Manda Riehl* (riehlar@uwec.edu). Distribution of distances under the Double Cut and Join model of genome rearrangement.

The Double Cut and Join model of genome rearrangement has the unique property that distances between genomes can be calculated via bipartite adjacency graphs. We answer the following question: How many genomes of length n are distance k from a starting genome A? We accomplish this by finding the number of these adjacency graphs with certain properties. We also show the resulting distance distributions for various starting genomes A. (Received September 24, 2012)