Visualization of RNA secondary structure is an open problem because there does not exist a well-defined description of the layout process. The layout accepted by the community is habitual. The approach implemented by the Traveler tool, developed at Department of Software Engineering MFF UK, is based on using existing structure with known layout as a template for laying out structure with unknown layout. The first version of the program had few issues that made it difficult to use. The goal of the thesis was to improve Traveler so that the tool is more accessible. Improvements include ability to process pseudoknots, intermediate format for images of secondary structures and modification of the layout-creating algorithm. We created a web application that serves as an user interface for Traveler. The application is able to automatically choose a template for the structure too.