

Double-Cut-and-Join (DCJ)

- Universal operation
- 1 DCJ:
 - Reversal, Translocation, Fission, Fusion
- 2 DCJ:
 - Transposition, Block interchange
- Linear time algorithms for distance & operations

DCJ Paper

- Synteny blocks (more general than genes)
- Caps for linear chromosomes
- Null chromosomes to equalize cap number
- Breakpoint: noncommon adjacency
- (Caps also equalize breakpoint number)

DCJ Paper

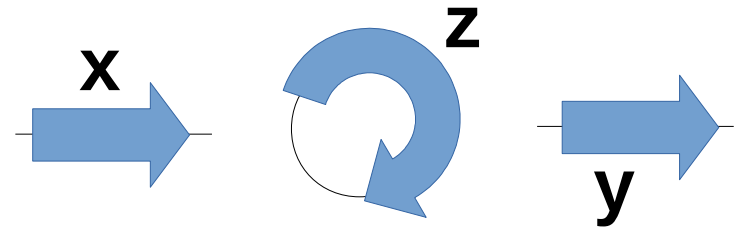
- Breakpoint graph (with caps)
- A – B adjacencies: black edges
- B – A adjacencies: gray edges
- Ignore common adjacencies
- Distance = $b - c$ (breakpoints – cycles)

DCJ Algorithm

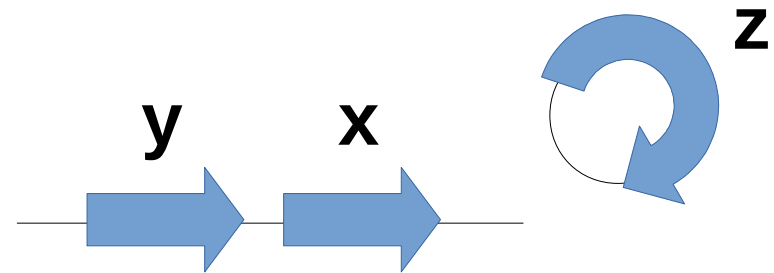
- Phase 0:
- Add caps to linear chromosomes
- Draw black and grey edges
- Identify ends of AB-paths
- Link ends of AA-paths with grey edges
- Link ends of BB-paths with black edges
- Other phases: proceed to reduce $b - c$

DCJ Algorithm: Computing distance

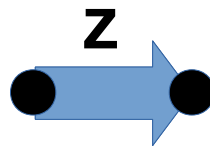
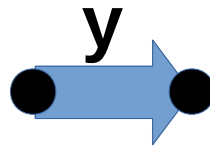
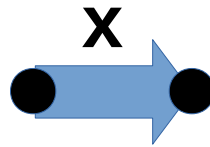
Genome A



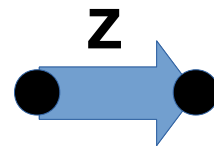
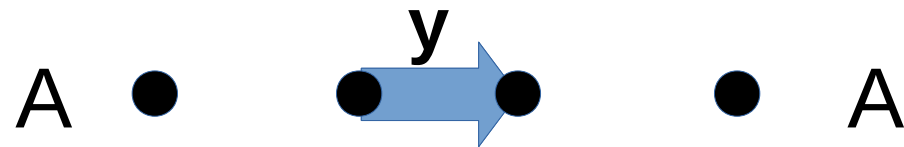
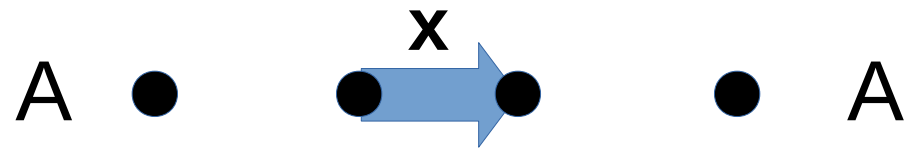
Genome B



