



Genome Rearrangements

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AGENDA

1. Summary
2. Genome comparison
3. Rearrangement events
4. Example: mouse vs. human (X-chromosome)
5. Rearrangement distance
6. Known results
7. Current research lines

SUMMARY

- One of the big challenges of contemporary Biology is to measure evolution
- Besides point mutations, evolution is known to occur by means of movements of large chunks of DNA (genome rearrangements)
- The advent of entire genomes brings a whole new facet to this issue
- As a first estimate of the amount of evolution between two species, one can use the formula

number of events

unit of time

- Our research focus on efficient ways of computing the number of rearrangement events between two or more genomes

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GENOME COMPARISON

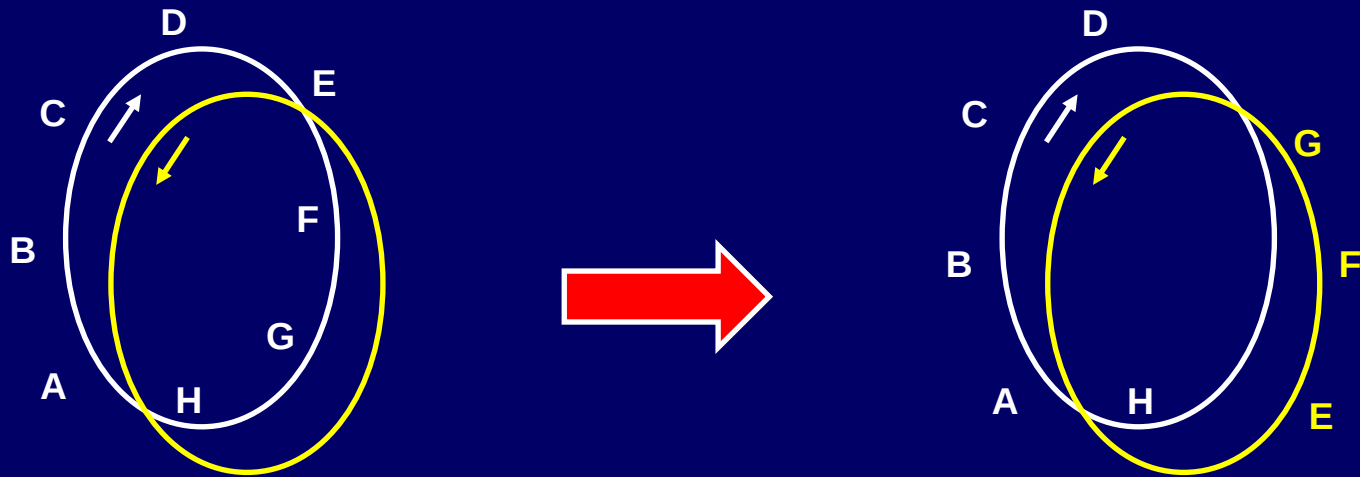
Point mutations

...TATC**G**ATAGAC**C**ACT**G**...

...TATC- -TAGAC**G**ACT**A**...

GENOME COMPARISON

Genome rearrangements



Movement of large segments within the genome.

