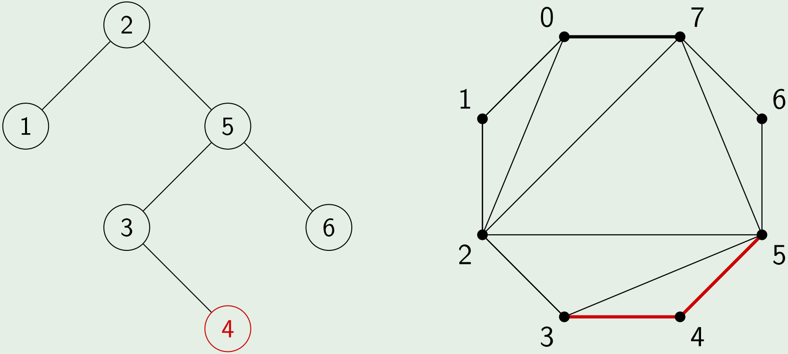

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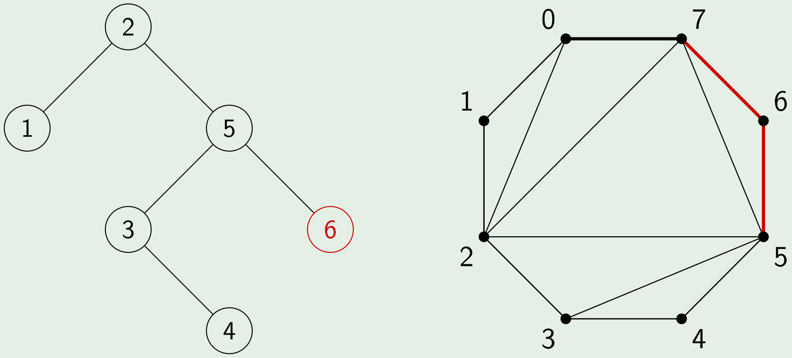

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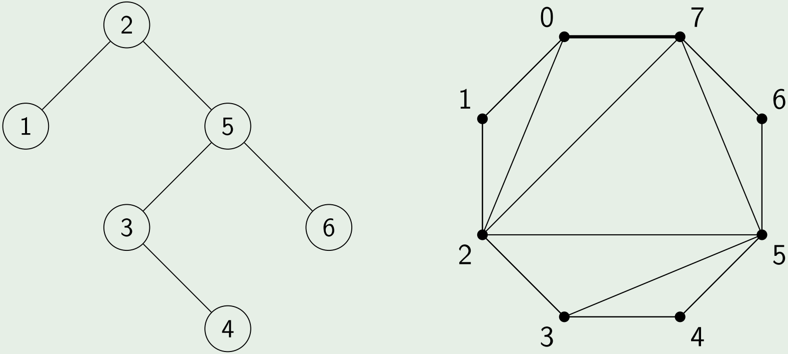

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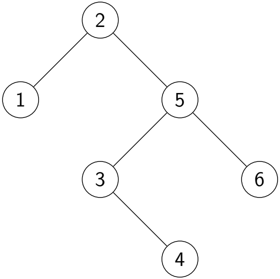

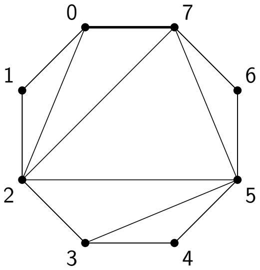

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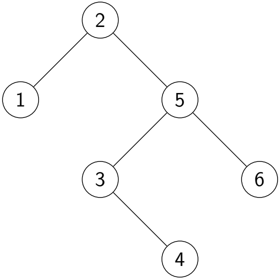

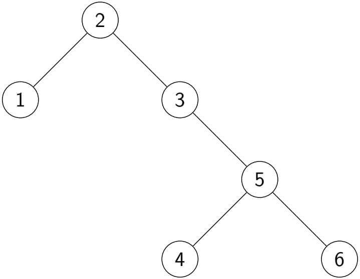

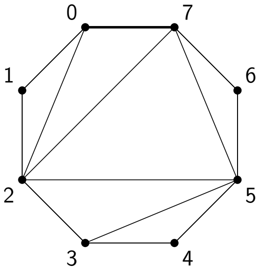

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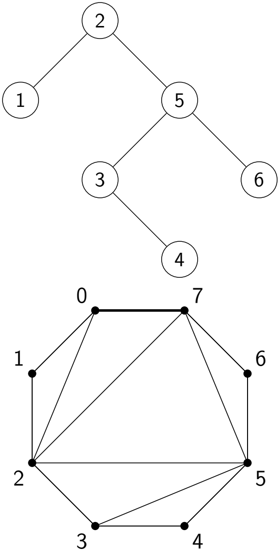

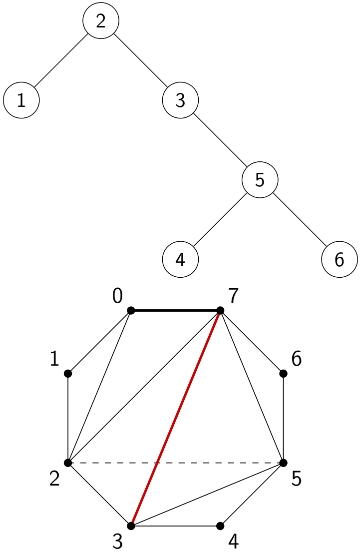

Flip Distance

Rotation distance between binary trees is equivalent to flip distance between triangulations

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Definition (Flip Distance)

The *flip distance* $\mathrm{fd}(\pi_1, \pi_2)$ is the minimum number of diagonal flips required to transform π_1 to π_2.

Flip Distance

Rotation distance between binary trees is equivalent to flip distance between triangulations

Definition (Flip Distance)

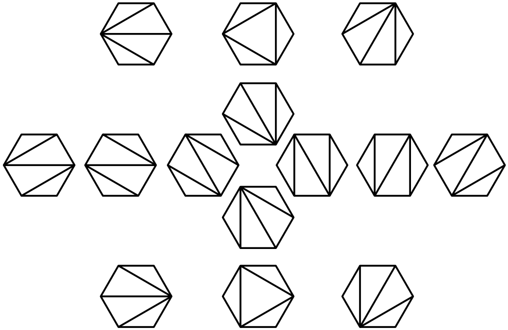
The *flip distance* $\mathrm{fd}(\pi_1, \pi_2)$ is the minimum number of diagonal flips required to transform π_1 to π_2.

Upper bound for two triangulations of the n-gon:

$$\mathrm{fd}(\pi_1, \pi_2) \leq 2n - 6$$

Breadth-First Search

Flip Graph $\mathcal{F}_6$:



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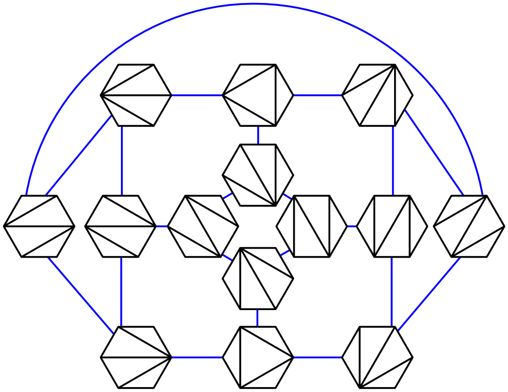

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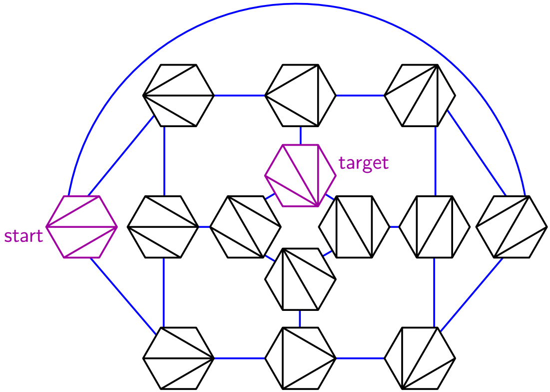

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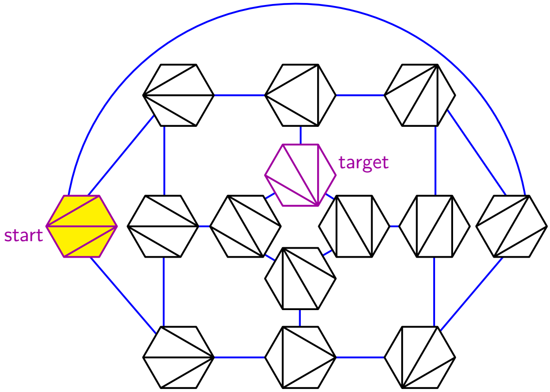

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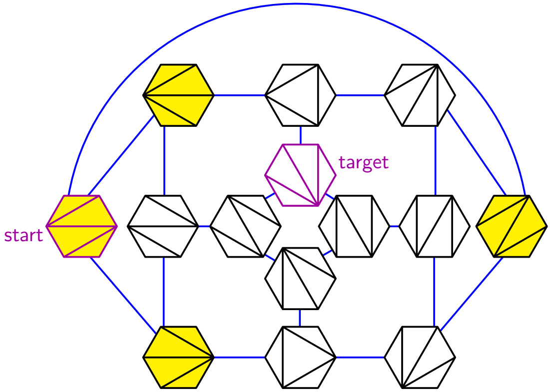

