Many research aim to RNA molecules and demand for tools enabling their analysis increased. First step is visual inspection of their secondary structure. In order to correctly lay out structure, the notion of optimal layout is required. However, this has never been formalized and is largely habitual. To tackle this problem we propose an algorithm capable of visualizing RNA structure using related one with known layout. Algorithm first converts both RNAs into a tree representation and using tree-edit-distance algorithm finds out the minimum number of operations to convert one structure into the other. All common motives are retained and the regions which differ are taken care of. Results show, that our algorithm is able to give good layouts even for relatively distant structures. It is well suited for visualization of homologous structures.