Above, segment E – F – G flips over

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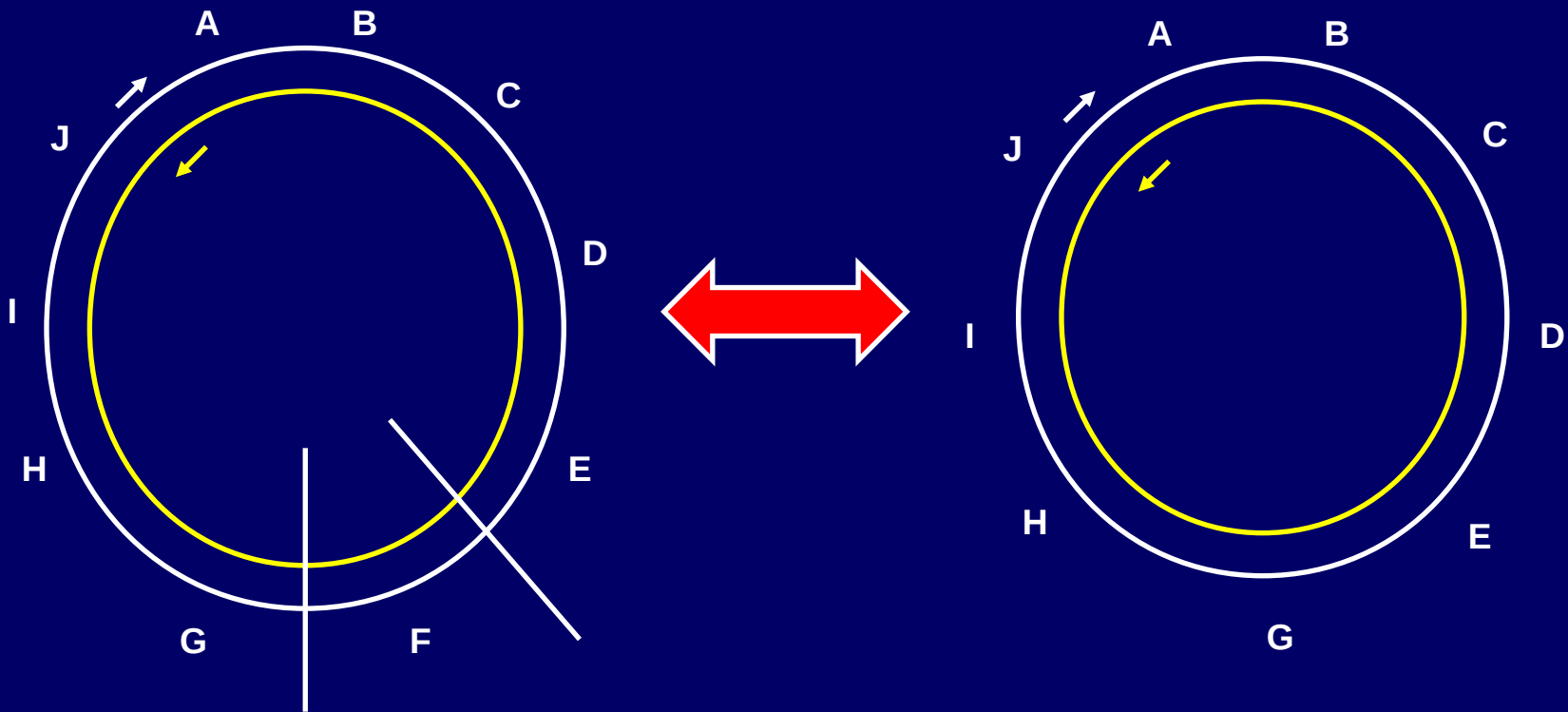
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REARRANGEMENT EVENTS

- **Insertion / Deletion**
- **Reversal**
- **Transposition**
- **Fission / Fusion**
- **Block Interchange**
- **Others: duplication, genome doubling**

