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

$$\frac{\text{number of events}}{\text{unit of time}}$$

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

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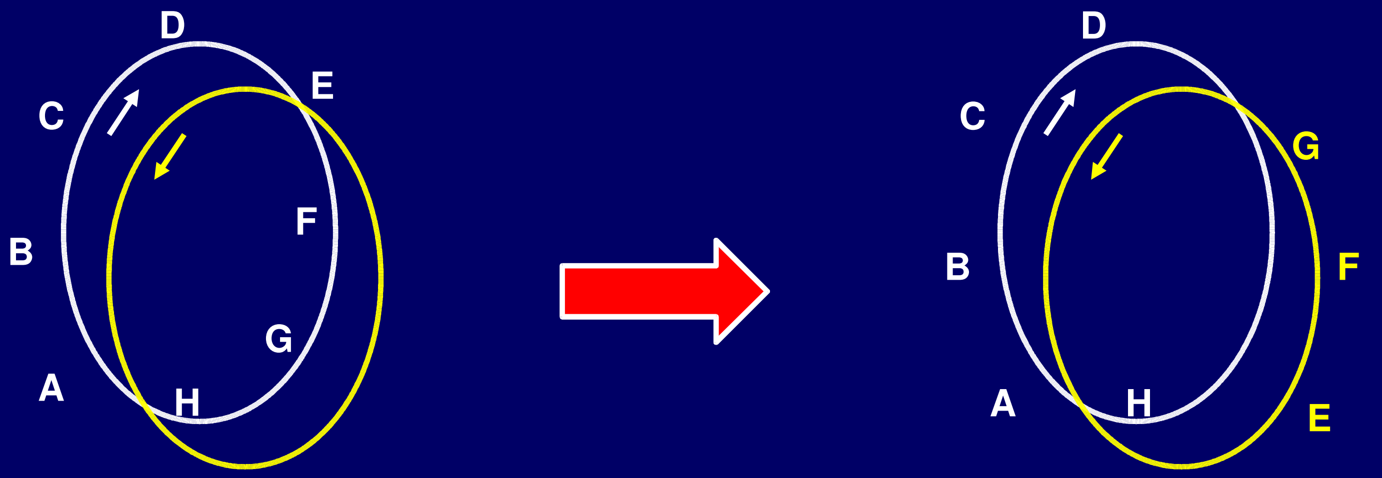
GENOME COMPARISON
Point mutations

```
...TATCGATAGACCACTG...
...TATC--TAGACGACTA...
```

GENOME COMPARISON
Genome rearragements



Movement of large segments within the genome.

