Sorting by Reversals

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Intro to CS: Bioinformatics

Genome Rearrangement

Turnips and Cabbages

- 99% identical
- Nearly identical gene sequences
- Genes in different order!

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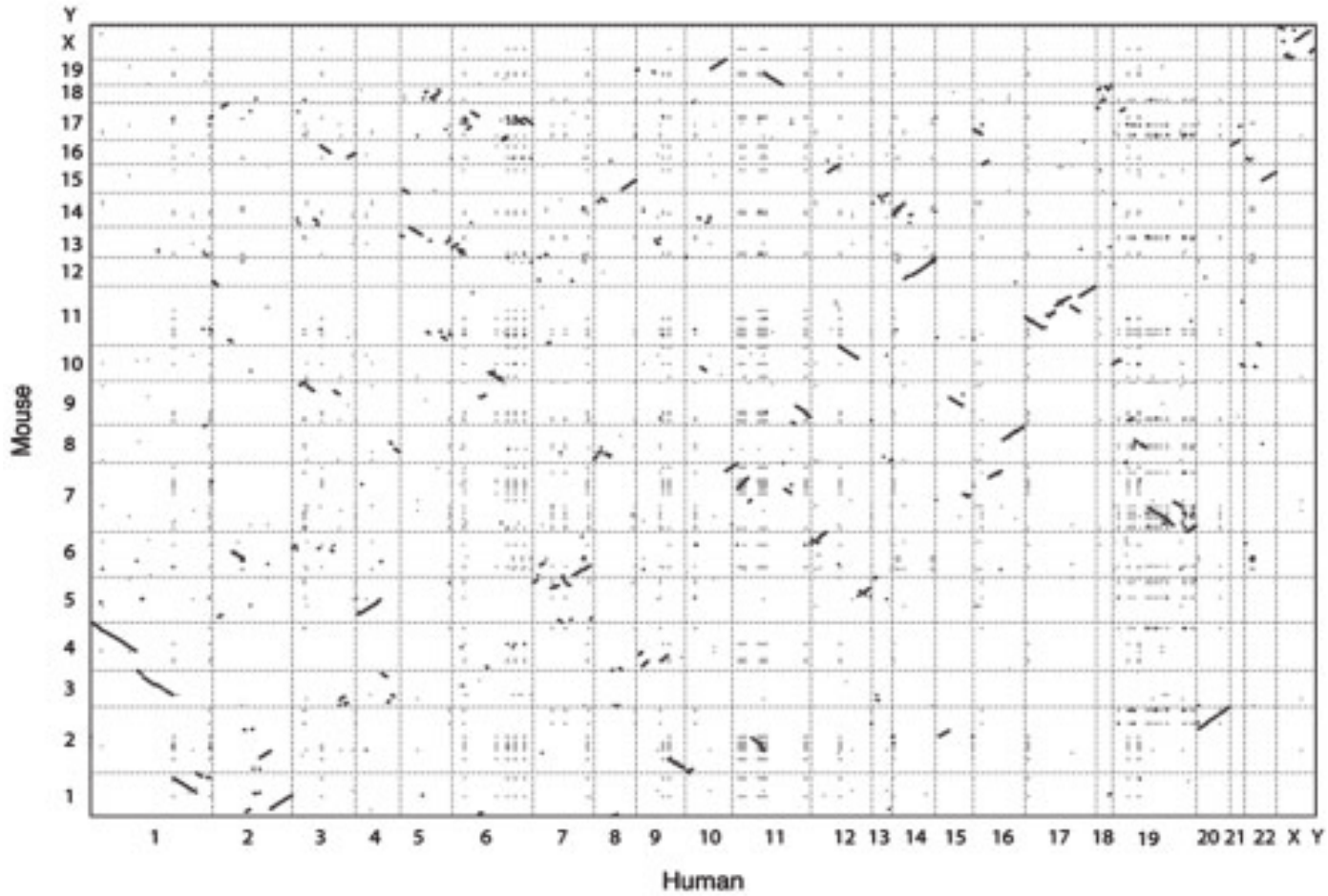
How does this happen

DNA forms loops and reversed a segment or two strands cross and swap segments.

