

Sorting Signed Permutations by Reversals in Nearly-Linear Time

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Input: Signed permutation π on n elements

Output: Shortest sequence of reversals sorting π

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Transforming cabbage into turnip

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Brassica oleracea (cabbage)



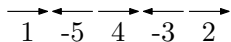
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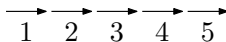
In the late 80s, Palmer et al. discovered that cabbage and turnip have almost identical gene sequence, **but different gene order**.



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Finding the shortest sequence of reversals

Early 90s: upper and lower bounds, approximation

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Some insights from Hannenhalli-Pevzner

The goal is to perform oriented reversals that create a new *adjacency*: $i, i + 1$ or $-(i + 1), -i$, e.g.:

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Sometimes such a reversal does not exist, but we can do an $\mathcal{O}(n)$ -time preprocessing and later focus only on finding the oriented reversals [Kaplan, Shamir, Tarjan 1999].

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Operations on a black-white graph

Input: Graph with nodes colored black or white

Output: The shortest sequence of toggle operations that transform it to an independent set of white nodes

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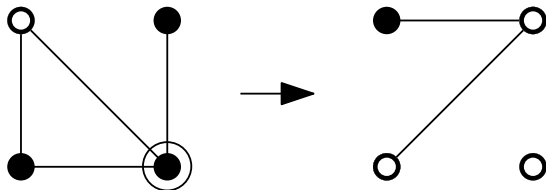
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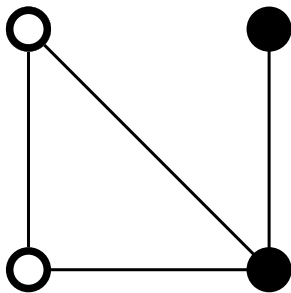
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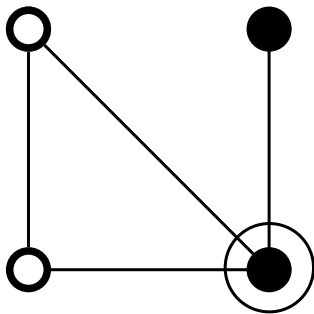
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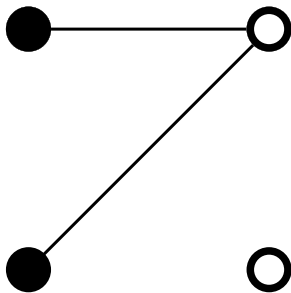
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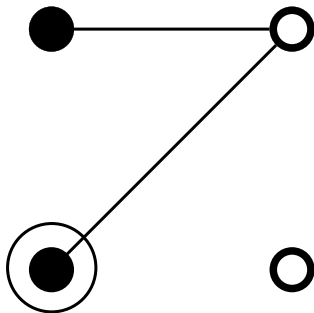
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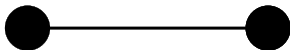
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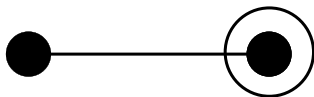
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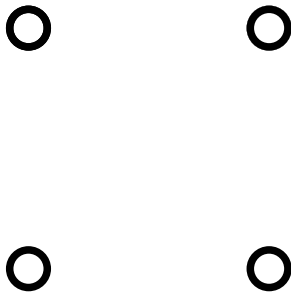
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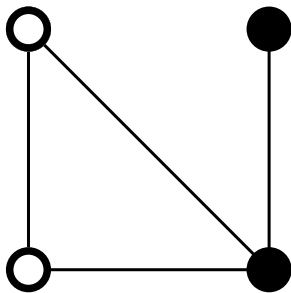
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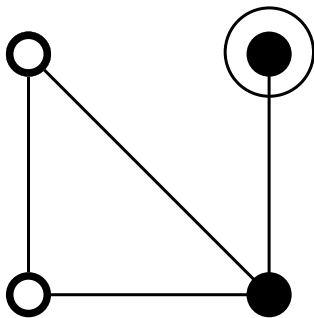
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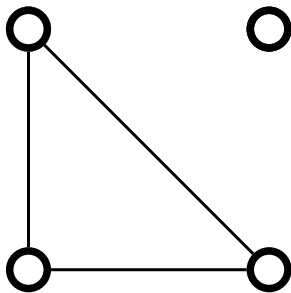
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Algorithm of Tannier, Bergeron and Sagot

```
1: function PROCESS(graph  $G$  with no non-singleton all-white connected components)
2:    $S := ()$ 
3:    $G' := G$ 
4:   while there is a black node  $v$  in  $G'$  do
5:     apply toggle( $v$ ) to  $G'$ 
6:      $S := S, v$ 
7:   while there is a non-singleton all-white connected component in  $G/S$  do
8:      $U :=$  set of nodes from non-singleton all-white connected components in  $G/S$ 
9:      $S_1, S_2 := S$  for the longest  $S_1$  s.t.  $G/S_1$  has a node of  $U$  in a not-all-white component
10:     $G_1 := G/S_1$ 
11:     $S_3 := ()$ 
12:    while there is a black node  $v$  from  $U$  in  $G_1$  do
13:      apply toggle( $v$ ) to  $G_1$ 
14:       $S_3 := S_3, v$ 
15:    if  $S_2[1]$  is white in  $G_1$  then
16:      remove the last element  $w$  from  $S_3$ 
17:      undo toggle( $w$ ) in  $G_1$ 
18:     $S := S_1, S_3, S_2$ 
19:  return  $S$ 
```