Above, segment E – F – G flips over

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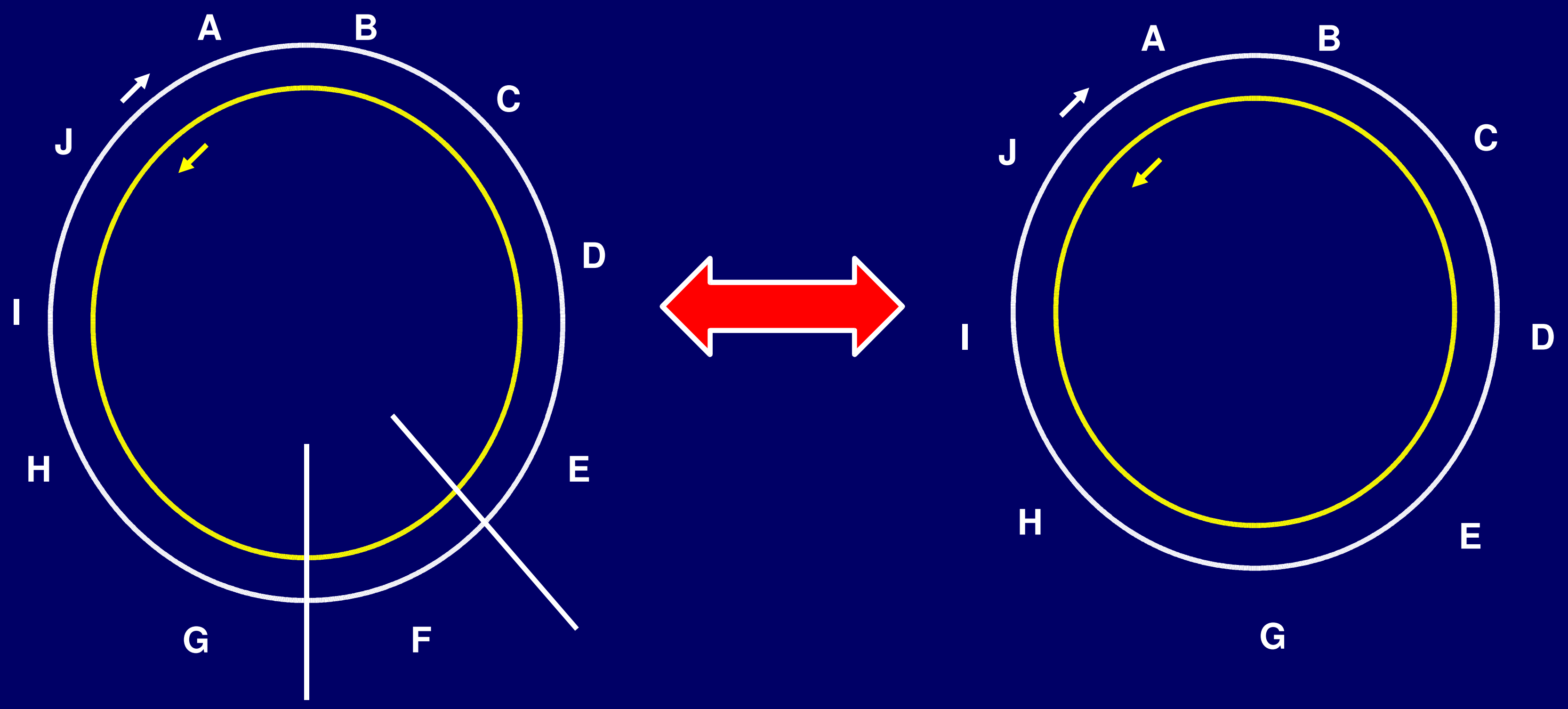
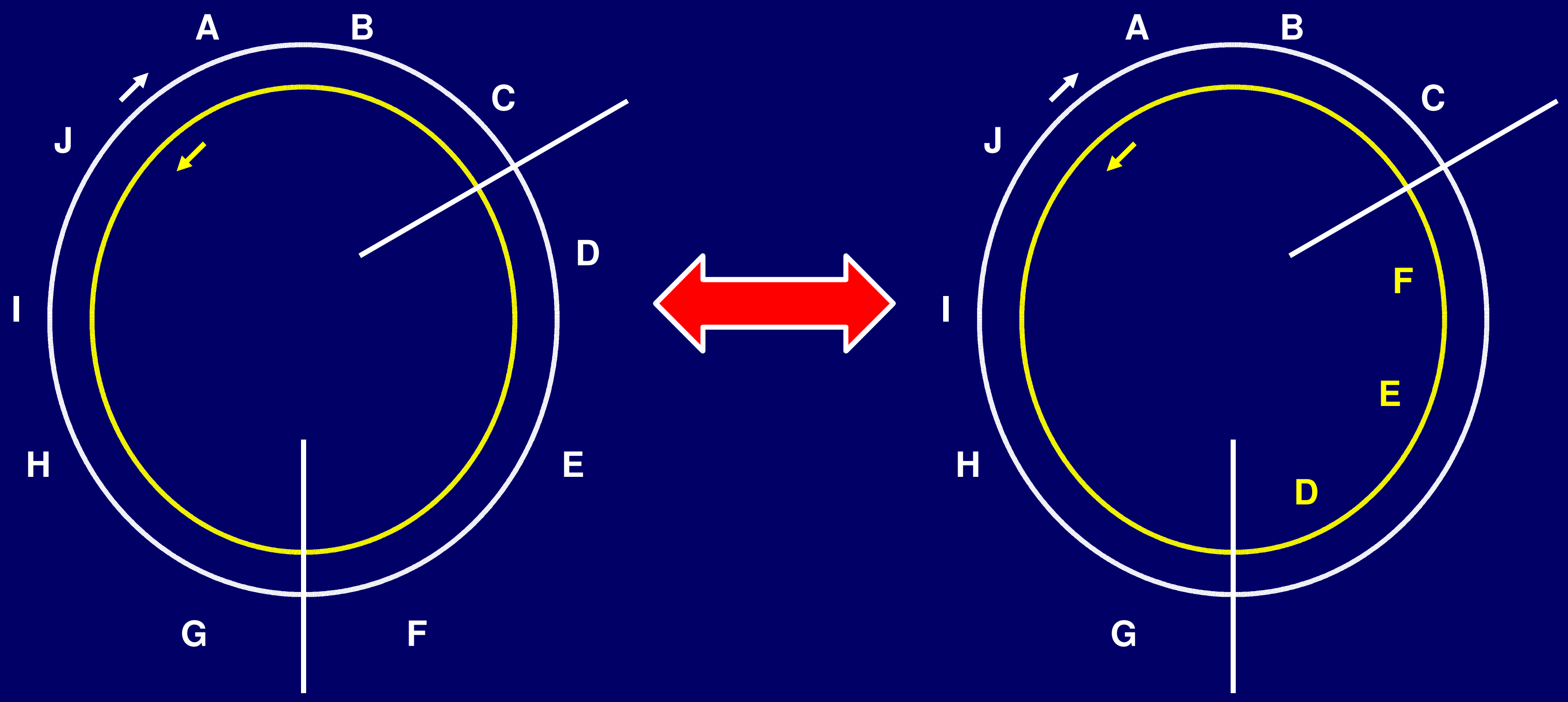
REARRANGEMENT EVENTS

