The inversion process in bacteria: distance metrics with group-theoretic models

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Phylomania

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Distance

Why think about distance?

- Science wants to quantify difference, to compare, to measure.
- We want to organise information and knowledge about life, relating organisms by phylogeny.

Distance provides the input to several important phylogeny methods.
(UPGMA, Neighbour-joining)

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- Large scale rearrangements are studied by identifying preserved regions ("locally colinear blocks") in a family of taxa.
- Inversions take a segment — a sequence of regions — and reverse their order.

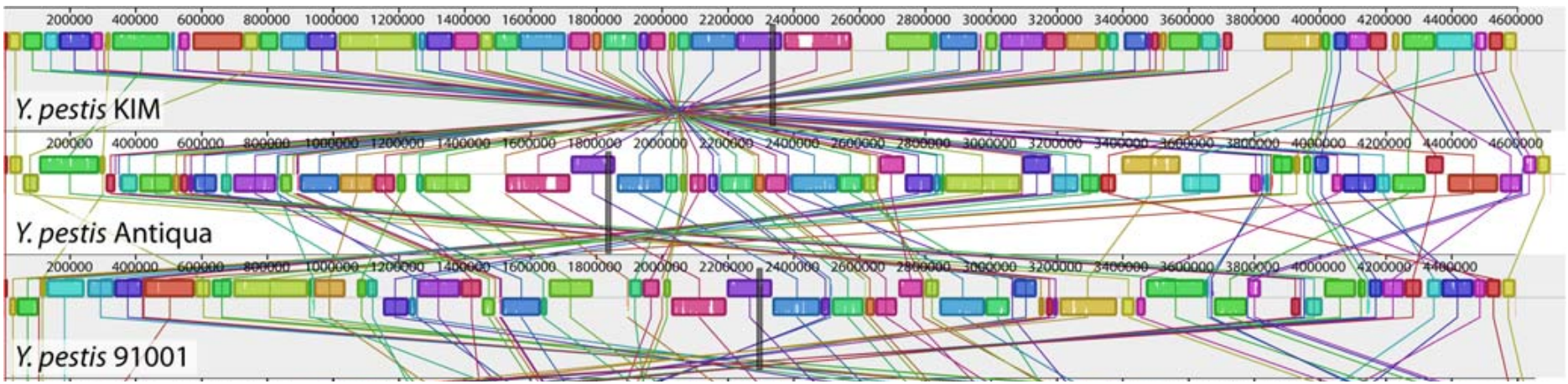

Figure from Darling et al, 2008.

Large-scale rearrangements $\longrightarrow$ genomes as permutations

- If we identify preserved regions we can treat each as a unit and regard all taxa as rearrangements of regions.
- Numbering regions $1, \ldots, n$ makes each genome a permutation.
  - Incorporating orientation of regions gives a *signed* permutation.
- This assumes
  - all regions are the same size, and
  - they are evenly distributed around the genome.

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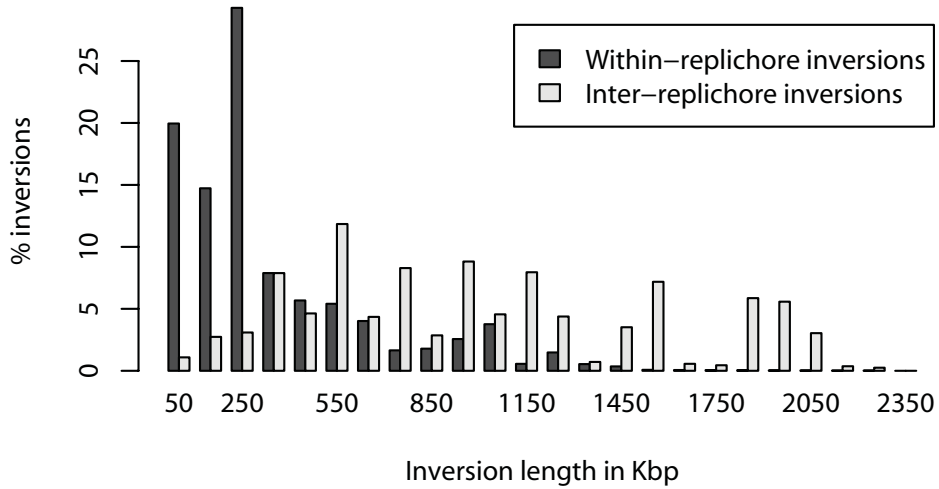
  - that all are equally probable.
- This means that circular arrangements can be dealt with as linear arrangements
  - because inversions across any given point can be performed on the complementary segment.
- There are fast algorithms for solving the inversion distance problem in this case, using the "breakpoint graph" (Bafna and Pevzner 1993).