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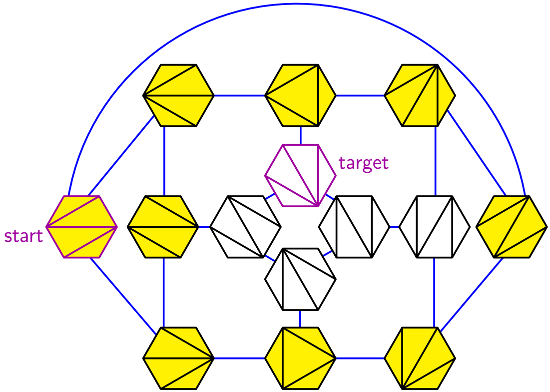

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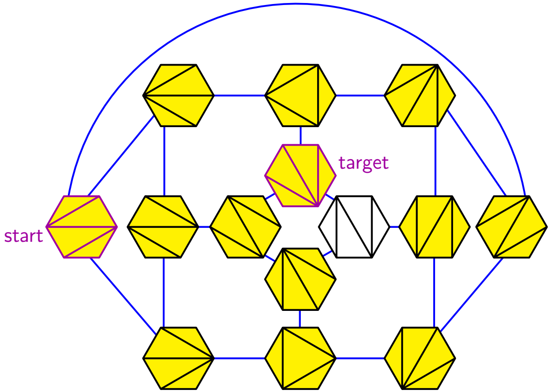

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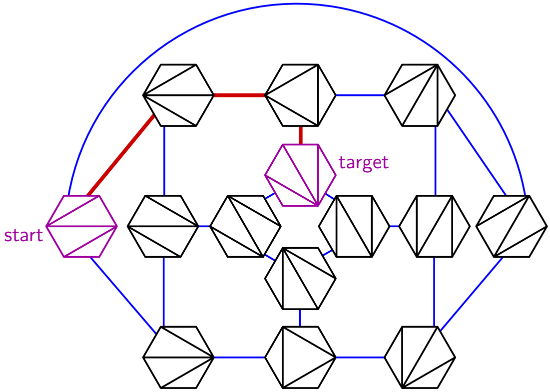

$\mathrm{fd}(\mathrm{start}, \mathrm{target}) = 3$

Breadth-First Search

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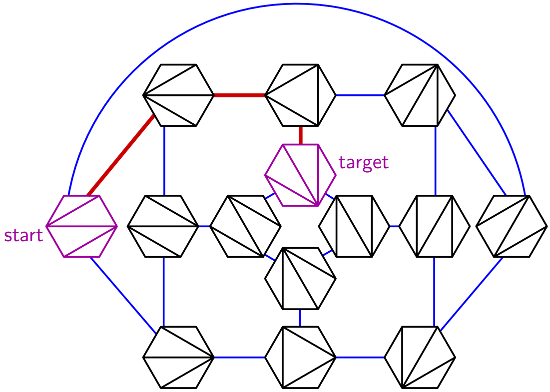

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Runtime

Number of nodes in $\mathcal{F}_{n+2}$:

$$C_n = \frac{1}{n+2}\binom{2n}{n}$$

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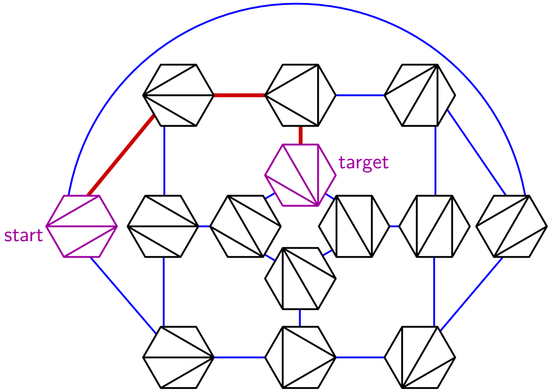

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Runtime

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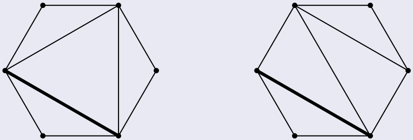
$$C_n = \frac{1}{n+2}\binom{2n}{n}$$

$$C_n \sim \frac{4^n}{\sqrt{\pi n^3}}$$

$\Rightarrow$ Exponential runtime

Simple Improvements

Common Diagonal



Do not flip this diagonal in BFS

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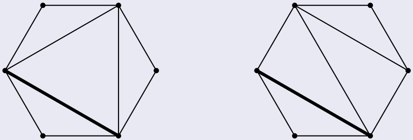

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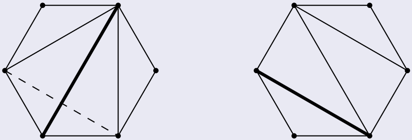
Flip-to-Match Diagonal



Flip only this diagonal in BFS

Two-Sided BFS

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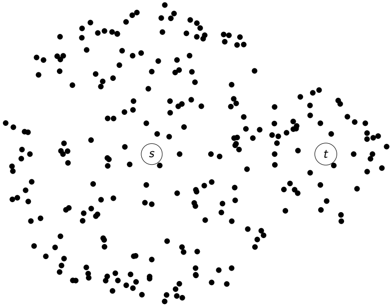

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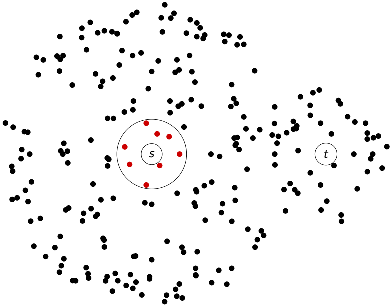

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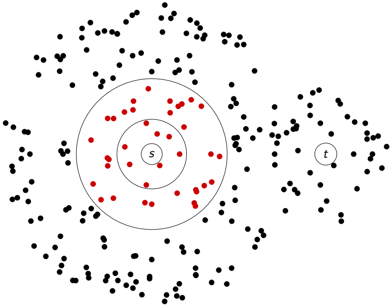

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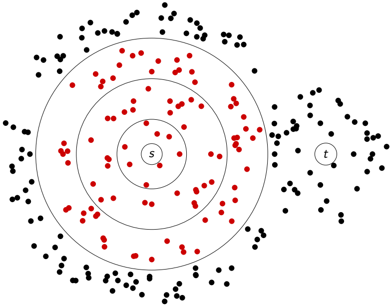

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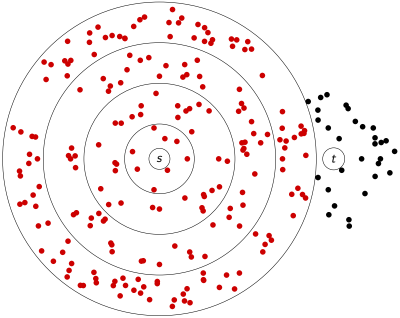

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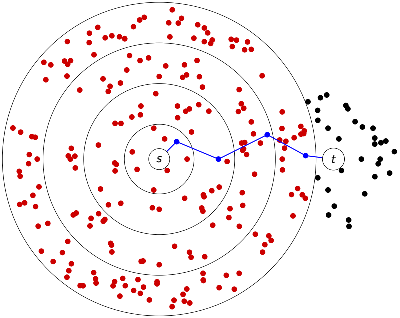

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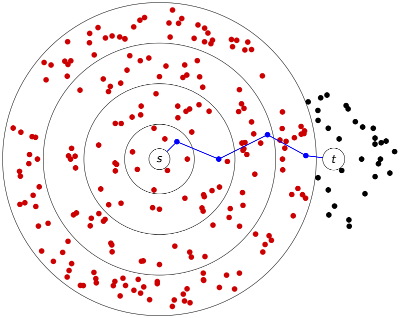

- Start BFS from start and target at the same time

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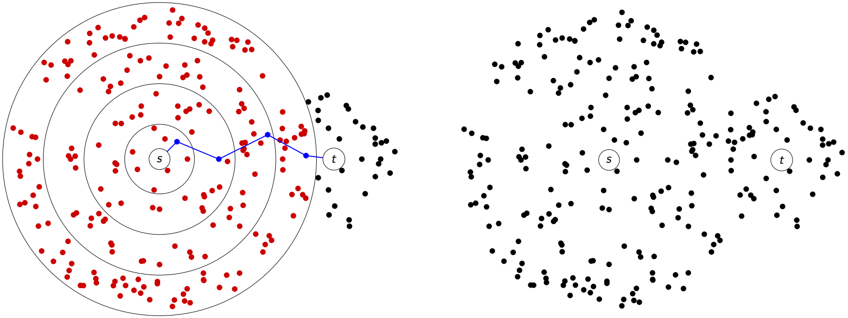