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

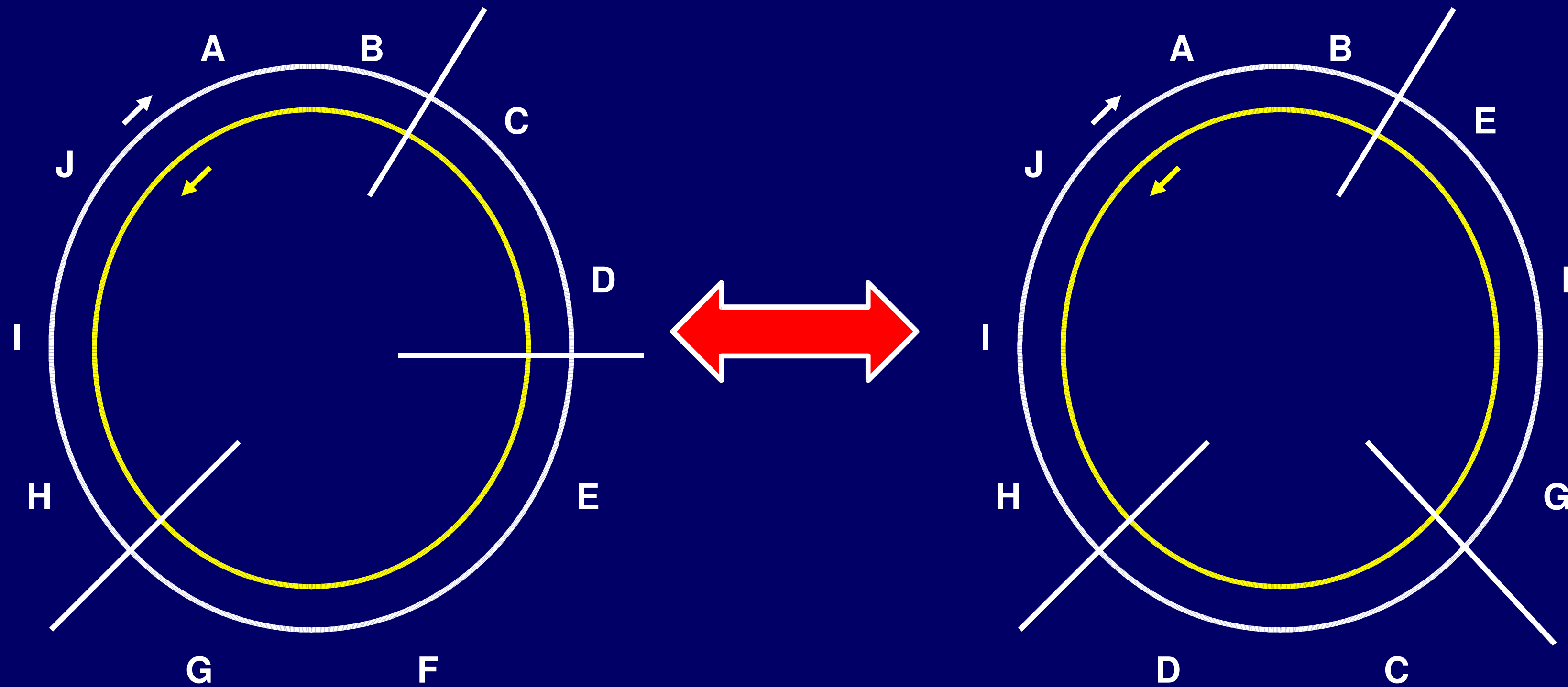
INSERTION / DELETION
Gene gain / loss between genomes