Interface of Tannier, Bergeron and Sagot

We need to efficiently maintain $\pi \in \mathcal{S}_n$ and a set $V \subseteq [n]$ under the following operations:

- 1 query for π_i or π_i^{-1} ,
- 2 apply to π a signed reversal of a given interval,
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$\mathcal{O}(\log n)$ time: splay tree + reverse flag

Operations 3 and 4 were previously implemented in $\mathcal{O}(\sqrt{n})$ time.

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Red-blue graph

For permutation $\pi = (0, -2, -5, 1, -4, 6, -3, 7)$ add the following nodes and blue edges:

0—2—5—1—4—6—3—7

0'—2'—5'—1'—4'—6'—3'—7'

Add red edges $\{i, (i+1)\}$ and $\{i', (i+1)'\}$ if i and $i+1$ have the same sign in π and $\{i, (i+1)'\}$ and $\{i', (i+1)\}$ otherwise.

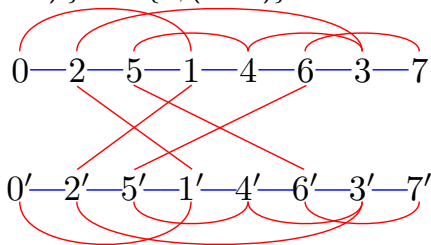
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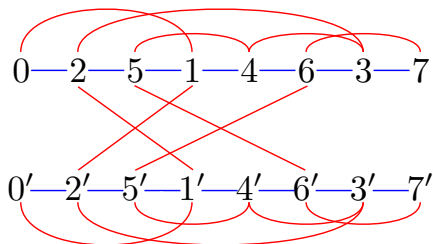
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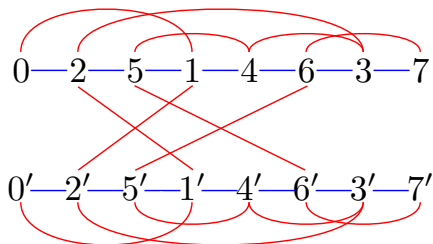
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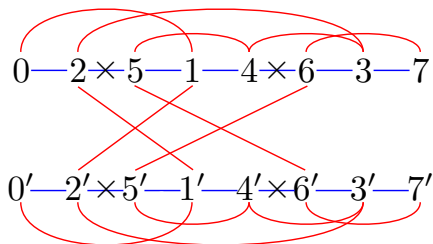
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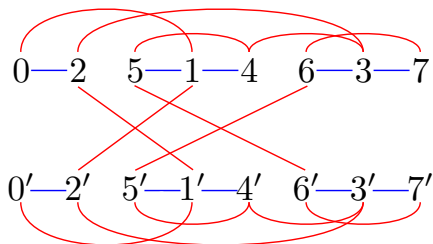
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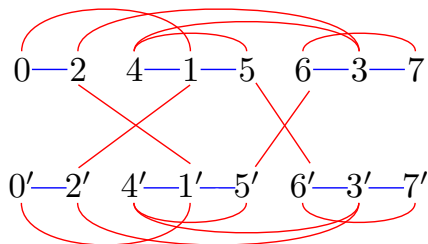
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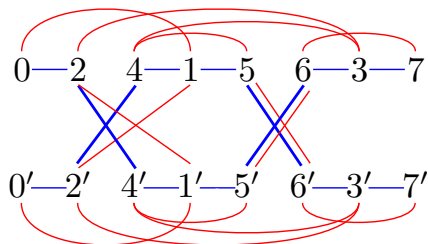
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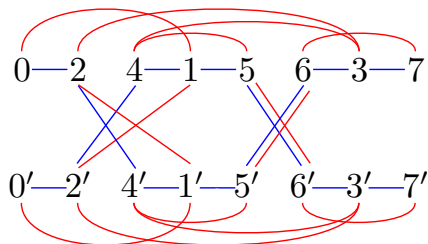
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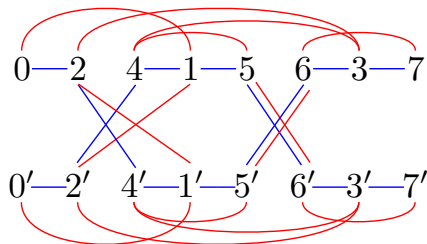
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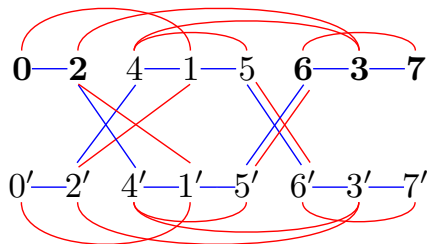
Property