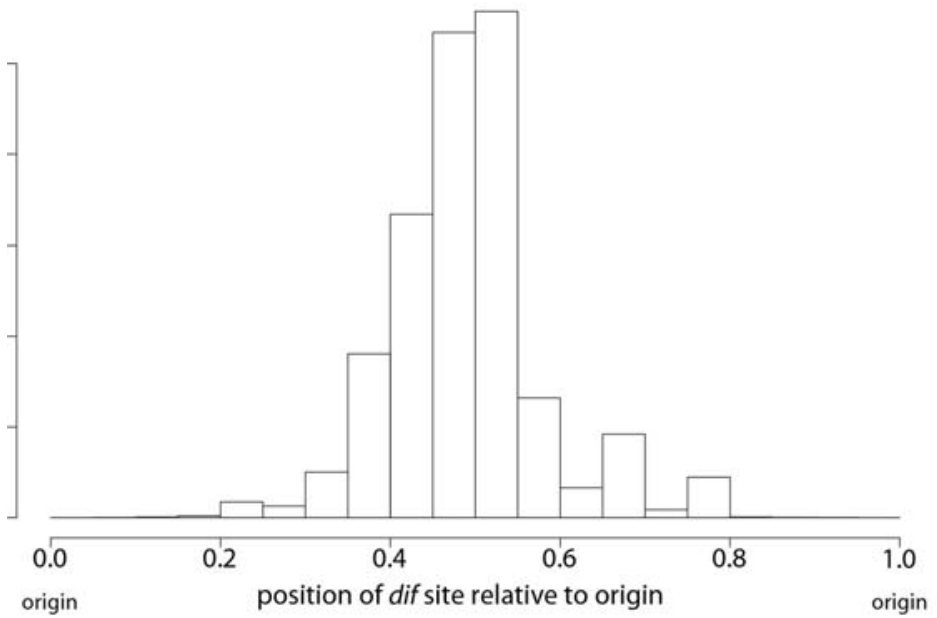
However

Not all inversions are equally likely.

- Length: shorter ones are more likely.



- Location: ones that fix terminus more likely.



[Figures from Darling *et al*, 2008.]

Group-theoretic approach

- Incorporating these constraints makes cutting-linearizing invalid.

  $\Longrightarrow$ We must model permutations on the circle.
- There are two features of permutations on a circle:
  - inversions can occur across any cut, e.g $(n, 1)$.
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- We also need to consider equivalence under the action of the dihedral group — not a normal subgroup so simply a (co)set of vertices on the Cayley graph.

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all colours and sizes to suit every household

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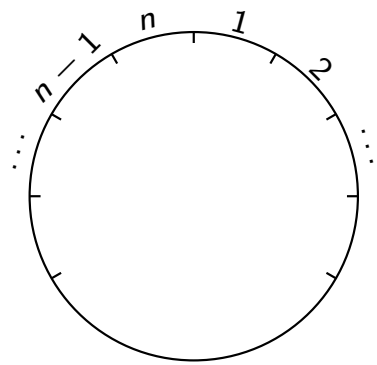
- The approach allows generalizations such as "Double-Cut-and-Join" (Bergeron-Mixtacke-Stoye, 2006).
  - [See talk by Sangeeta Bhatia after lunch]

Example

Two region inversion model

- The 2-region inversions that generate the group are the simple transpositions of adjacent regions.

- . . . noting that they now include $s_n = (n\ 1)$, because we are on the circle.
- We need to use the affine symmetric group.