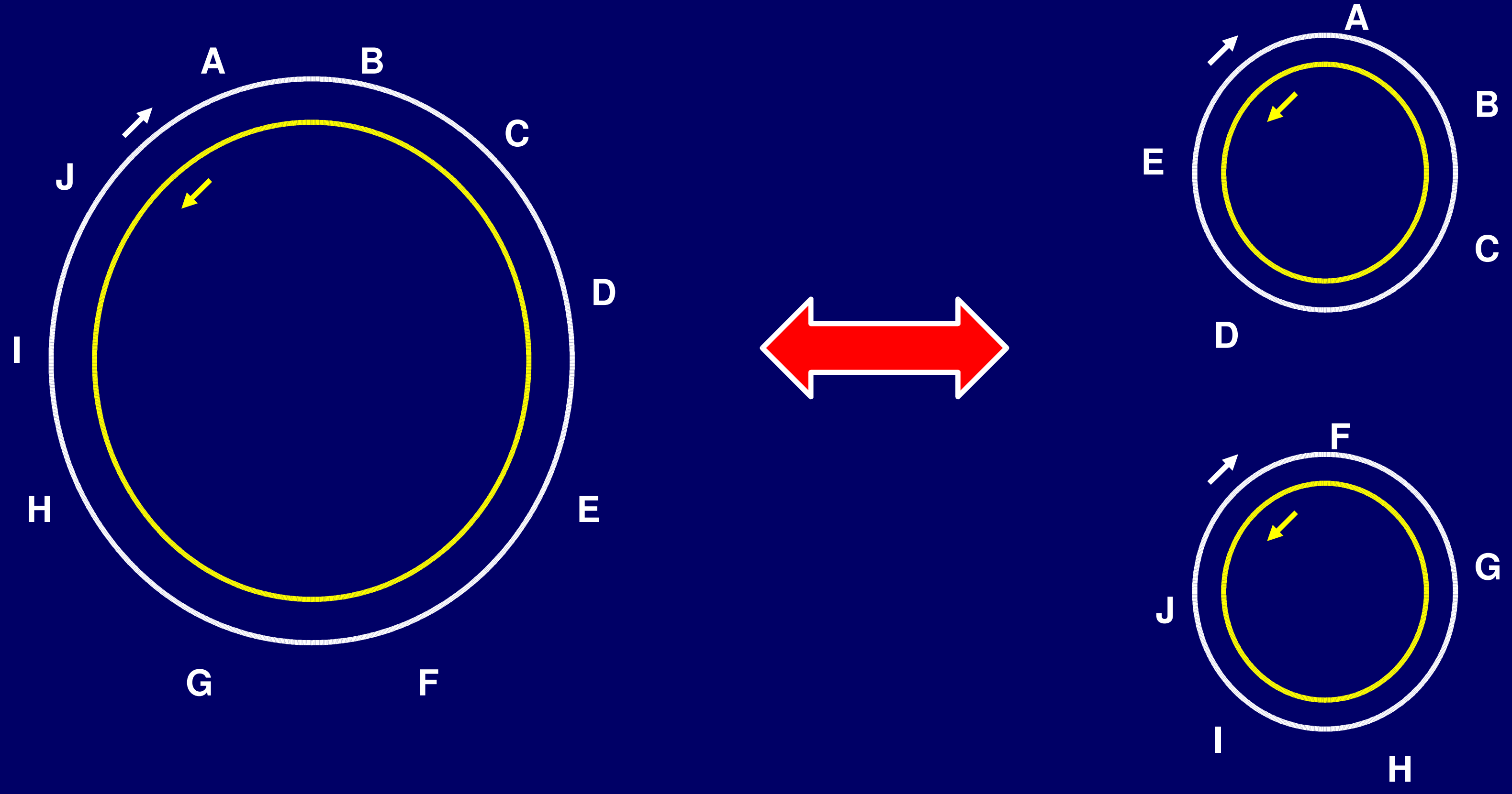
REVERSAL
A segment is reversed between genomes



