

1086-VN-1956 **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)