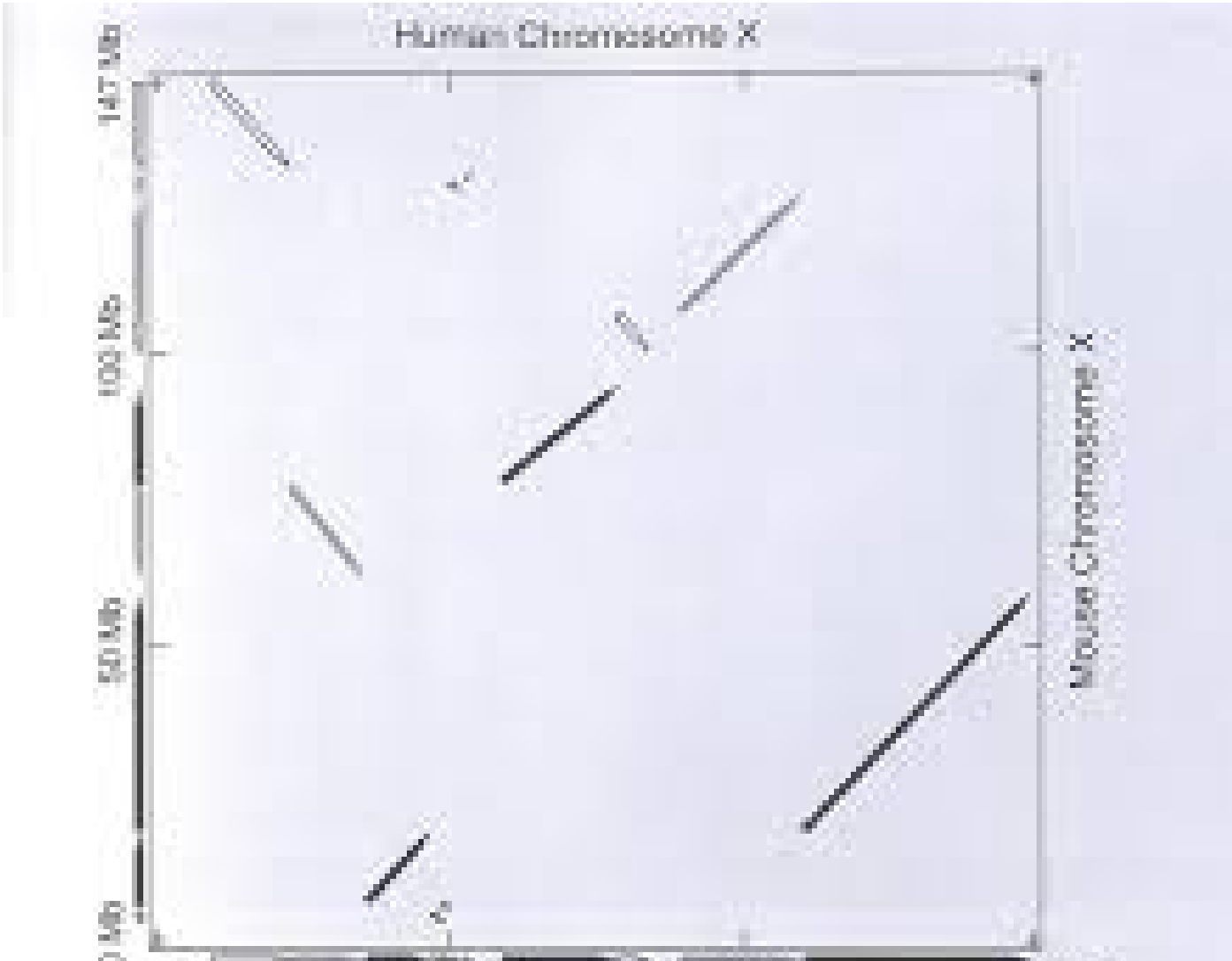
Genome Rearrangement

Human and Mouse Genome

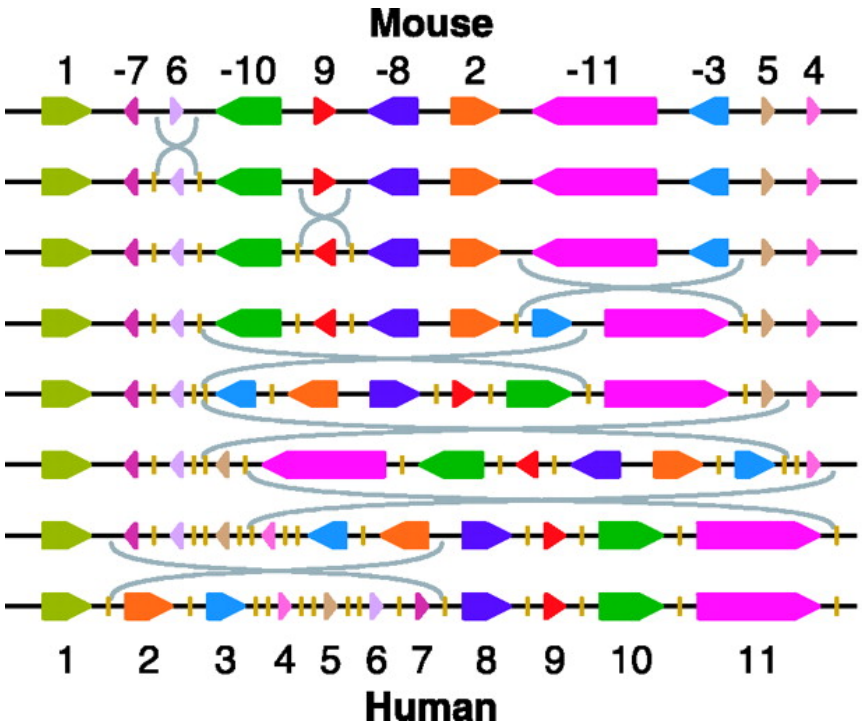


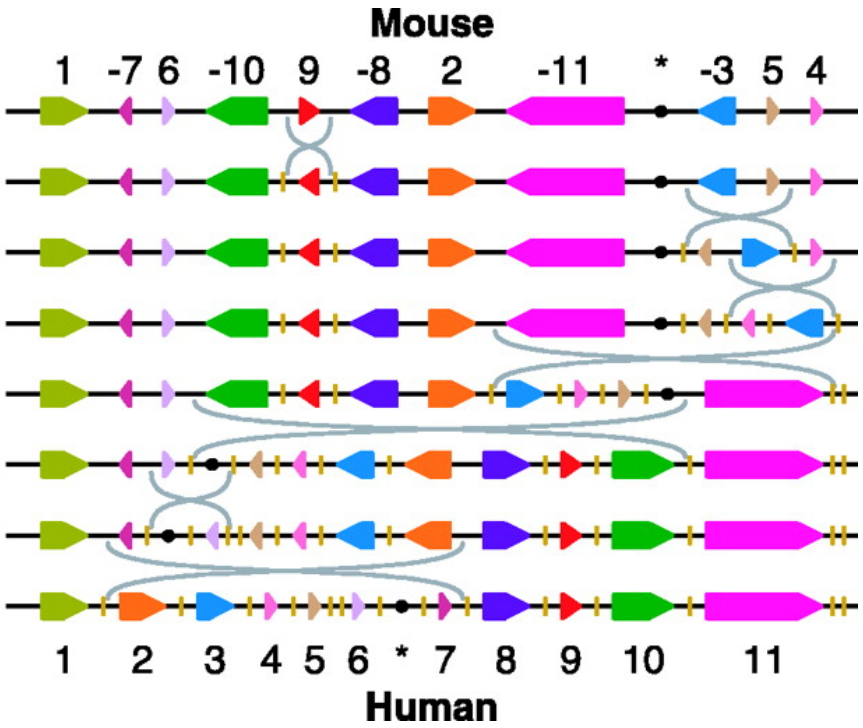
Genome Rearrangement

Human and Mouse X Chromosomes



Reversals


Mouse
1 -7 6 -10 9 -8 2 -11 -3 5 4
1 2 3 4 5 6 7 8 9 10 11
Human


Mouse
1 -7 6 -10 9 -8 2 -11 * -3 5 4
1 2 3 4 5 6 * 7 8 9 10 11
Human

Reversals

The more reversals, the further back their common ancestor lived.

Parsimony assumption

Want to count the minimum number of reversals needs to convert one sequence to another.

Related Problem: Sorting by Reversals

Sort a sequence of numbers by reversing segments

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Sort a sequence of numbers by reversing segments

An example

$$\underline{5\ 2\ 1}\ 3\ 4$$
$$1\ 2\ 5\ \underline{3\ 4}$$
$$1\ 2\ \underline{5\ 4\ 3}$$
$$1\ 2\ 3\ 4\ 5$$

Related Problem: Sorting by Reversals

Sort a sequence of numbers by reversing segments

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What's the minimum number of reversals needed?