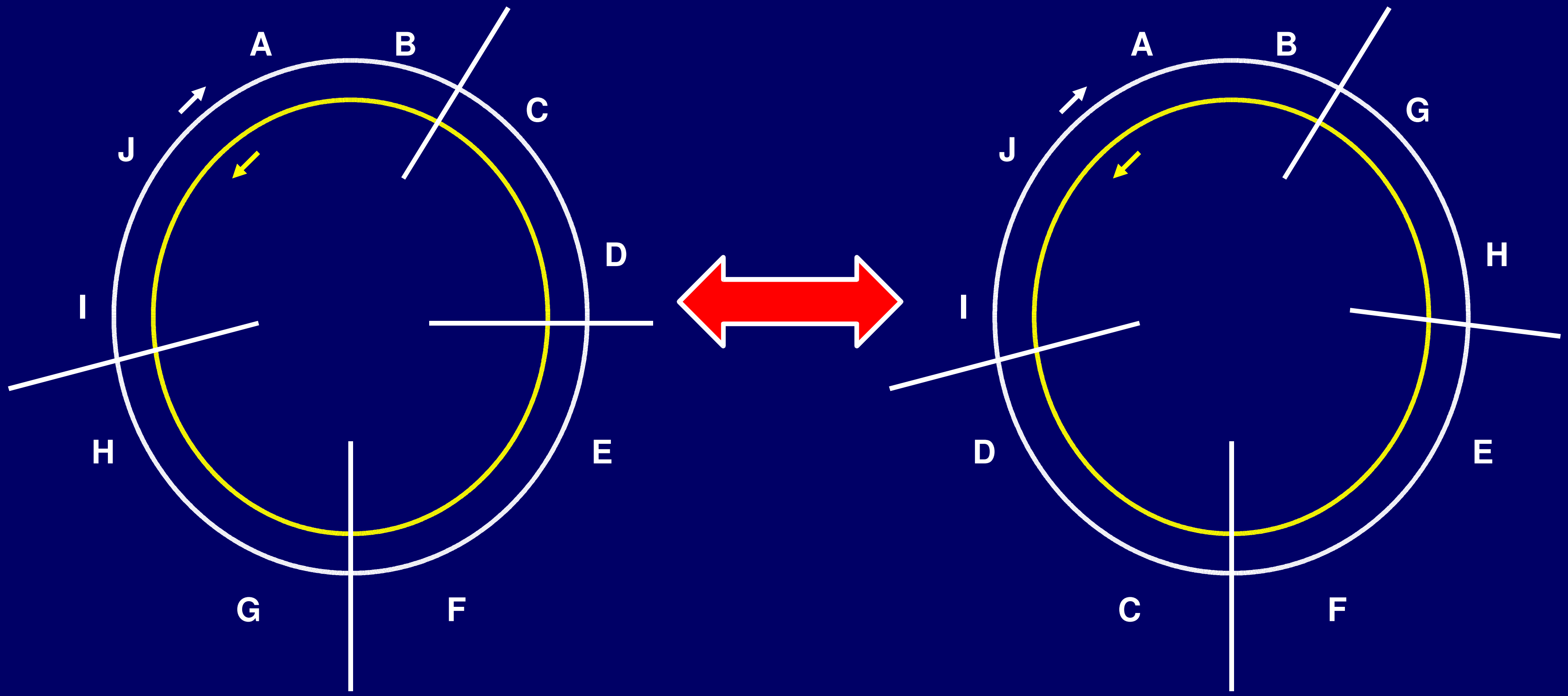
TRANSPOSITION
A segment moves to a new position
(or: exchange of two adjacent segments)