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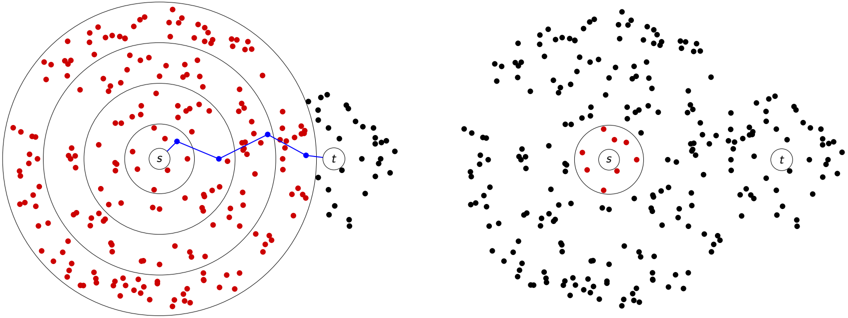

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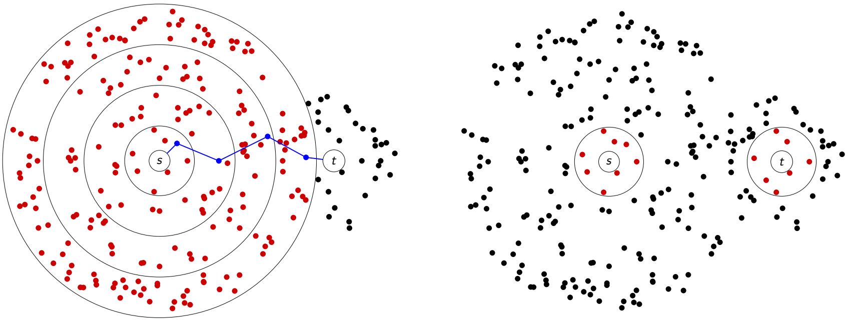

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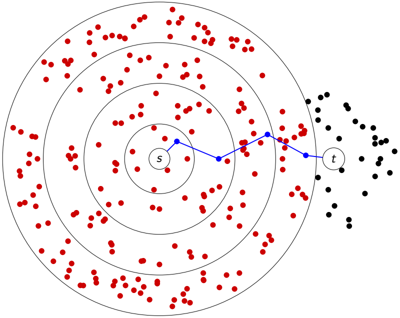

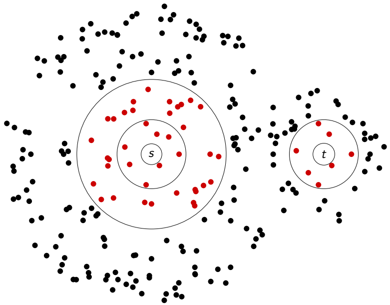

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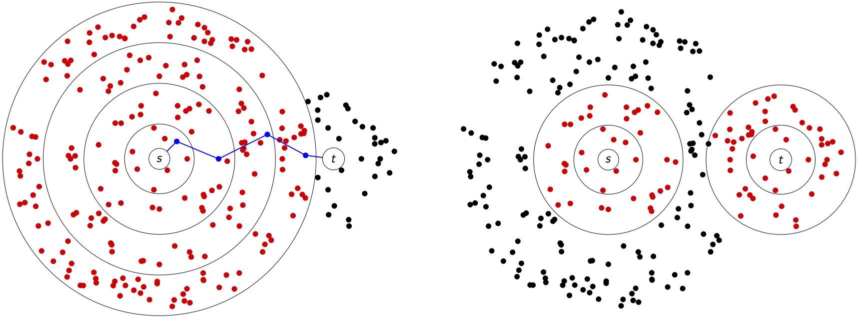

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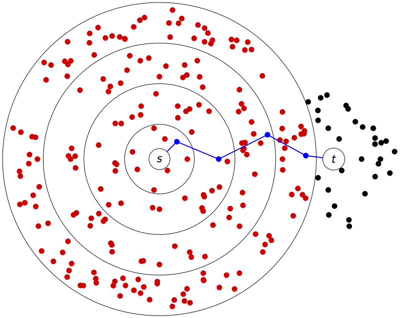

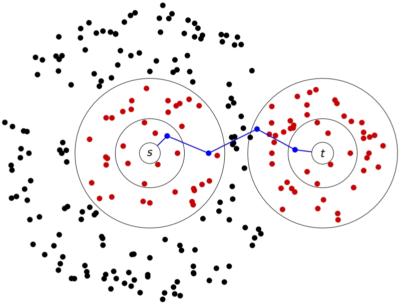

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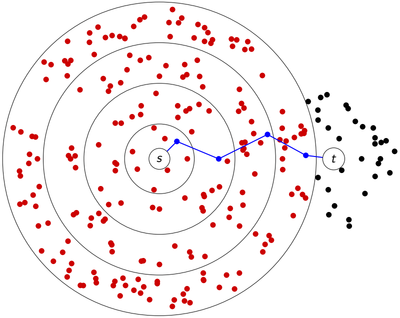
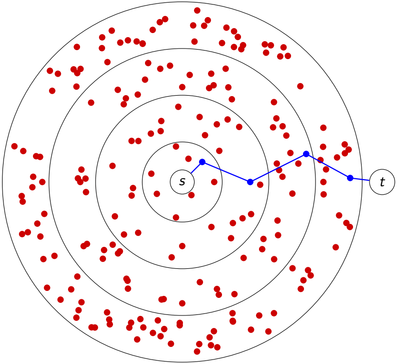


- Start BFS from start and target at the same time
- Reduces the number of visited nodes

A* search algorithm



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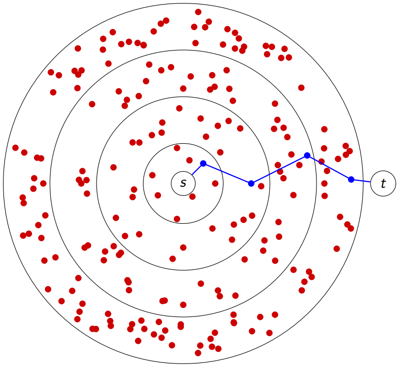

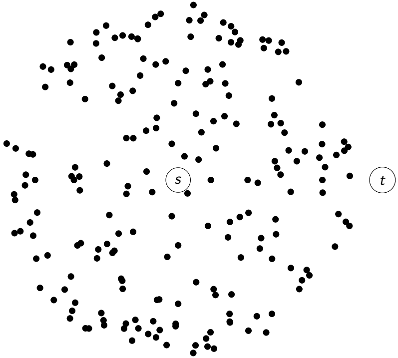

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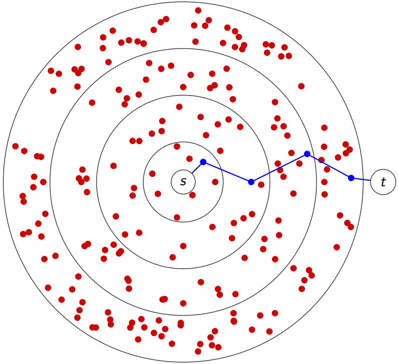

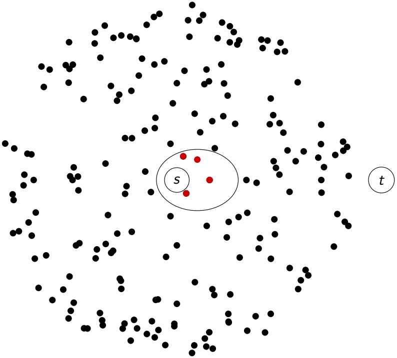

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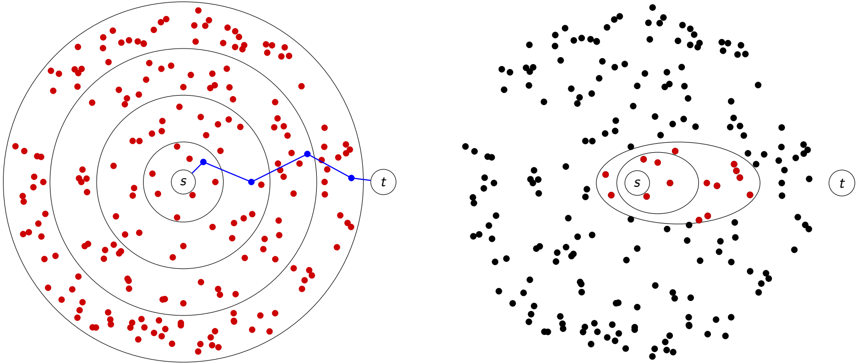

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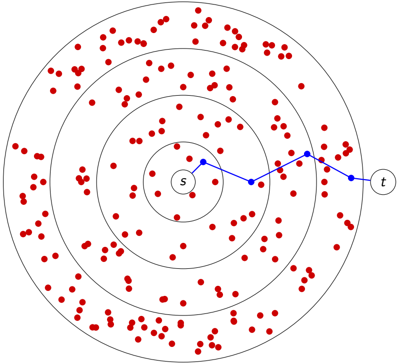

