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Diffusion on the DCJ Lattice

In the DCJ (double cut and join) model of genome rearrangement, the segment ends can be treated as independent entities so that a rearrangement is defined by how these 2N entities are paired at synapses. A DCJ step is made by cutting any two pairs and reconnecting the 4 cut ends. Each possible rearrangement corresponds to one of the (2N-1)!! complete pairings. Treating each pairing as a graph vertex and the DCJ operation as specifying the graph edges, one can study diffusion on the graph by random DCJ operations. The diffusion equation is

$$\frac{d}{dt}P_\alpha = -P_\alpha + M^{-1}\Sigma_{\beta\wedge\alpha}P_\beta \tag{1}$$

where P_α is the probability of being at site α, $\wedge$ denotes DCJ neighbors, and $M = N(N-1)$ is the number of neighbors. Starting with all probability at site 0, we seek the probability of being at any site α at time t.

Symmetries of the DCJ lattice are inherited from S_{2N} acting on the segment ends. Eigenfunctions of $-d/dt$ belong to a set A of the irreps of S_{2N}. The eigenvalue corresponding to the irrep R is $\Lambda_R = (1-\lambda_R(2))(2N-1)/(2N-2)$ where $\lambda_R(2)$ is the character of single pair exchange in R. Thus

$$P_\alpha(t) = \Sigma_R^A e^{-\Lambda_R t}P_\alpha^R(0) \tag{2}$$

where $\Sigma_R^A P_\alpha^R(0) = \delta_{0\alpha}$. The bulk of the calculation consists in finding the numbers $P_\alpha(0)$.