Node i is in the blue component of 0 if and only if i has the same sign in π as in π_0 .

Corollary

The endpoints of a red edge $i - (i + 1)/(i + 1)'$ are in distinct blue components iff i and $i + 1$ have different signs in π .

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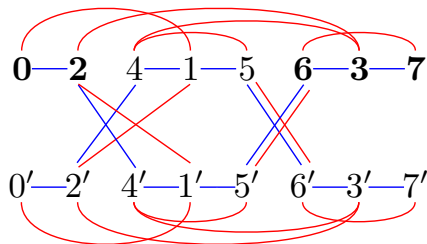
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Reformulation of the problem

New goal

Find a red edge connecting distinct blue components under insertions and deletions of blue edges and deletions of red edges.

Algorithm

Put weights on edges:

- 0 on blue edges
- i on i -th red edge

If the graph is connected:

⇒ its MST has exactly one red edge

⇒ weight of MST gives the index of the red edge.

Use the algorithm by Holm, Lichtenberg and Thorup for dynamic MST in amortized $\mathcal{O}(\log^4 n)$ time.

⇒ $\mathcal{O}(n \log^4 n)$ total time.

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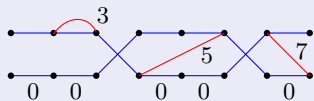
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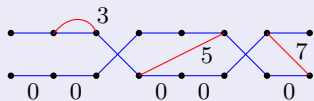
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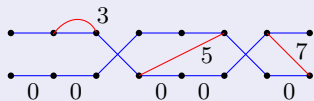
New goal

Find a red edge connecting distinct blue components under insertions and deletions of blue edges and deletions of red edges.

Algorithm

Put weights on edges:

- 0 on blue edges
- i on i -th red edge



If the graph is connected:

⇒ its MST has exactly one red edge

⇒ weight of MST gives the index of the red edge.

Use the algorithm by Holm, Lichtenberg and Thorup for dynamic MST in amortized $\mathcal{O}(\log^4 n)$ time.

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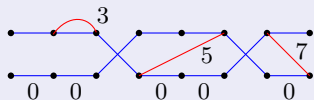
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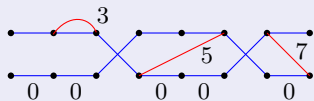
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Faster approach

Instead of MST: maintain a spanning forest of the graph on blue and red edges in a link-cut tree in amortized $\mathcal{O}(\log^2 n)$ time (using a data structure for fully-dynamic graph connectivity).

How to find a red edge connecting blue components of 0 and $0'$?

Recall:

- 1 Node i is in the blue component of 0 if and only if i has the same sign in π as in π_0 .
- 2 We maintain π under signed reversals on a splay tree.

Solution: binary search over the path connecting 0 and $0'$!

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In the previous approach:

- 1 $\mathcal{O}(n \log n)$ queries about the sign of i in π
- 2 $\mathcal{O}(n)$ updates

Idea: maintain shortcuts of length $\varepsilon \log \log n$ up the splay trees

- 1 $\mathcal{O}(\log n / \log \log n)$ time per query
- 2 $\mathcal{O}(\log^{1+\varepsilon} n)$ time per update

$\implies \mathcal{O}(n \log^2 n / \log \log n)$ total time for all operations on splay trees.

For the graph: use dynamic connectivity structure by Wulff-Nilsen:
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Open questions

- 1 Can we improve the time complexity even further?
 - Our solution runs in $\mathcal{O}(n \log^2 n / \log \log n)$ but counting the number of reversals takes $\mathcal{O}(n)$ time
 - Swenson [arXiv '24]: $\mathcal{O}(n \log n)$
- 2 Does randomization help?
 - Can we utilize the $\mathcal{O}(n \log n \log^2 \log n)$ time algorithm for dynamic connectivity by Huang, Huang, Kopelowitz, Pettie, and Thorup?

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