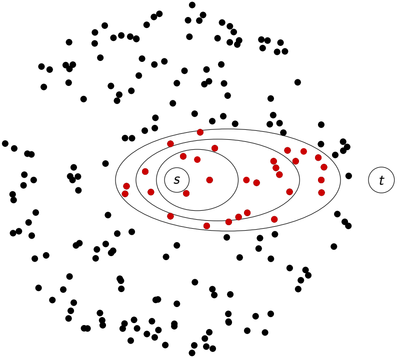

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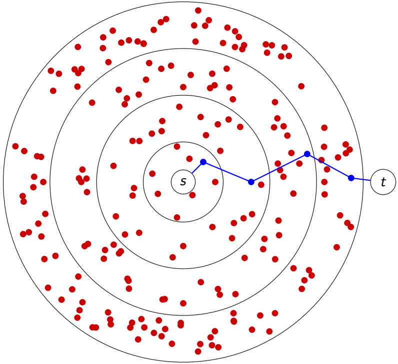

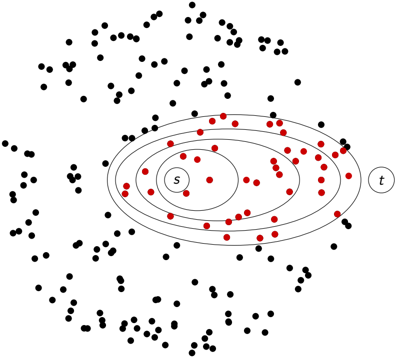

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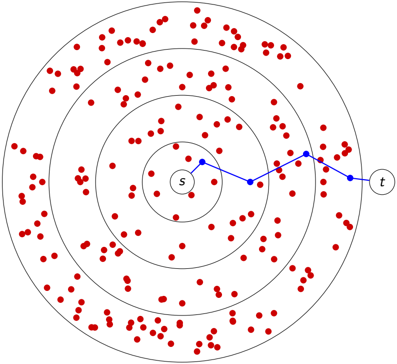

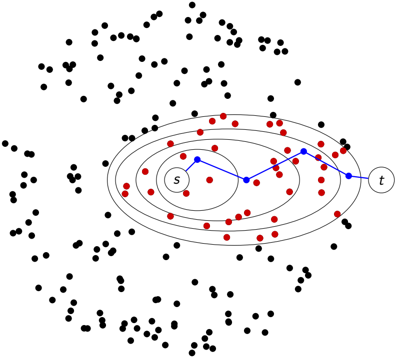

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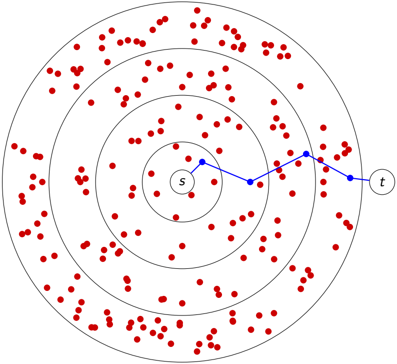

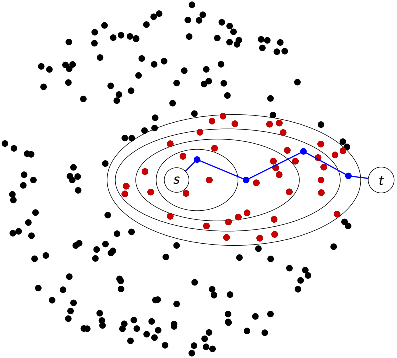

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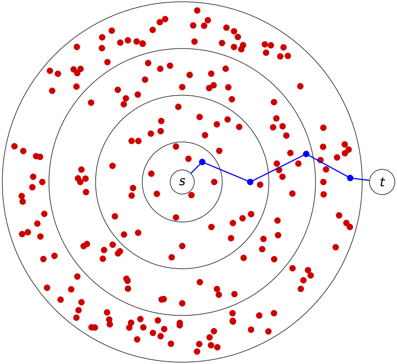
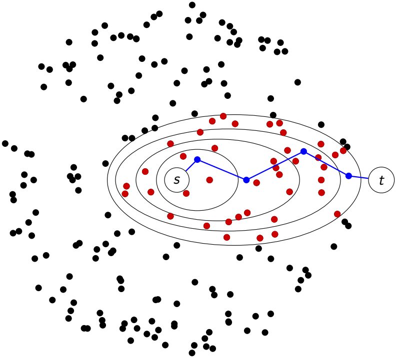
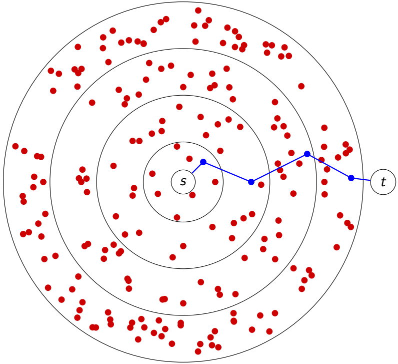
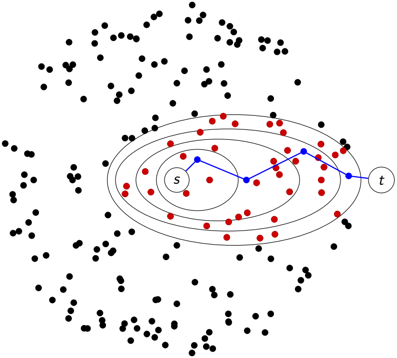




- Reduces the number of visited nodes
- Needs lower bound for distance from an arbitrary node to target

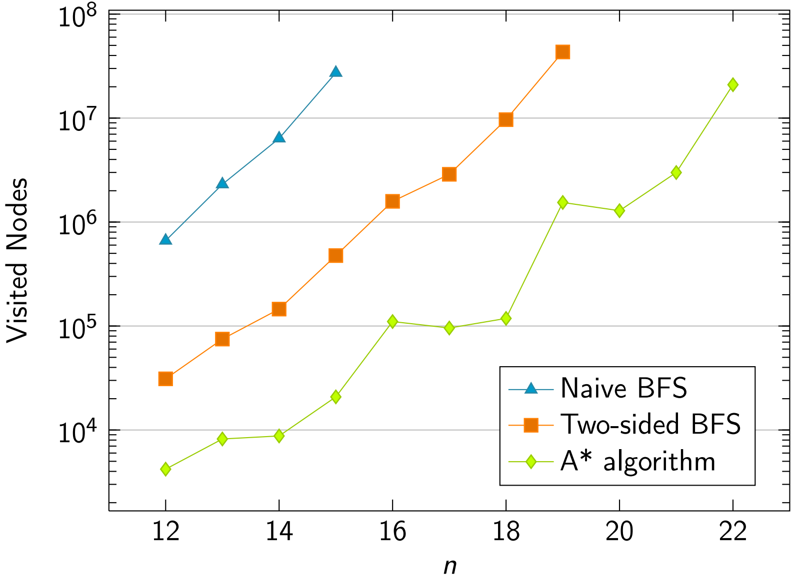
A* search algorithm





- Reduces the number of visited nodes
- Needs lower bound for distance from an arbitrary node to target
- Easy lower bound: number of diagonals that are not common

Effects of these improvements



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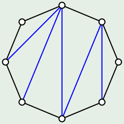

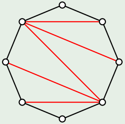

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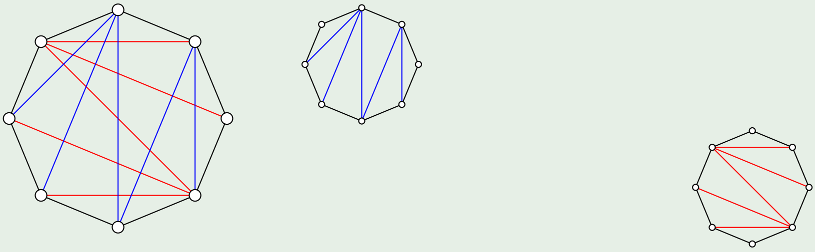

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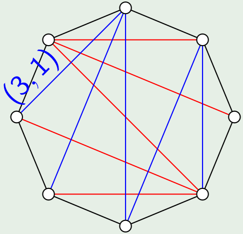

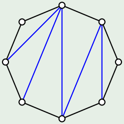

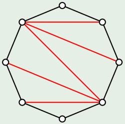

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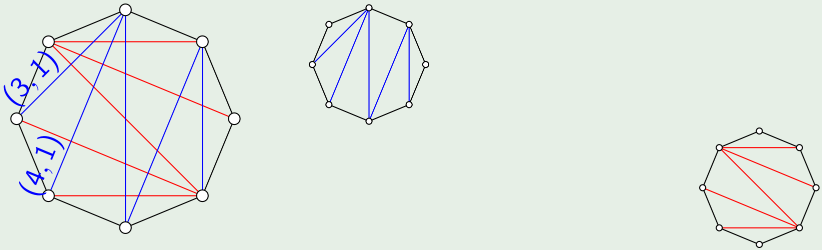

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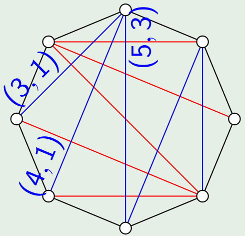

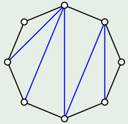

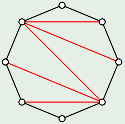

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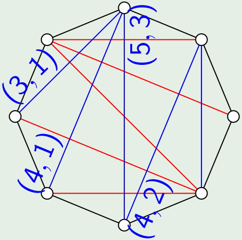