Challenge

Find the minimum number of reversals to sort

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

Notation

Permutation

$\pi = \pi_1 \pi_2 \pi_3 \ldots \pi_{n-1} \pi_n$

$$\begin{aligned} \pi &= 1\ 4\ 6\ 5\ 7\ 8\ 3\ 2 \\ \pi_1\ \pi_2\ \pi_3\ \pi_4\ \pi_5\ \pi_6\ \pi_7\ \pi_8 &= 1\ 4\ 6\ 5\ 7\ 8\ 3\ 2 \end{aligned}$$

Breakpoints

Extending permutations

For a permutation of 1..n, add a 0 at the beginning and n+1 at the end.

1 9 3 4 7 8 2 5 6 becomes 0 1 9 3 4 7 8 2 5 6 10

This changes the permutation to $\pi_0\ \pi_1\ \pi_2\ \pi_3\ \ldots\ \pi_{n-1}\ \pi_n\ \pi_{n+1}$

Breakpoints

Positions in the extended permutation where numbers are not consecutive:

0 1 | 9 | 3 4 | 7 8 | 2 | 5 6 | 10

This sequence has 6 breaks points.

How many breakpoints can a reversal remove?

Lower Bounds

$b(\pi)$ Number of breakpoints in the (extended) permutation π

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Each reversal removes at most 2 breakpoints so

$$d(\pi) \geq b(\pi)/2$$

An Example

$\pi = 231465$

0 2 3 1 4 6 5 7	5 breakpoints
0 1 3 2 4 6 5 7	4 breakpoints
0 1 2 3 4 6 5 7	2 breakpoints
0 1 2 3 4 5 6 7	0 breakpoints

Can we always remove a break point?

Strips

Strip A sequence between consecutive breakpoints

Increasing strip a strip where the numbers are in increasing order

Decreasing strip a strip where the numbers are in decreasing order

An example: $\pi = 1\ 9\ 8\ 7\ 3\ 4\ 2\ 5\ 6$

0 1 9 8 7 3 4 2 5 6 10 has 6 strips

Increasing strips: 0 1, 3 4, 2, 5 6, 10

Decreasing strips: 9 8 7, 10

Strips

Fact 1

If a sequence has a decreasing strip then there is a reversal that removes a breakpoint

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If a sequence has a decreasing strip then there is a reversal that removes a breakpoint

1. Find the smallest number k in any decreasing strip
2. Find $k-1$ in the sequence
3. Perform the reversal that make $k-1$ and k adjacent

0 1 4 6 5 7 8 3 2 9
0 1 2 3 8 7 5 6 4 9

0 1 6 5 4 2 3 7 8 9
0 1 6 5 4 3 2 7 8 9

Strips

Fact 2

If there is no decreasing strips then reversing an increasing strip will not change the number of breakpoints

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If there is no decreasing strips then reversing an increasing strip will not change the number of breakpoints

0 1 2 5 6 7 3 4 8 9
0 1 2 7 6 5 3 4 8 9

Notice that to remove a breakpoint either the strip before or after must have been increasing.

A Greedy Algorithm

1. While $b(\pi) > 0$
2. If π has a decreasing string
3. Among all possible reversals choose one that removes the most breakpoints
4. Else
5. Perform a reversal of an increasing strip

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Note, if you're trying to remove a breakpoint, use the idea a couple of slides ago to quickly find one. Find the smallest element k of a decreasing strip and perform the reversal that makes $k-1$ and k adjacent.

Note that at most two reversals are needed in the algorithm to remove a breakpoint.

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Note that at most two reversals are needed in the algorithm to remove a breakpoint. So $d(\pi) \leq 2b(\pi)$

Challenge

Try this algorithm on

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

1. How many breakpoints are in each sequence?
2. How many reversals does the greedy algorithm take to sort the sequence?
3. What is the minimum number of reversals needed?

Approximation Algorithms

How many reversals are necessary?

$$b(\pi)/2 \leq d(\pi) \leq 2b(\pi)$$

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This algorithm has an **approximation factor** of 4.

Can We Do Better?

In the previous algorithm we either have a decreasing strip and can remove a breakpoint. If this is all we every saw, then we would have $d(\pi) \leq b(\pi)$.

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But, we don't always have a decreasing strip. So it might take two reversals to remove a breakpoint

Think about what happens to create a sequence with no decreasing strips.

Can We Do Better? YES

Claim

If every reversal that reduce the number of breakpoints results in a permutation without decreasing strips then there is a reversal that removes two breakpoints!

If true, this would show $b(\pi)/2 \leq d(\pi) \leq b(\pi)$ and give an algorithm with approximation factor 2.
If you're interested in how to show this is true, I'm happy to show you.

Multiple Sequences

Goal

Simulate multiple DNA strands and how many changes are required to put each strip on the correct chromasome and in the correct order.