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

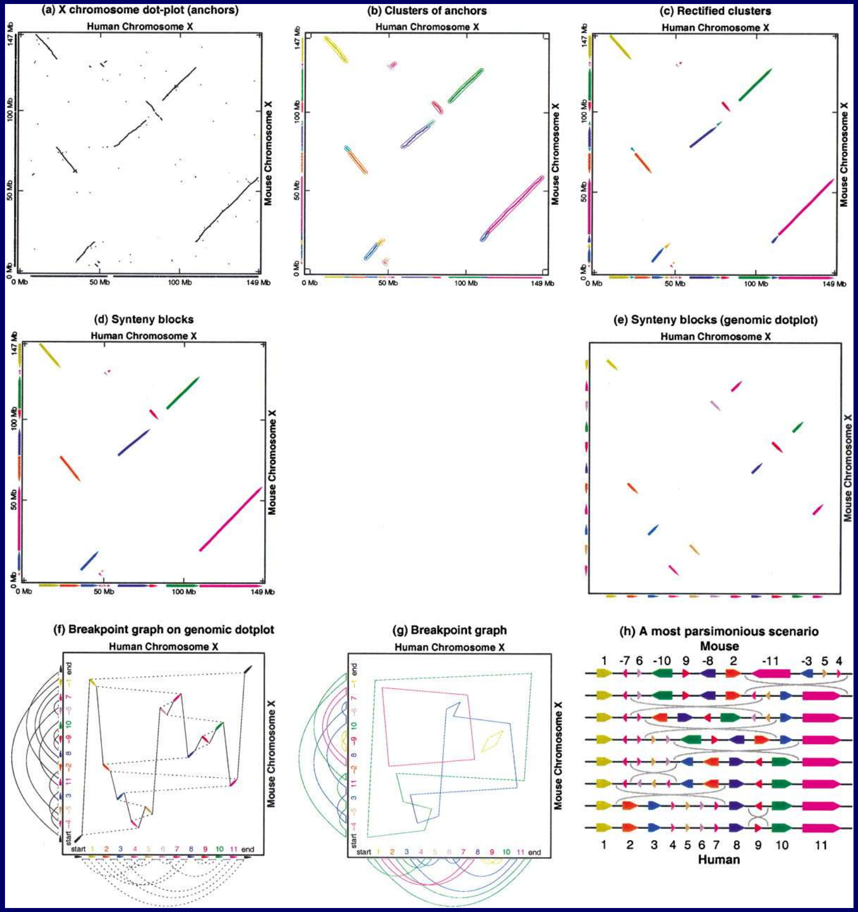

Figure 2. X-chromosome: from local similarities, to synteny blocks, to breakpoint graph, to rearrangement scenario

Thanks to:

Cold Spring Harbor Laboratory Press

CSHL 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: no efficient algorithm known; approximative algorithms
- Fission / Fusion distance : efficient algorithm known
- Block Interchange distance : efficient algorithm known

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CURRENT RESEARCH LINES

- Solve transposition distance problem
- Comparions of three or more genomes
- Sets with more than one operation, e.g., reversal and transposition distance