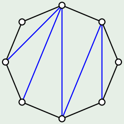

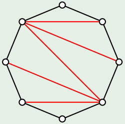

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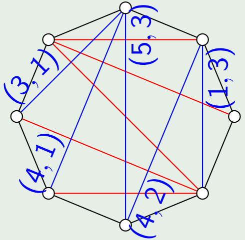

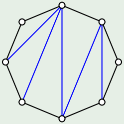

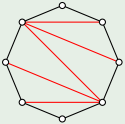

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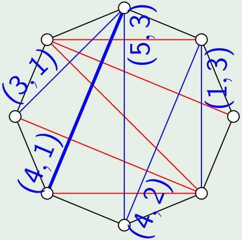

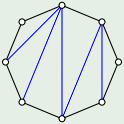

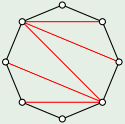

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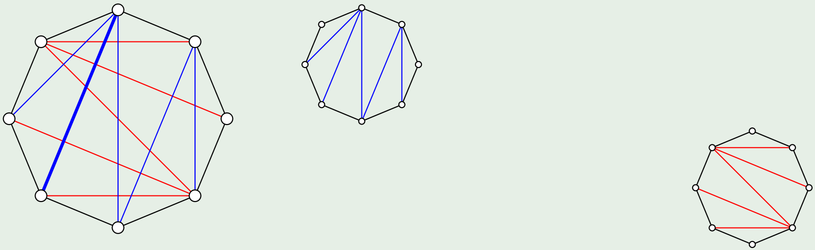

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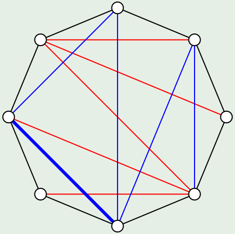

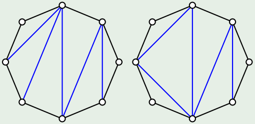

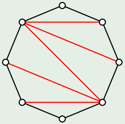

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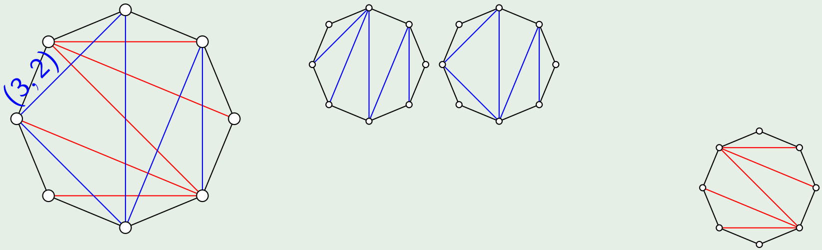

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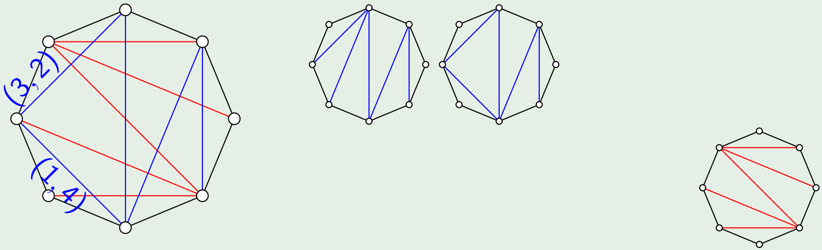

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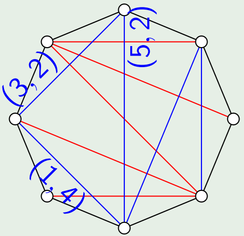

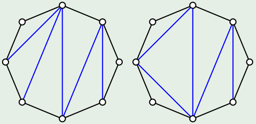

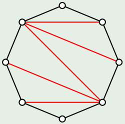

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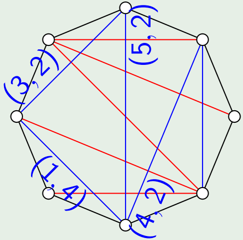

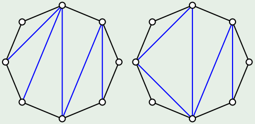

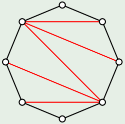

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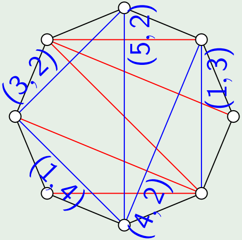

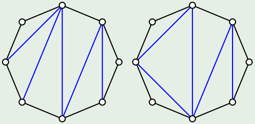

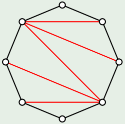

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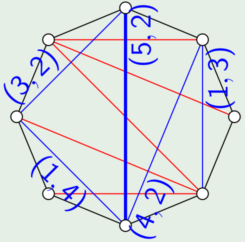

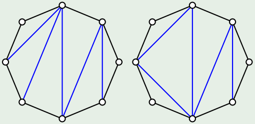

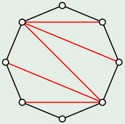

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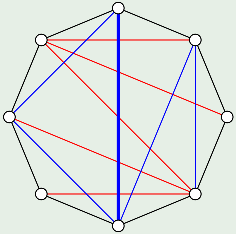

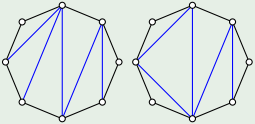

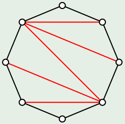

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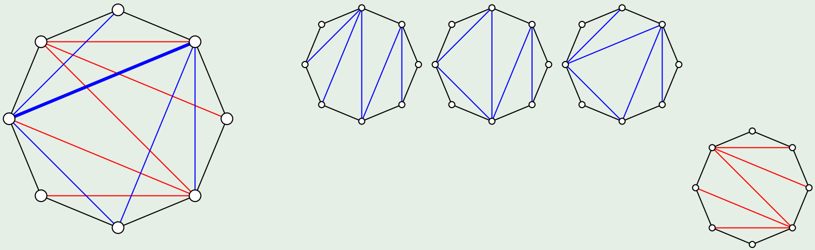

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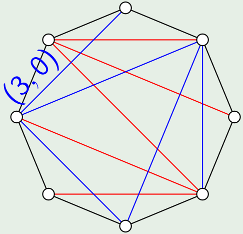

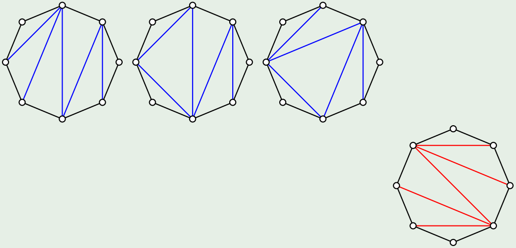

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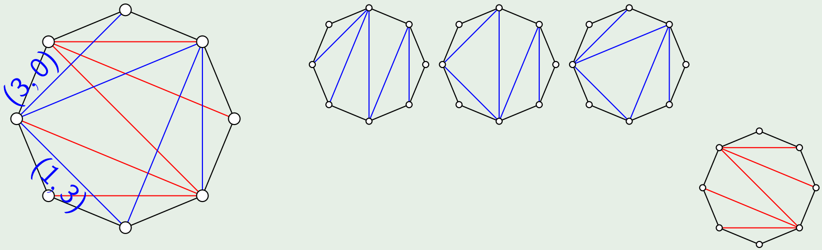

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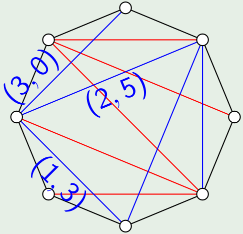

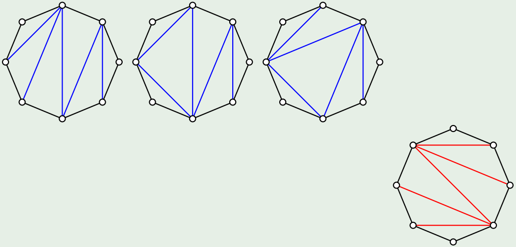

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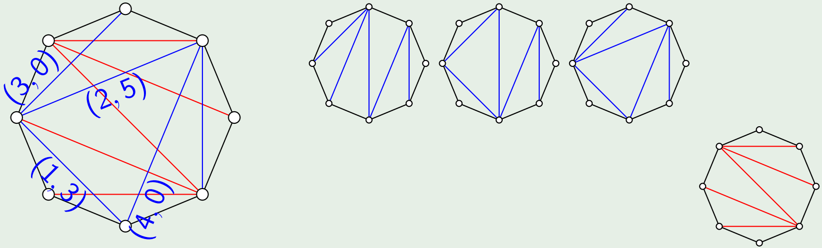