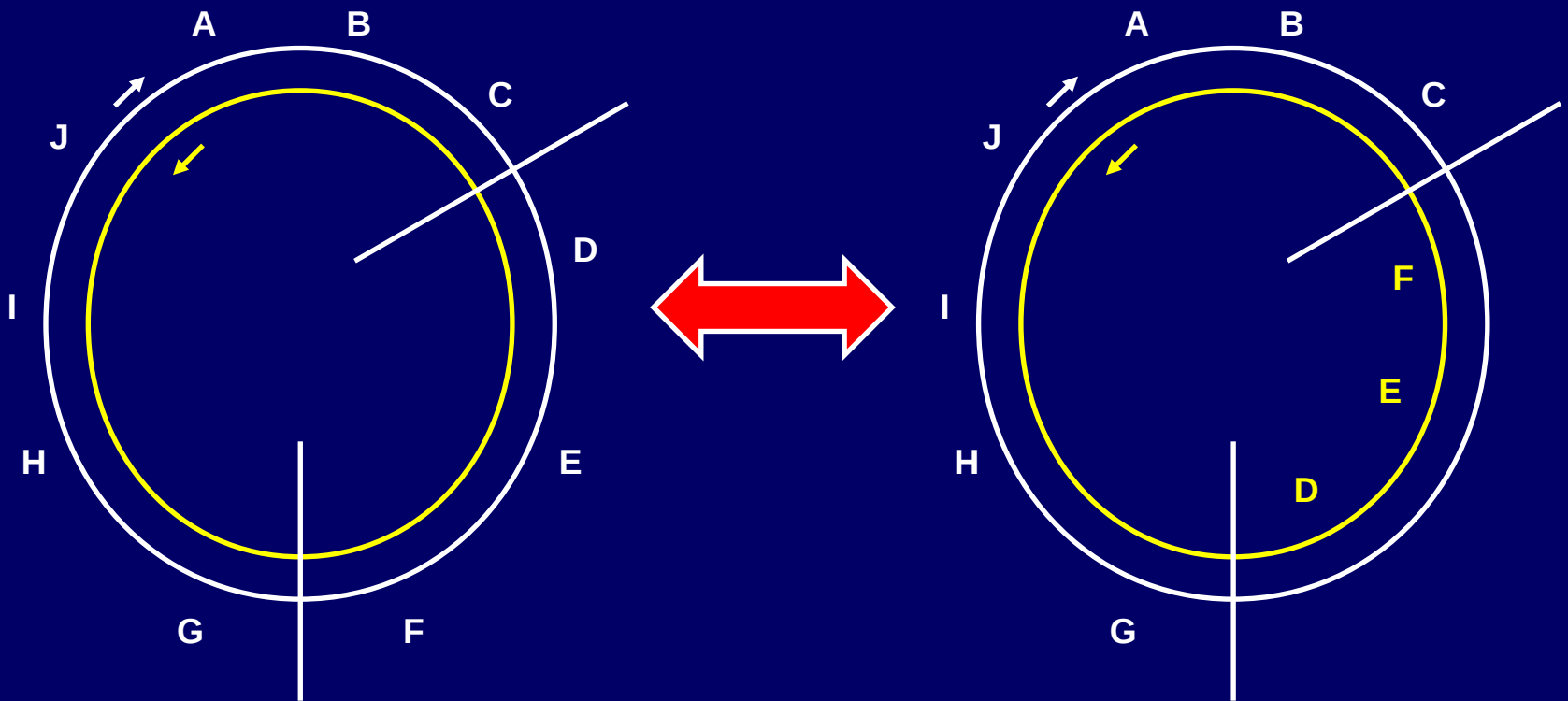
INSERTION / DELETION

Gene gain / loss between genomes



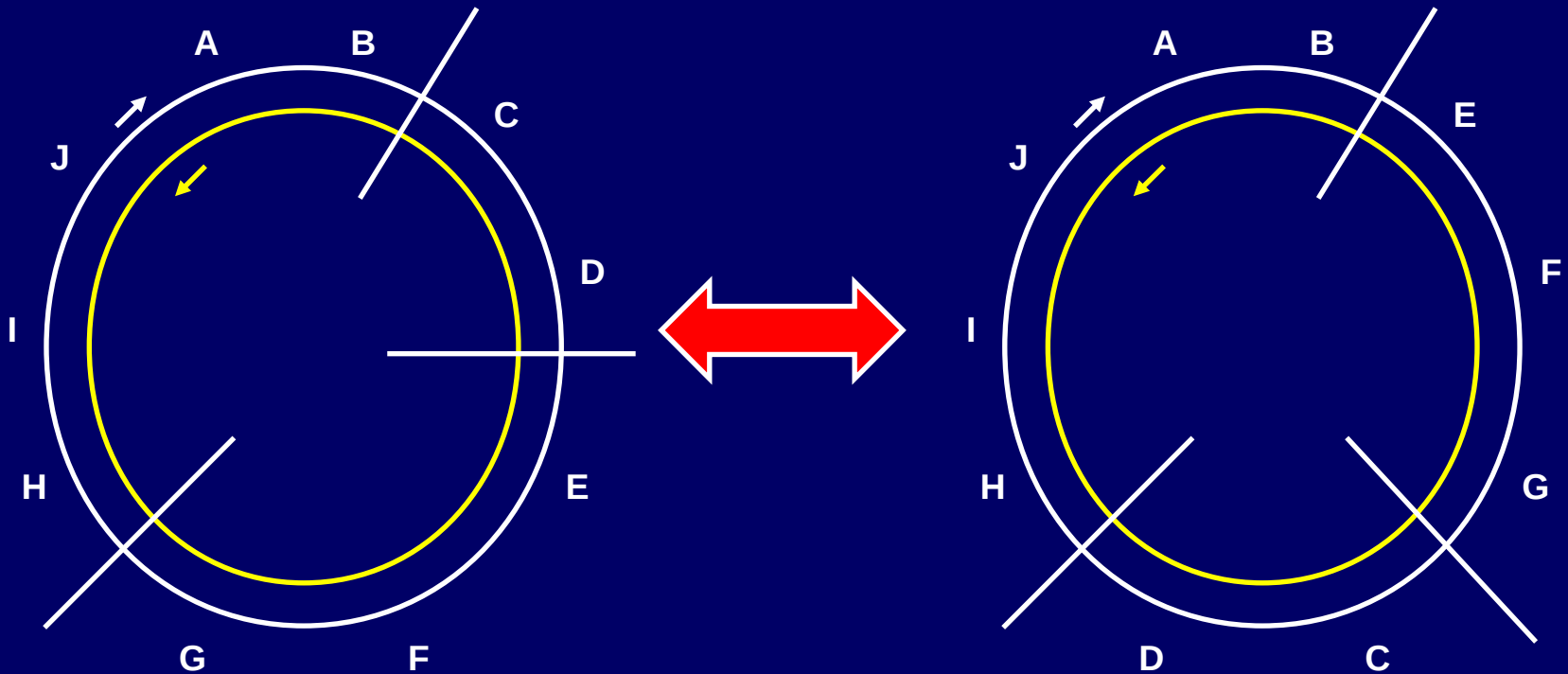
REVERSAL

A segment is reversed between genomes



