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A classical problem in computational biology is the construction of a phylogenetic tree from a sequence alignment of  $n$  species. The work by Billera, Holmes, and Vogtmann (2001) provides a construction of a space  $BHV_n$  of such metric trees, which is shown to have a CAT(0)-structure, enabling the computation of geodesics and centroids. An alternate phylogenetic tree space introduced by Kim (2000), known as the “space of phylogenetic oranges”, is a more general tree space that captures forests rather than trees. We study the connection between these two tree spaces in terms of combinatorial moves on trees induced by infinite edge, producing a “discrete path tree space” in the process. The image of a chamber can be described in terms of a product of cubes and simplices that allow straightforward descriptions of the collapsing map. (Received September 23, 2012)