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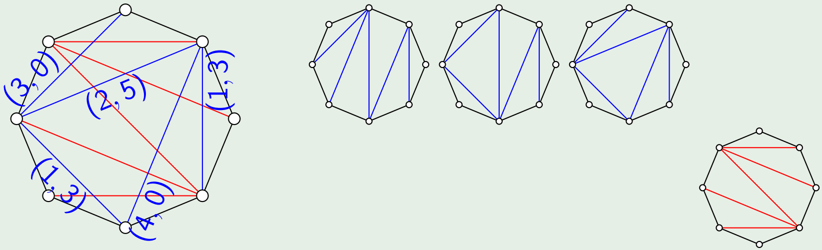

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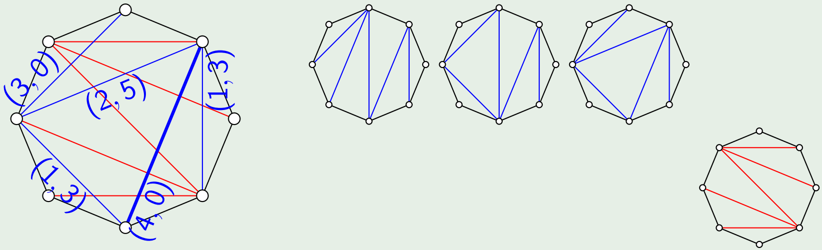

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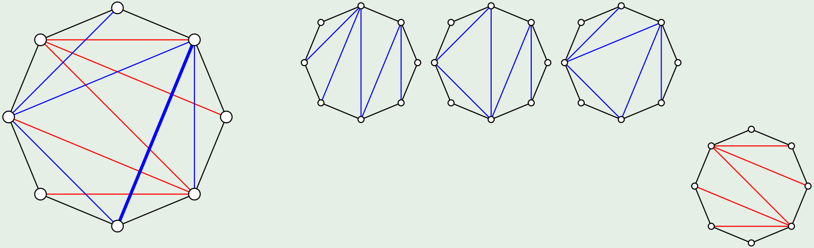

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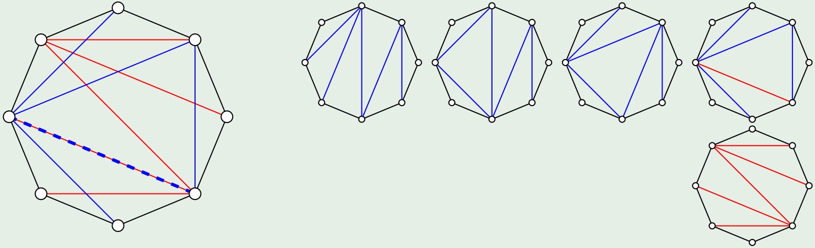

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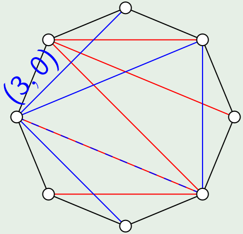

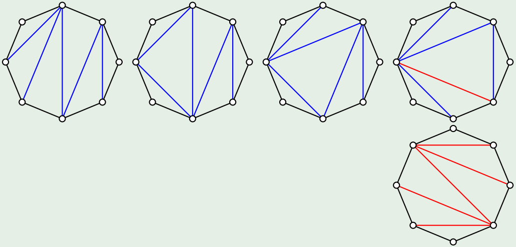

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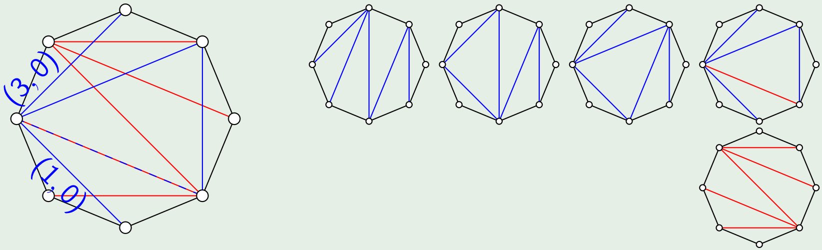

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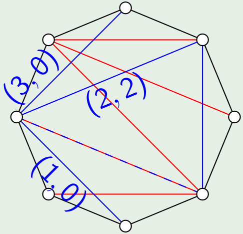

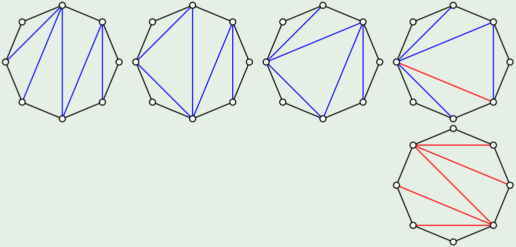

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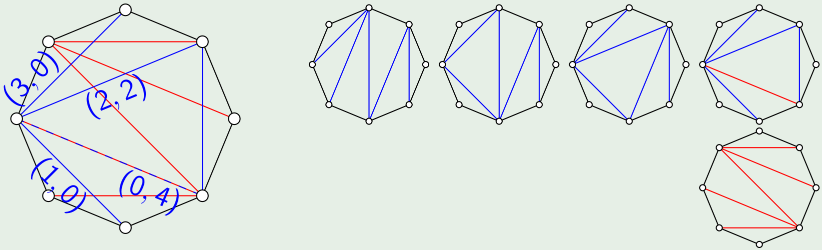

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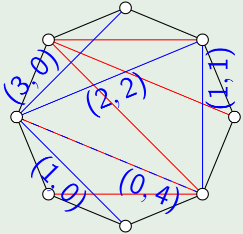

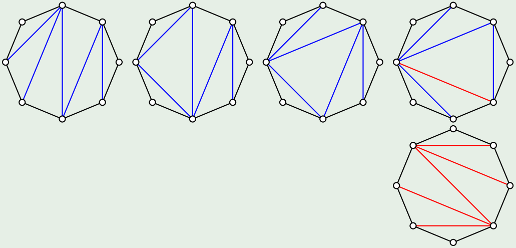

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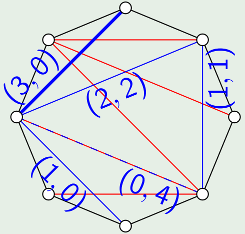

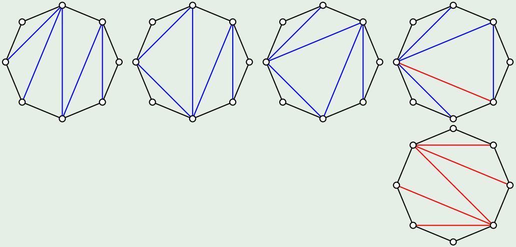

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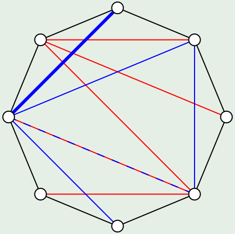

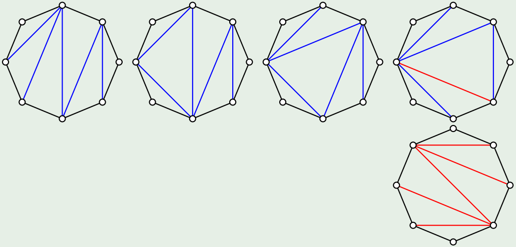

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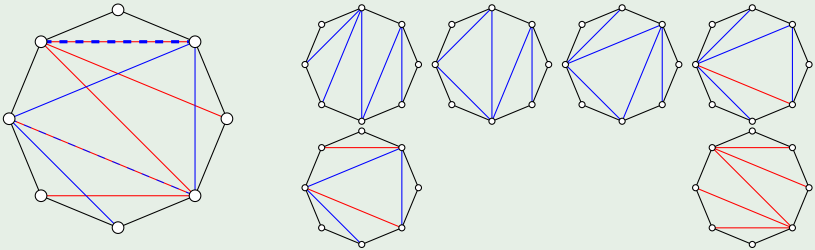

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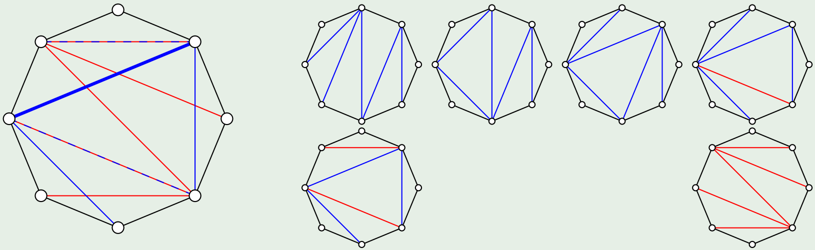

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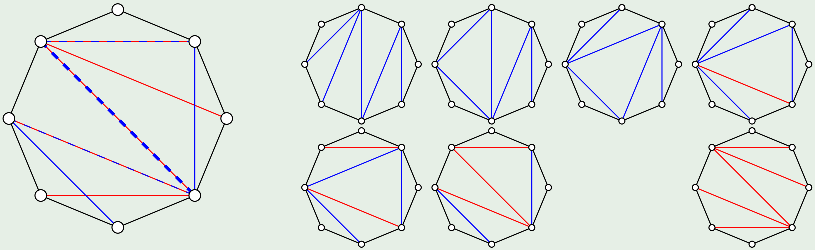