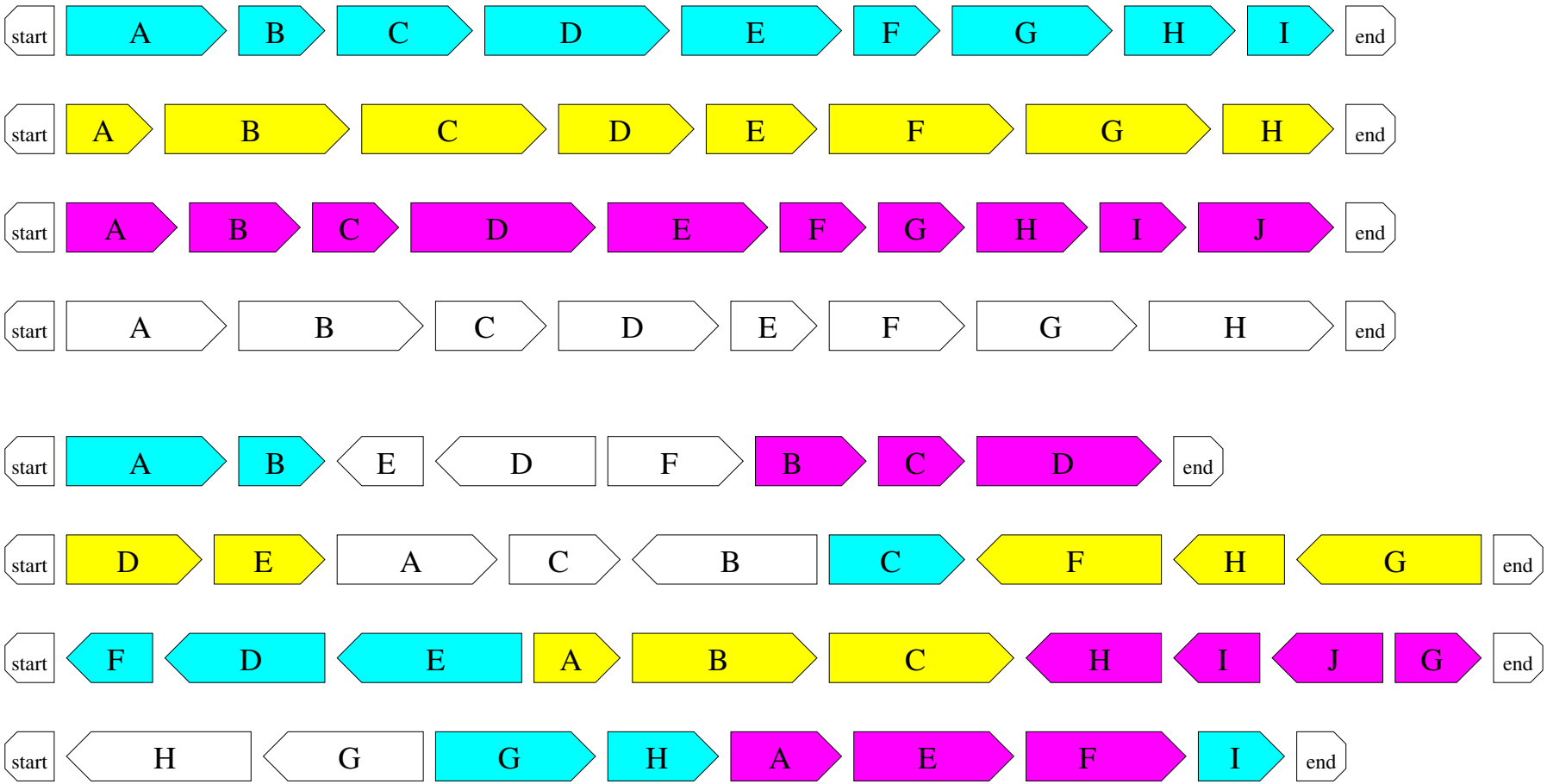
Moves

1. Reversal on a single strand
2. Cut two strands and swap the ends
3. Cut two strands combining the front ends together and and back ends together

Breakpoints

How should we define the number of breakpoints

In particular, what do we do at the ends?



Bounds

What the most breakpoints that can be removed by a single reversal or other move?

What's the most moves need to remove a breakpoint?

Can we bound the distance to the sorted order based on the number of breakpoints?

Challenge

How many breakpoints? Bounds? What's the shortest move sequence?