In this talk we focus on a tree metric called $k$-interval cospeciation ($k$-IC). The notion of the $k$-IC came from the host-parasite analysis. Biologically, it is highly unlikely that a large number of consecutive speciations can accumulate in a host lineage, without any reactionary speciation in parasite. Thus, when reconstructing host and parasite trees, we might assume that only a bounded number of consecutive speciations can occur in any host lineage before a reactionary speciation in parasite (and vice versa). Combinatorially this implies that for each pair of host species $A, B$, and corresponding parasite species $a, b$, the number of edges between $A, B$ is within $k$ of the number of edges between $a, b$. We say such a cophylogeny satisfies $k$-interval cospeciation.

Here we will compare the $k$-IC tree distance with other tree metrics, and then we will discuss the distribution of the $k$-IC metric between two randomly generated trees if we fix $n$. (Received September 02, 2014)