Draw syntenic blocks



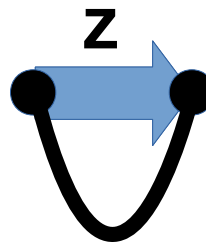
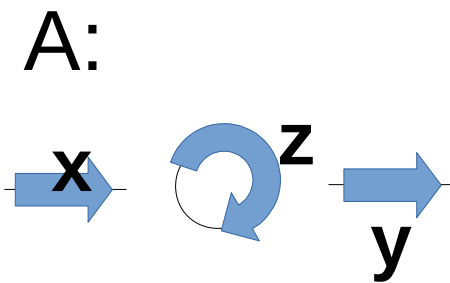
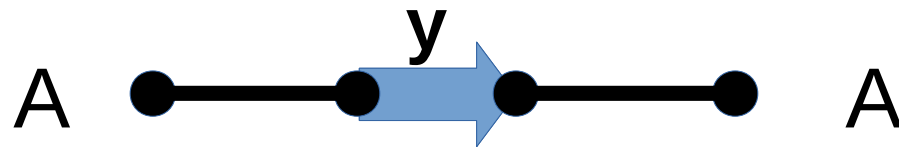
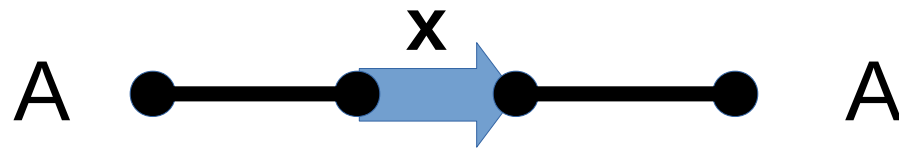
Genome A: add caps



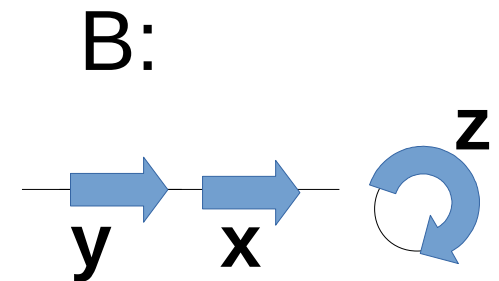
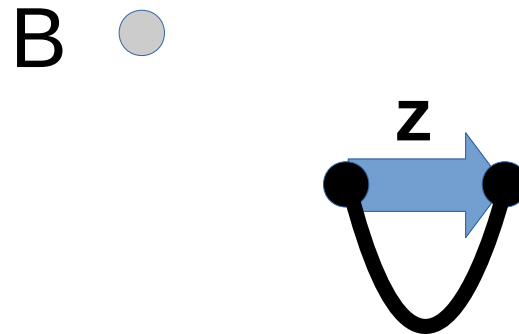
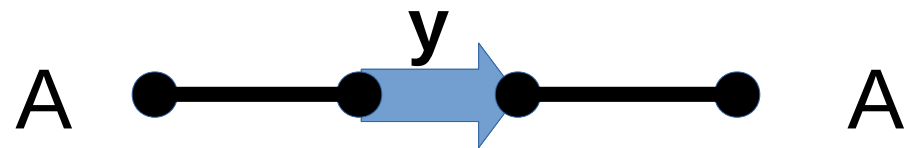
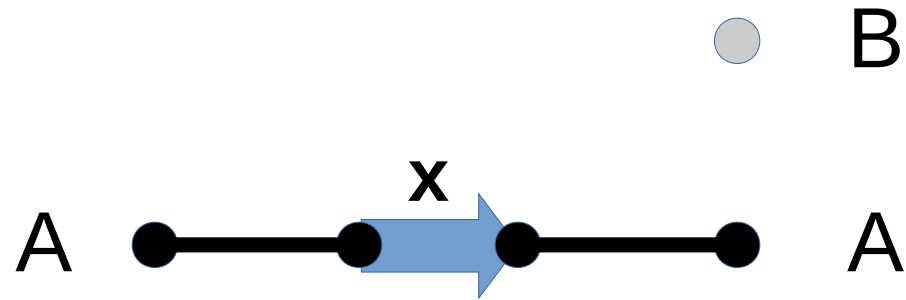
A:



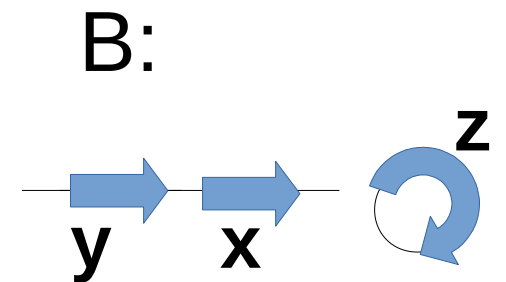
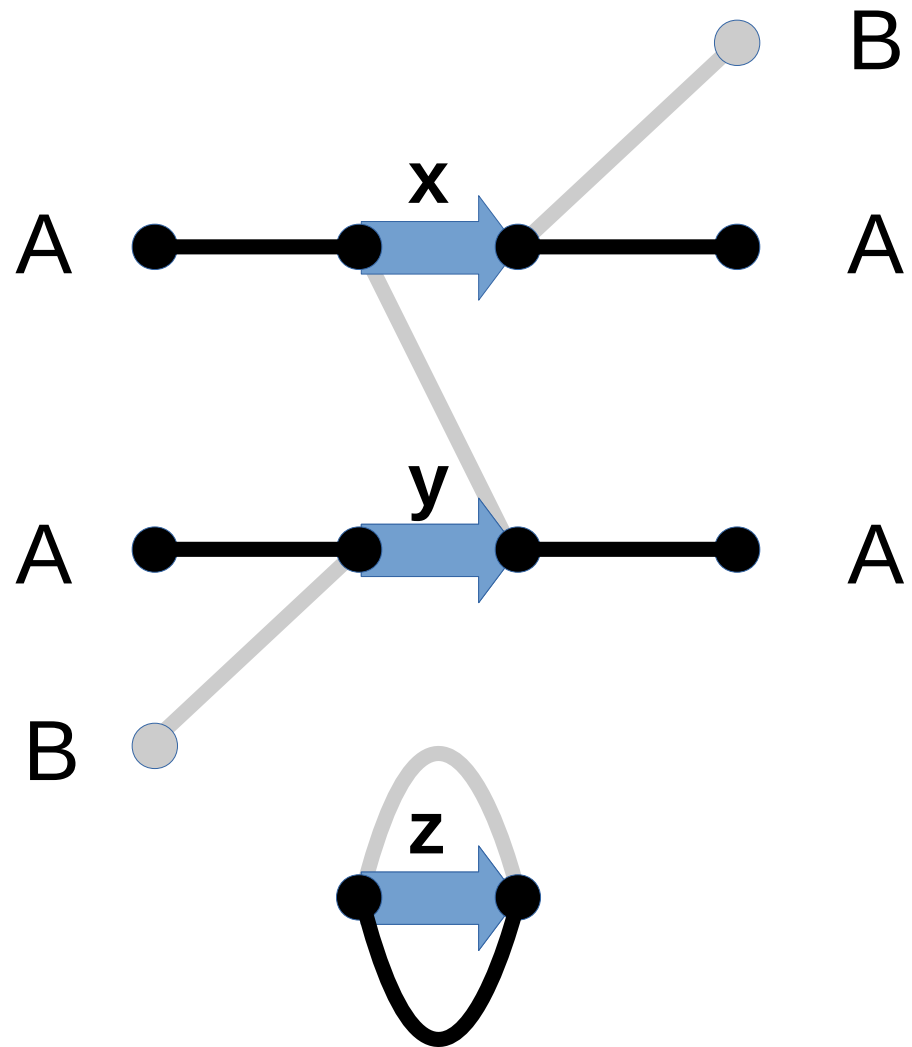
Genome A: add adjacencies