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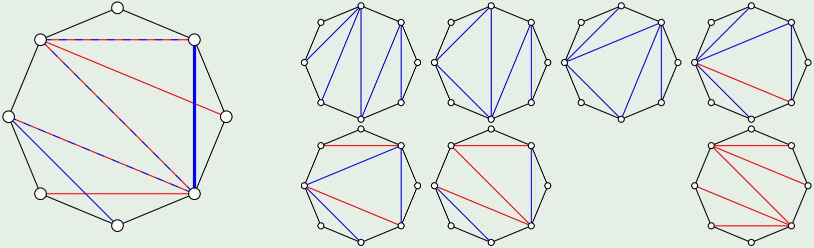

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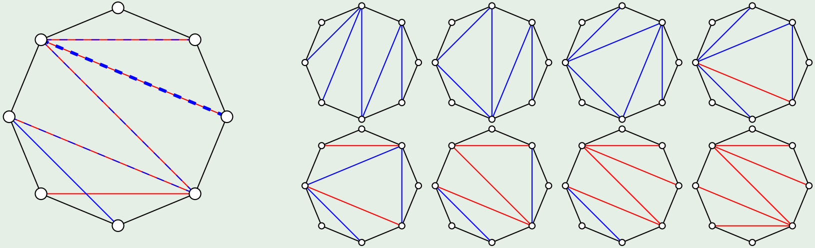

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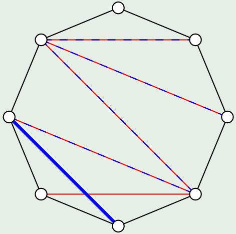

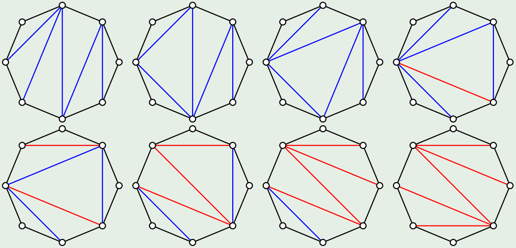

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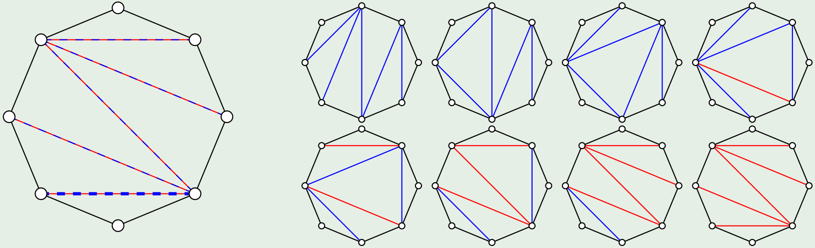

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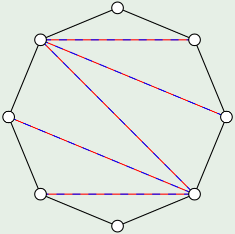

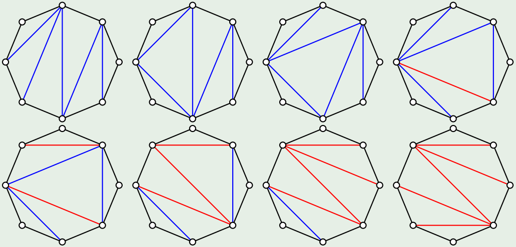

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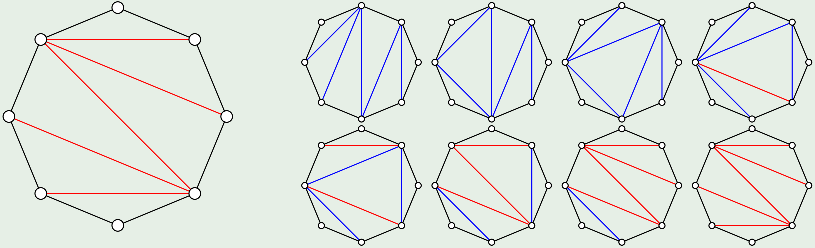
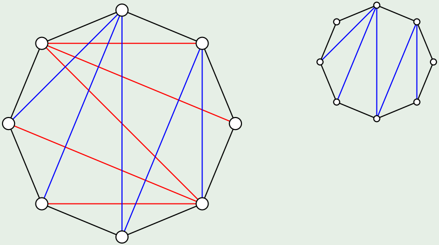


Optimal flip sequence



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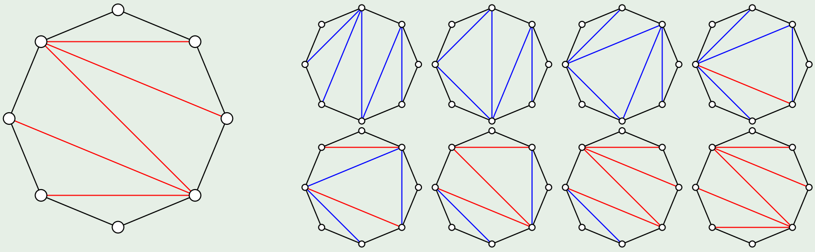

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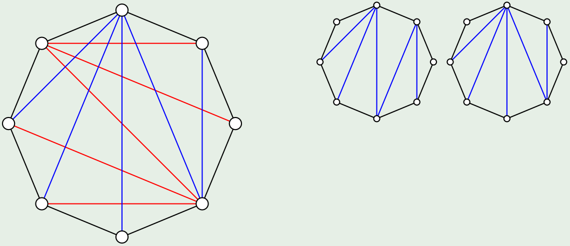

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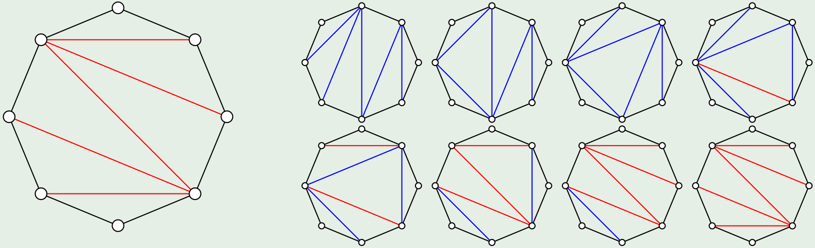

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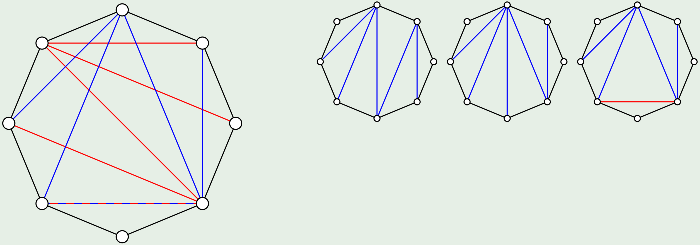

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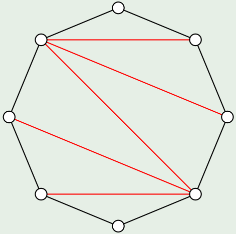

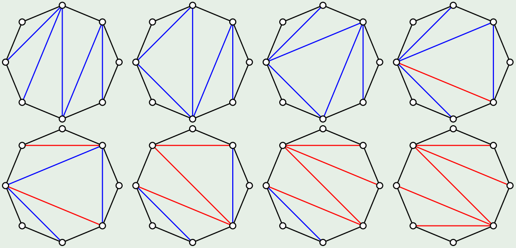

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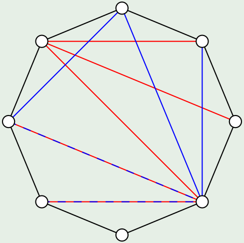

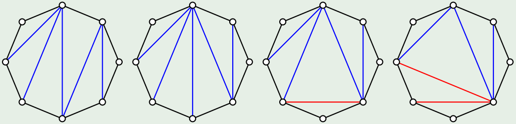

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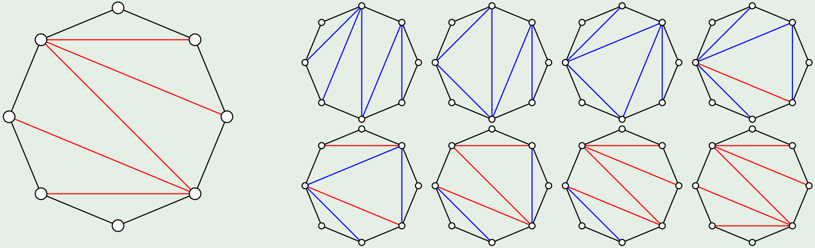

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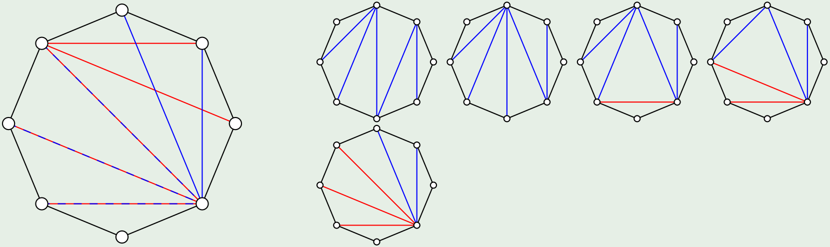