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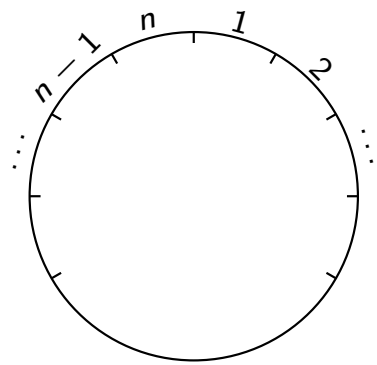


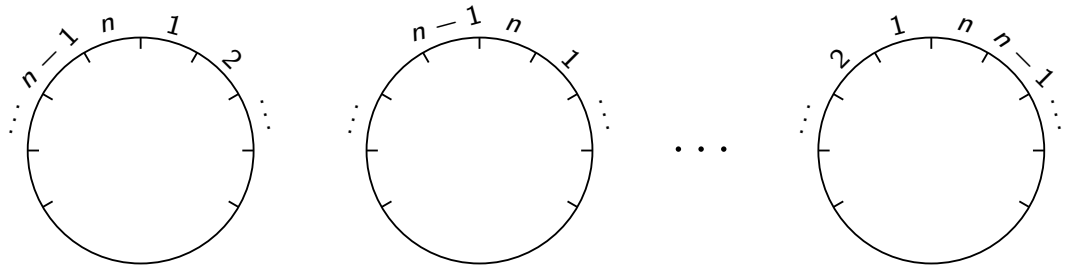
Theorem

If σ *is a minimal length affine permutation representing a circular permutation,* **then** σ *takes the shortest distance between each* i *and* $\sigma(i)$ mod n.

Group-theoretic models of the inversion process in bacterial genomes, Egri-Nagy, Gebhardt, Tanaka & Francis, *J Mathematical Biology*, Online June 2013.

The resulting algorithm

1. For each frame of reference,



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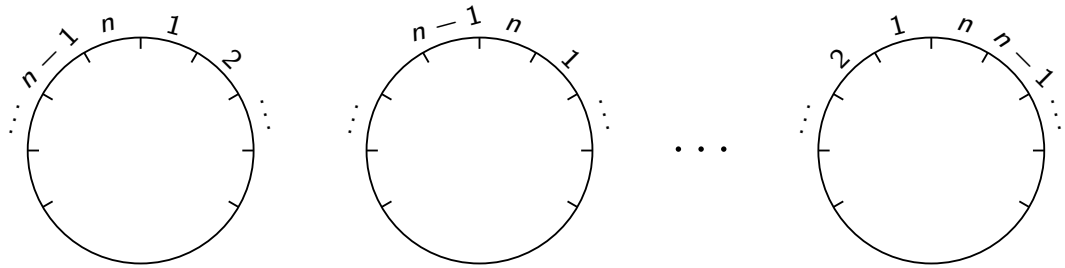

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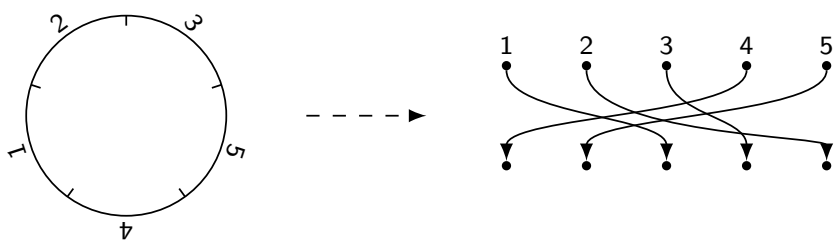

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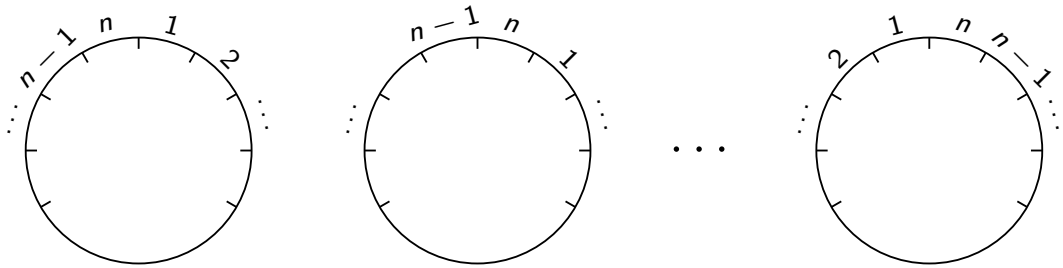