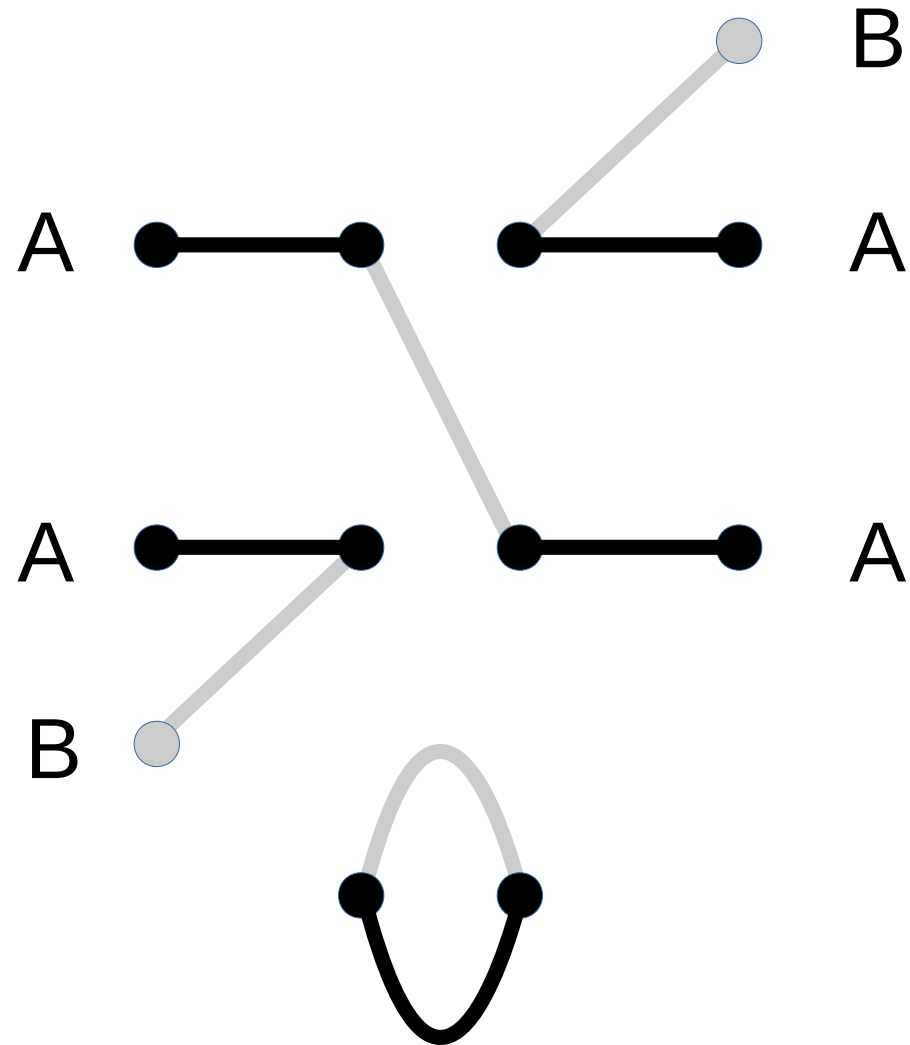
Genome B: add caps



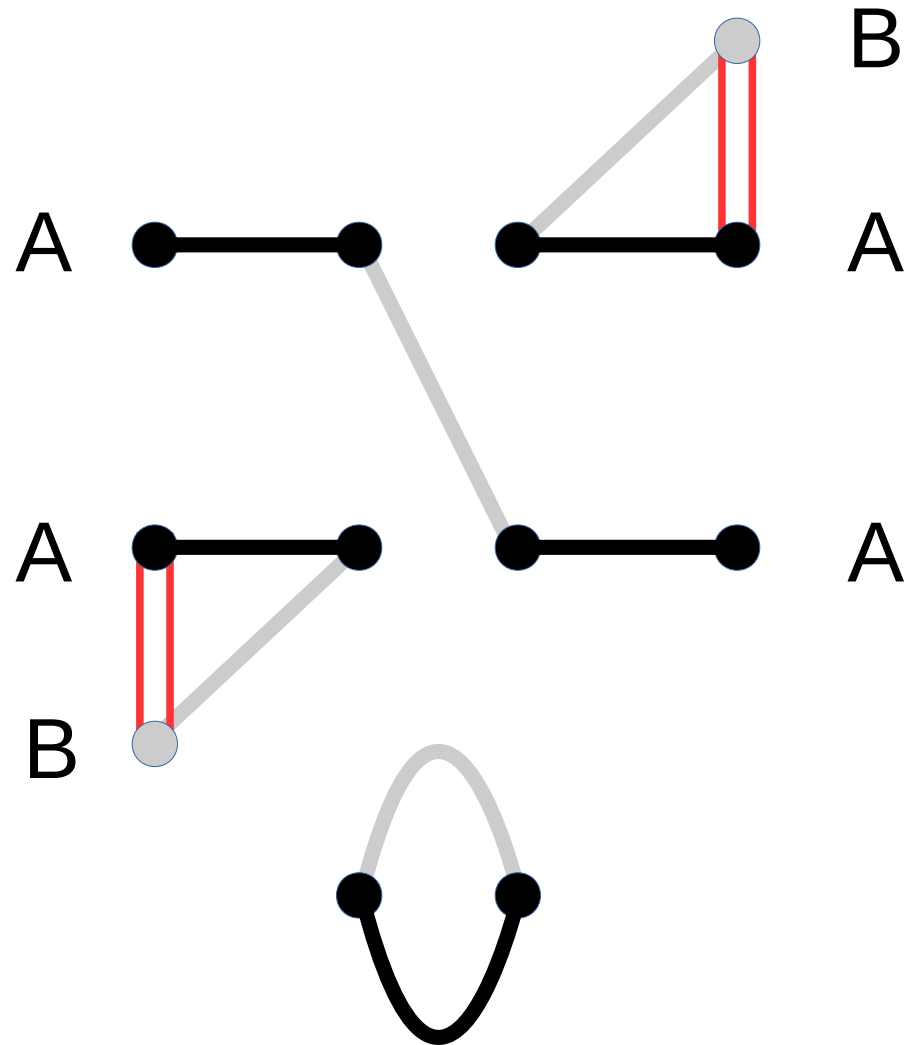
Genome B: add adjacencies



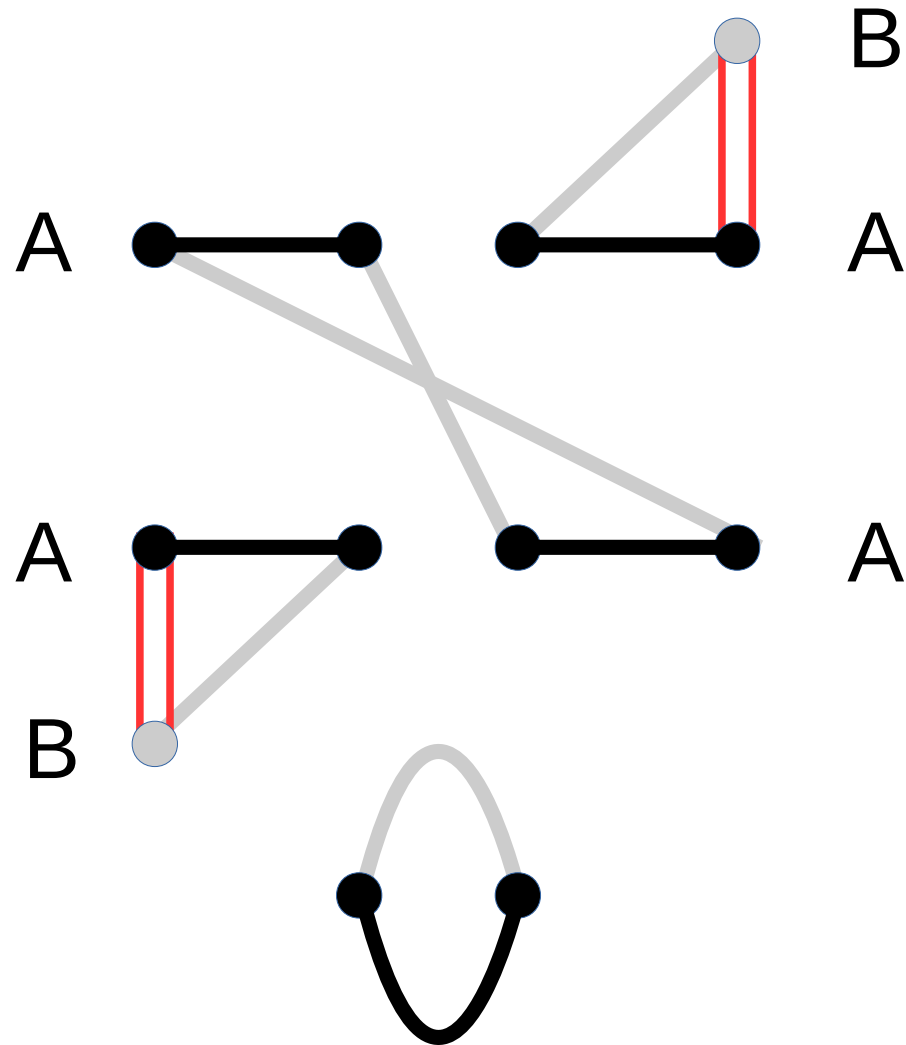