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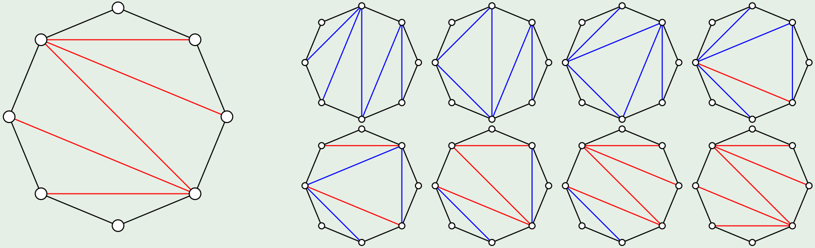

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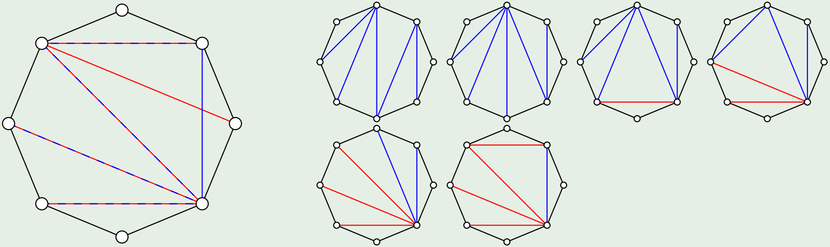

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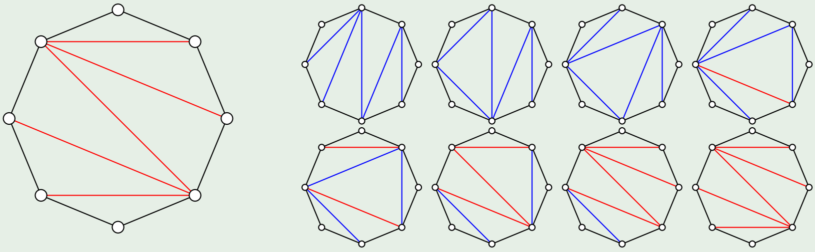

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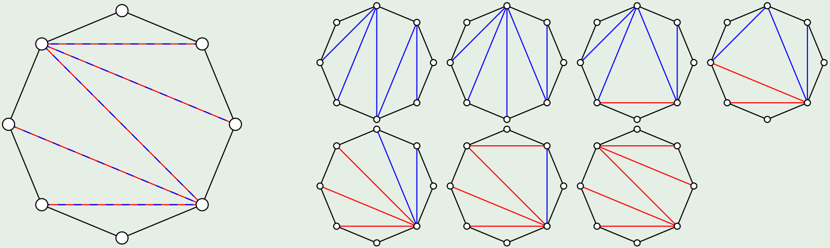

Variants of the Heuristic

Input: start triangulation s, target triangulation t
Output: short flip sequence from s to t

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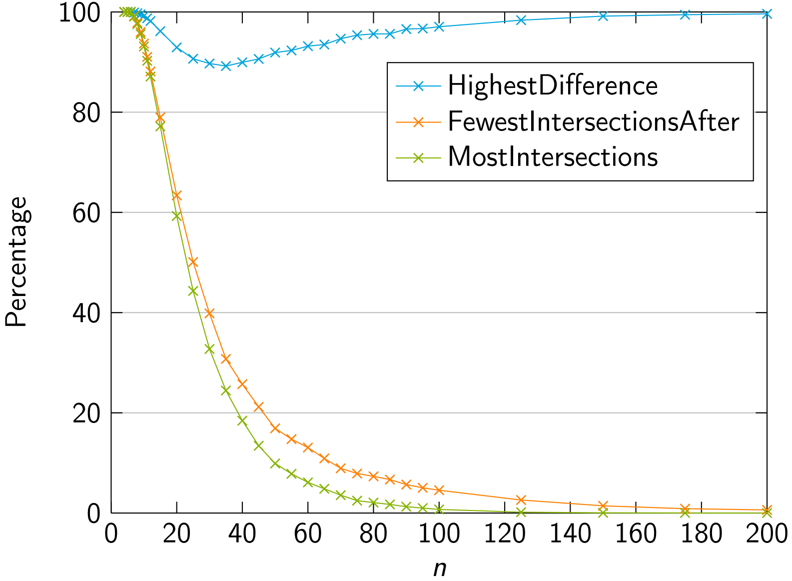
Runtime: $O(n^2)$

Comparing the Variants



Heuristics of Baril and Pallo

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  - Works on weight sequences representing binary trees
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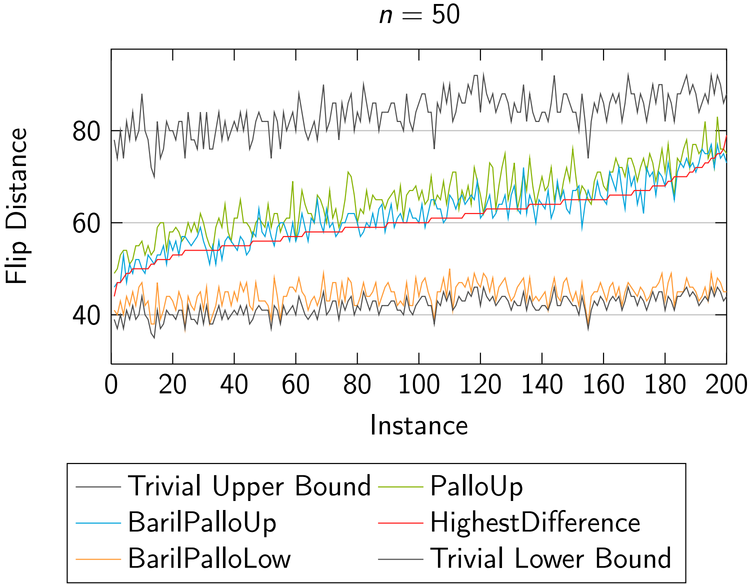
Comparing to other Heuristics



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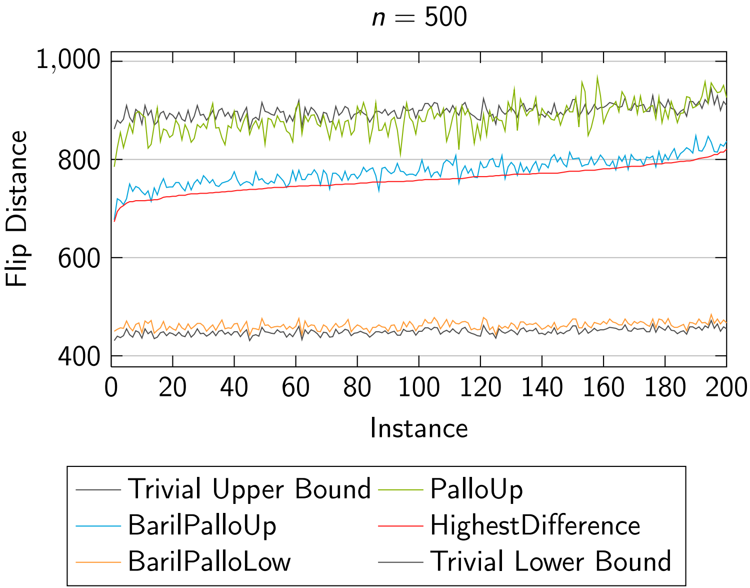

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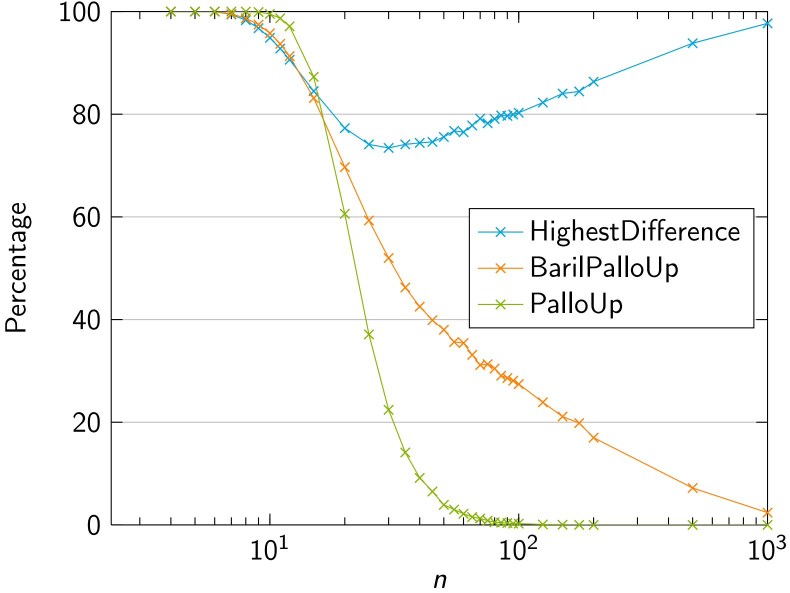

Conclusion

Summary

- Exact Algorithms: Improvements to BFS
- Heuristics: HighestDifference
  - Efficient compared to other heuristics
  - Easy to implement

Open Problems

- Polynomial-time algorithm
- NP-hardness proof
- Algorithms with approximation ratio < 2

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