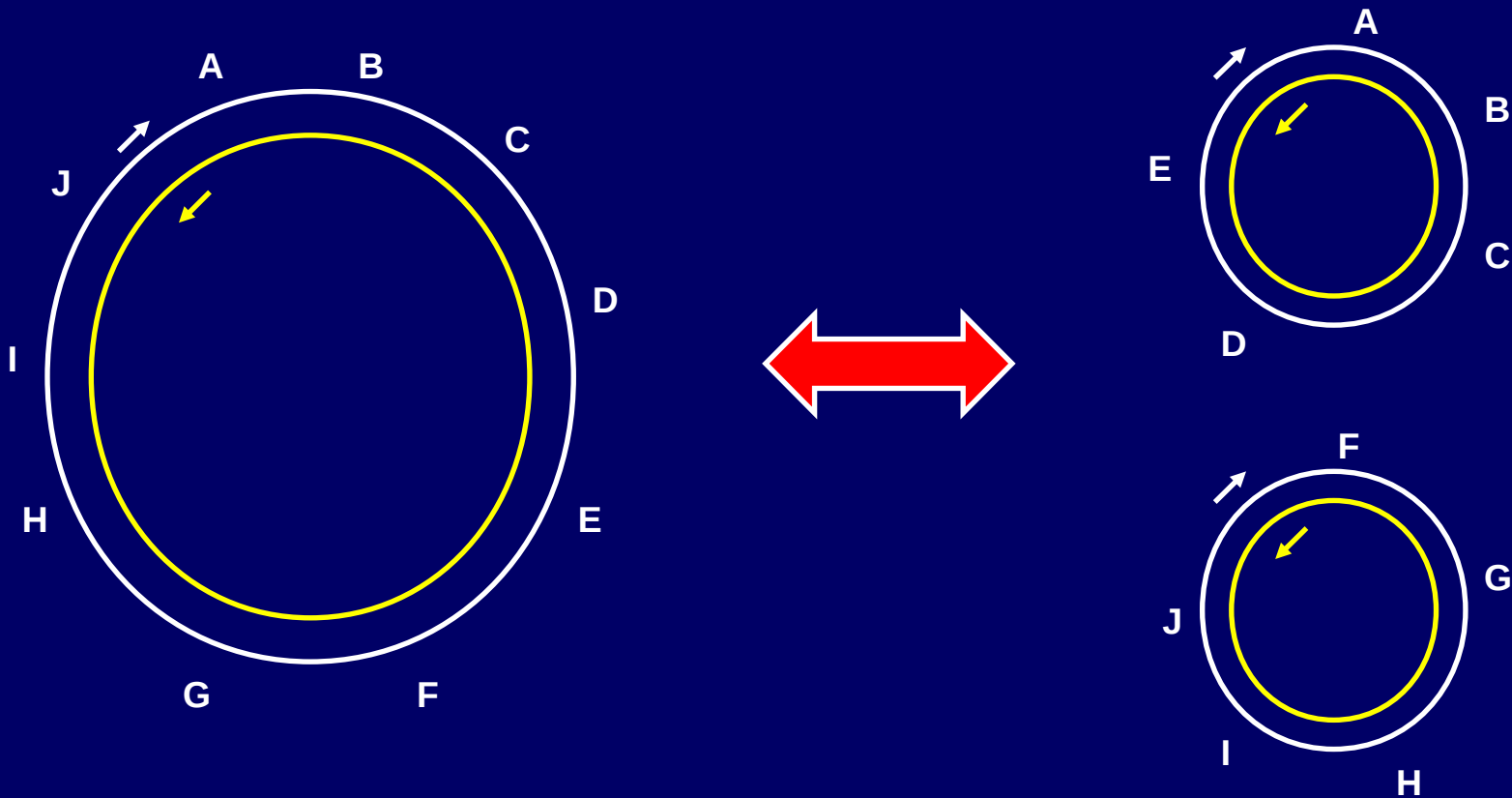
TRANSPOSITION

A segment moves to a new position
(or: exchange of two adjacent segments)



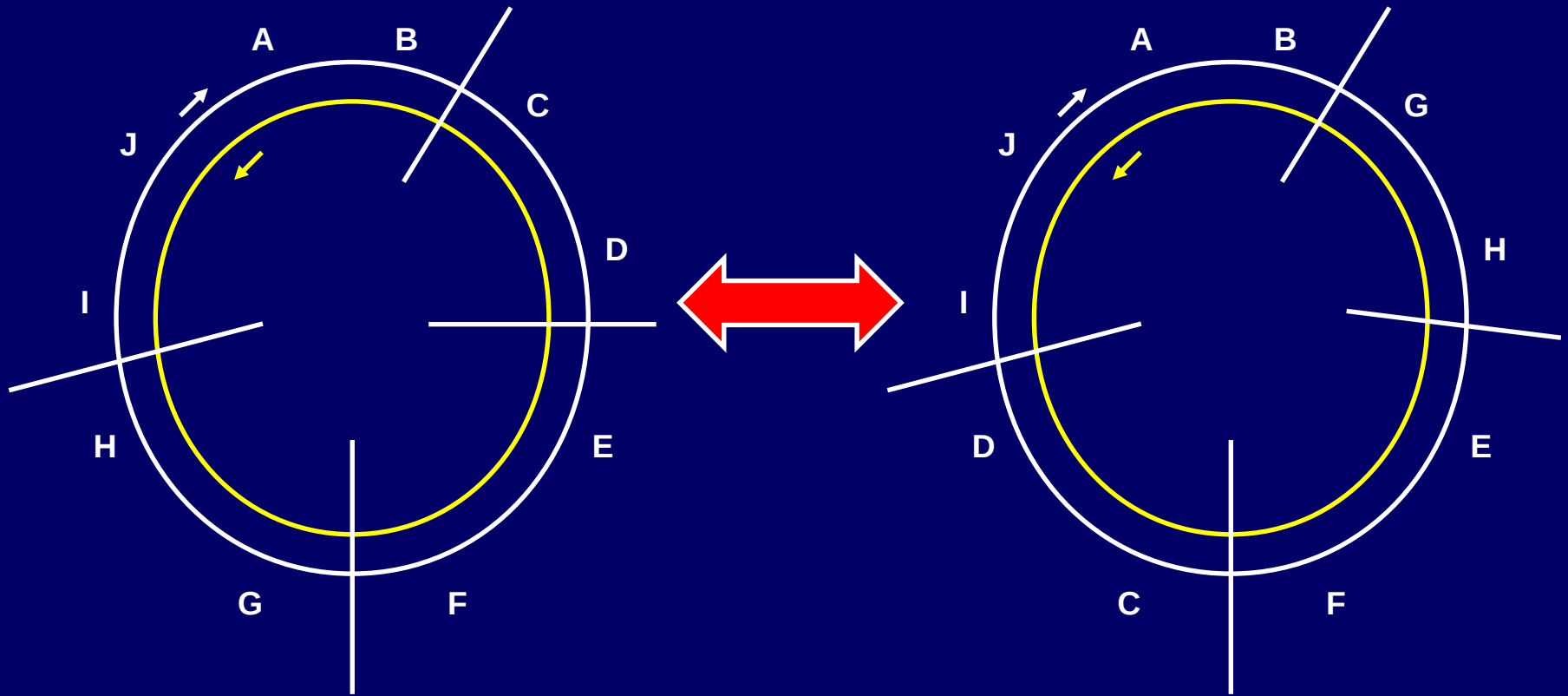
FISSION / FUSION

Genome breaks in two / Two genomes join



BLOCK INTERCHANGE

Exchange of two nonadjacent segments



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EXAMPLE: HUMAN AND MOUSE X-CHROMOSOME