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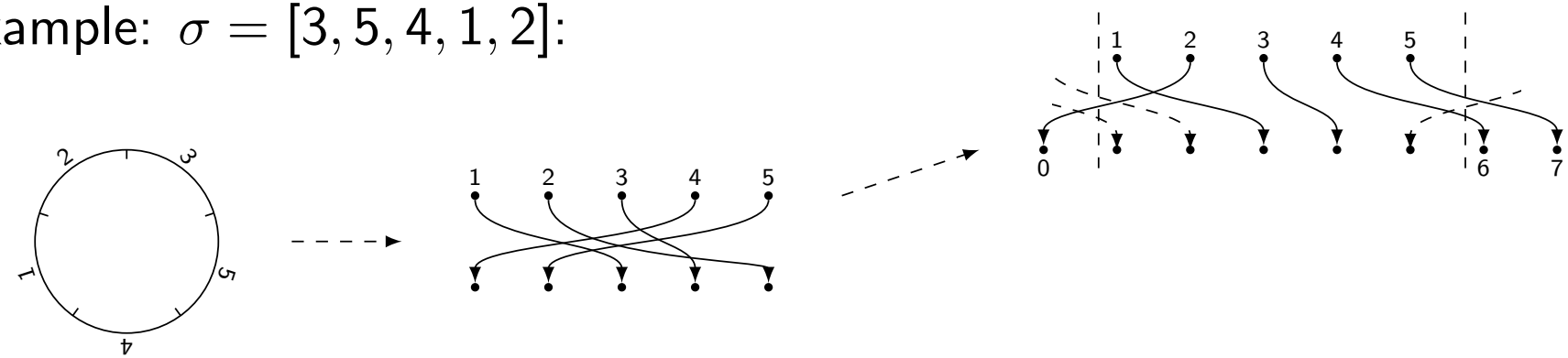

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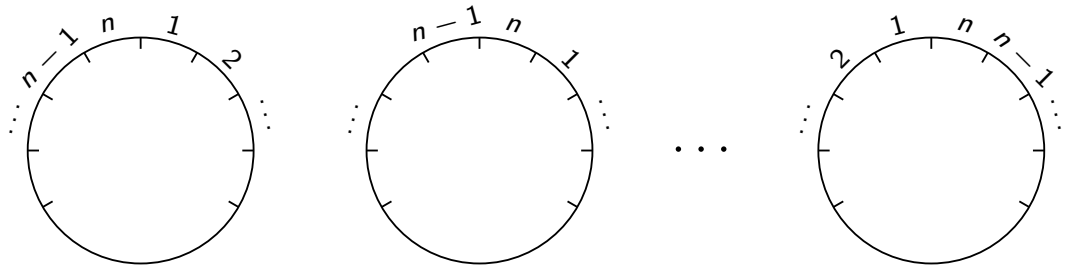

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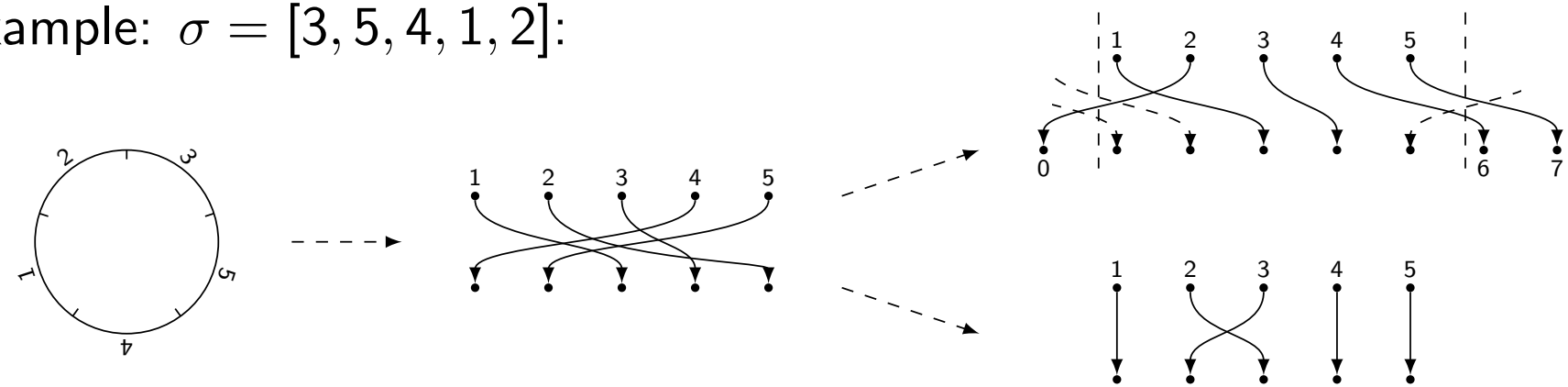

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Thank you for listening, thanks to the organisers for organising, and thanks to the ARC for funding.