

# Algebraic Theory

- Modeling of genomes, rearrangement operations using **permutation group theory**
- Leads to a novel notion of distance
- Very similar to DCJ
- Differs from DCJ in linear fissions, linear fusions, circularizations, and linearizations

# Permutation group theory

- Permutations are bijective functions  $\alpha: E \rightarrow E$
- Representation:  $\alpha = (1\ 2\ 5)\ (4\ 7)$
- Cycles:  $(5\ 2\ 8\ 9\ 3)$
- Orbits
- $k$ -cycles: cycles involving  $k$  elements
- Fixed elements:  $\alpha(x) = x$
- Support: set of elements not fixed

# Permutation group theory

- Product is composition:  $\alpha\beta(x) = \alpha(\beta(x))$
- Identity: **1**
- Disjointness
- Unique cycle decomposition
- Conjugation
- 2-cycle decomposition
- Norm:  $||\alpha||$

# Norm properties

- $\|\alpha\| = 0$  if and only if  $\alpha = \mathbf{1}$
- $\|\alpha^{-1}\| = \|\alpha\|$
- $\|\alpha\beta\| \leq \|\alpha\| + \|\beta\|$
- $\|\alpha\beta\| = \|\beta\alpha\|$
- $\|\alpha\beta\alpha^{-1}\| = \|\alpha\|$
- $\|\alpha\| = |E| - |\text{orb}(\alpha)|$
- Constructiveness

# Divisibility

- Notation:  $\alpha \mid \beta$
- $\alpha \mid \beta$  when  $\|\beta\alpha^{-1}\| = \|\beta\| - \|\alpha\|$
- $\alpha \mid \beta$  when:
  - $\text{orb}(\alpha)$  refines  $\text{orb}(\beta)$
  - Edges of  $\alpha$  go in the same direction as  $\beta$
  - Edges of  $\alpha$  do not cross in  $\beta$

# Modeling genomes

- Genes: 1, 2, 3, ...
- $k_t = +k$ ,  $k_h = -k$
- $E = \{k_h, k_t \text{ for all genes } k\}$
- $\Gamma = (-1 +1) (-2 +2) (-3 +3) \dots (-n +n)$

# Chromosomal method

- Genes: 1, 2, 3, ...
- $k_t = +k$ ,  $k_h = -k$
- $E = \{k_h, k_t \text{ for all genes } k\}$
- $\Gamma = (-1 +1) (-2 +2) (-3 +3) \dots (-n +n)$
- $\Gamma^2 = \mathbf{1}$
- $\pi_{\text{chr}}$  is a genome when  $\Gamma \pi_{\text{chr}} \Gamma = \pi_{\text{chr}}^{-1}$

# Adjacency method

- Genes: 1, 2, 3, ...
- $k_t = +k$ ,  $k_h = -k$
- $E = \{k_h, k_t \text{ for all genes } k\}$
- $\Gamma = (-1 +1) (-2 +2) (-3 +3) \dots (-n +n)$
- $\Gamma^2 = \mathbf{1}$
- $\pi_{\text{adj}}$  is a genome when  $\pi_{\text{adj}}^2 = \mathbf{1}$



# Relationship between methods

- $\pi_{\text{adj}} \Gamma = \pi_{\text{chr}}$
- $\pi_{\text{chr}} \Gamma = \pi_{\text{adj}}$

# Rearrangement operations

- $\rho$  is a rearrangement operation on genome  $\pi$  when  $\rho\pi$  is a genome
- Weight of  $\rho$  is  $\|\rho\|/2$