Pavel Pevzner et al. *Genome Res.* 2003; 13: 37-45

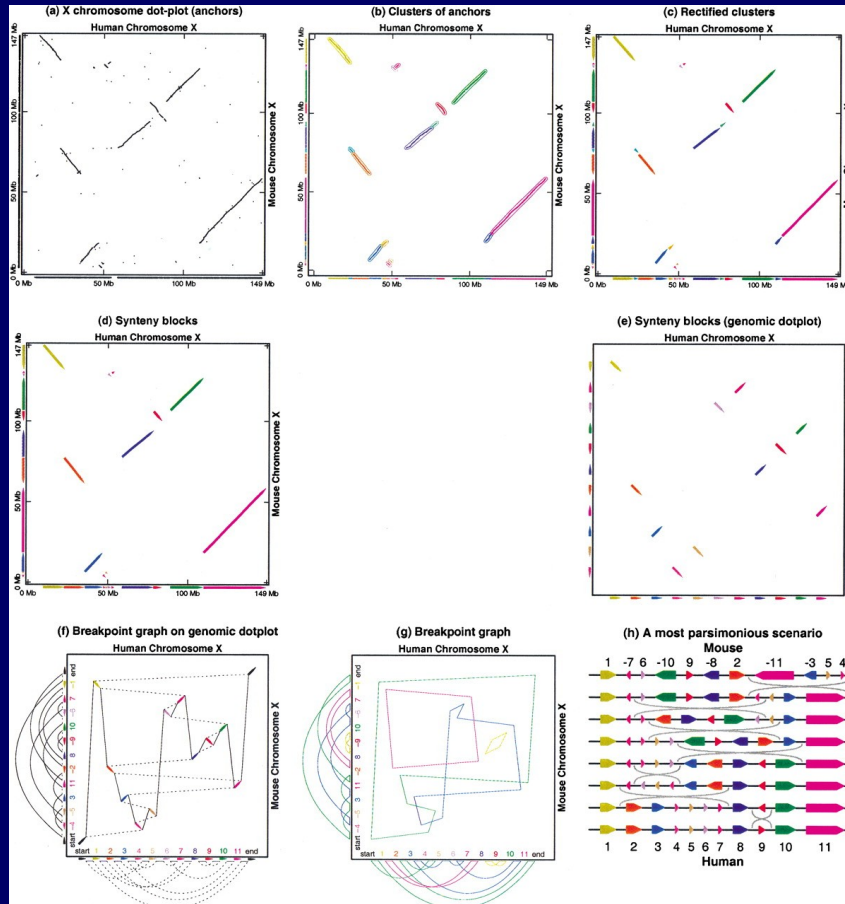


Figure 2. X-chromosome:
from local similarities, to
synteny blocks, to
breakpoint graph, to
rearrangement scenario

Thanks to:

Cold Spring Harbor Laboratory Press



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REARRANGEMENT DISTANCE

Maximum parsimony approach

Given two genomes, and a set of events, the rearrangement distance between the genomes is the length of the shortest series of events that transforms one genome into the other.

In the previous example:

Genome 1: mouse X-chromosome

Genome 2: human X-chromosome

Set of events: reversals only

Distance: 7 events

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KNOWN RESULTS

- **Insertion / Deletion distance : efficient algorithm known**
- **Reversal distance : efficient algorithm known**
- **Transposition distance : NP-hard; approximative algorithms**
- **Fission / Fusion distance : efficient algorithm known**
- **Block Interchange distance : efficient algorithm known**

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CURRENT RESEARCH LINES

- **Comparisons of three or more genomes**
- **More realistic models with several operations, or basic operations that can form several others, e.g., DCJ or SCJ**