Get rid of block bodies



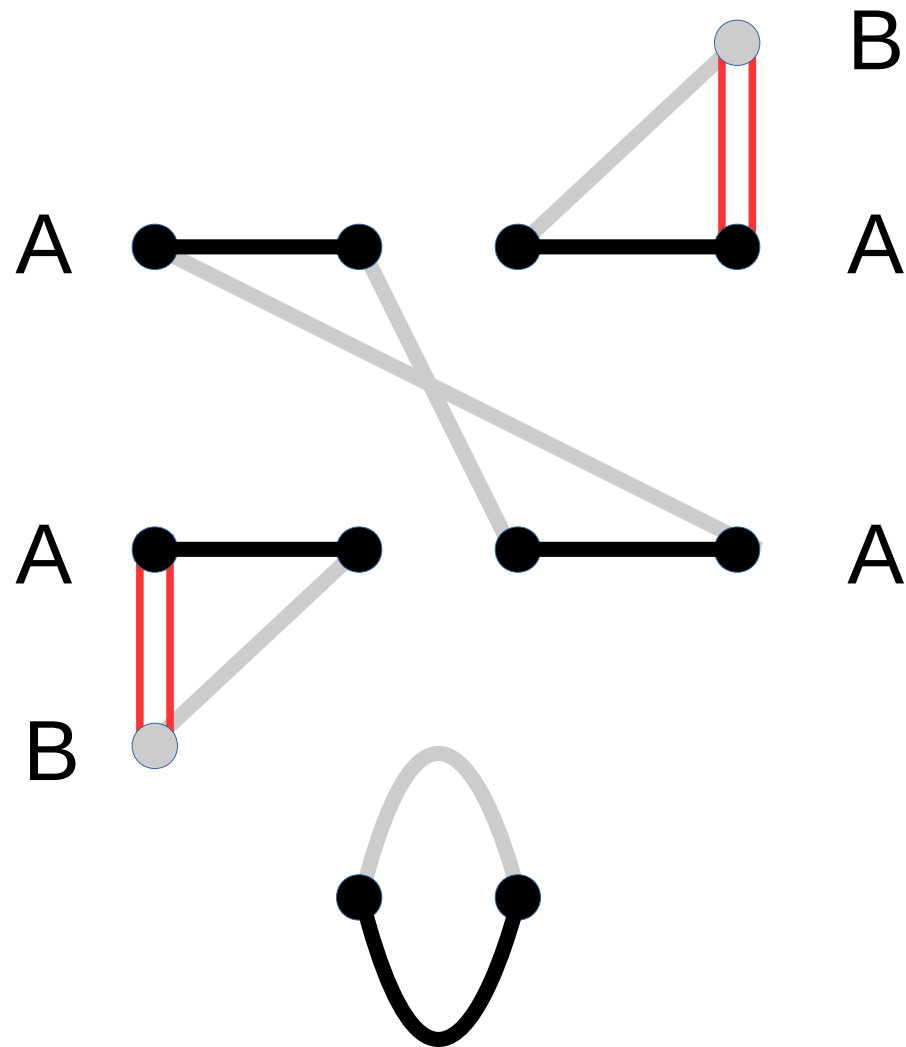
Identify ends of AB-paths



Connect ends of AA-, BB-paths



Compute: $b - c = 2 - 1 = 1$



Tips

- Breakpoints:
 - Noncommon adjacencies in A and not in B, or
 - Noncommon adjacencies in B and not in A
- It will be the same number (b)
- Cycles composed solely of common adjacencies do not count