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 $T_n$ of such trees, which was shown to have a CAT(0)-structure, enabling the computation of geodesics and centroids. Due to its conical structure, the combinatorial characteristics are encoded in its cross-section $L_n$, a simplicial complex, which from an operadic viewpoint corresponds to fully-grown trees. We provide a novel construction of $L_n$ in the language of the associahedron and the permutohedron, famous classical polytopes that encapsulate algebraic information. These polytopes themselves appear in numerous contexts, ranging from root systems and knot theory to Floer homology and moduli spaces of curves. We prove that $L_n$ is covered by $n!$ associahedra, with the discrete fiber over this map keeping track of the planarity of the tree structure. Moreover, permutohedra are shown to be embedded in $L_n$, each corresponding to a caterpillar tree. Finally, we reinterpret the topological results regarding $L_n$ of Robinson and Whitehouse (1996), demonstrating that each permutohedron completely captures the homotopy structure of $L_n$ as a wedge of spheres. (Received September 25, 2012)