



## ***RnaViz 2: an improved representation of RNA secondary structure***

*Peter De Rijk\*, Jan Wuyts and Rupert De Wachter*

*Departement Biomedische Wetenschappen, Universiteit Antwerpen (UIA),  
Universiteitsplein 1, B-2610 Antwerpen, Belgium*

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### **ABSTRACT**

**Summary:** RnaViz has been developed to easily create nice, publication quality drawings of RNA secondary structure. RnaViz 2 supports CT, DCSE, and RNAML input formats and improves on many aspects of the first version, notably portability and structure annotation. RnaViz is written using a hybrid programming approach combining pieces written in C and in the scripting language Tcl/Tk, making the program very portable and extensible.

**Availability:** Source code, binaries for Linux and MS Windows, and additional documentation are available at <http://rrna.uia.ac.be/rnaviz/>

**Contact:** [derijkp@uia.ua.ac.be](mailto:derijkp@uia.ua.ac.be)

Several formats for storing RNA secondary structure information exist that are not really suitable for eye-ball comparison and publication of structures. A new version of RnaViz (De Rijk and De Wachter, 1997) is presented. RnaViz 2 will read files containing the secondary structure, extract the structure information, and automatically draw the structure contained in the file. The structure drawings can then be edited and annotated into publication quality 2D drawings. RnaViz supports reading files in the DCSE (De Rijk and De Wachter, 1993) format that incorporates special symbols indicating the secondary structure in an RNA sequence alignment. It can also read CT files as produced by the mfold program (Jacobson and Zuker, 1993). The detection of helices in CT files has become more advanced: helices consisting of several segments will now be detected as one helix, reducing clutter and improving layout. The new version also supports loading RNAML (Waugh *et al.*, 2002) formatted files. RNAML is a new XML-based format for storing RNA structure. Some of these formats can contain more than one structure; in this case, the user can select to either draw a number of these structures on one page, or batch process them into different pages. Structure drawings are by default saved in the new, more efficient file format, although loading of files in the old format is

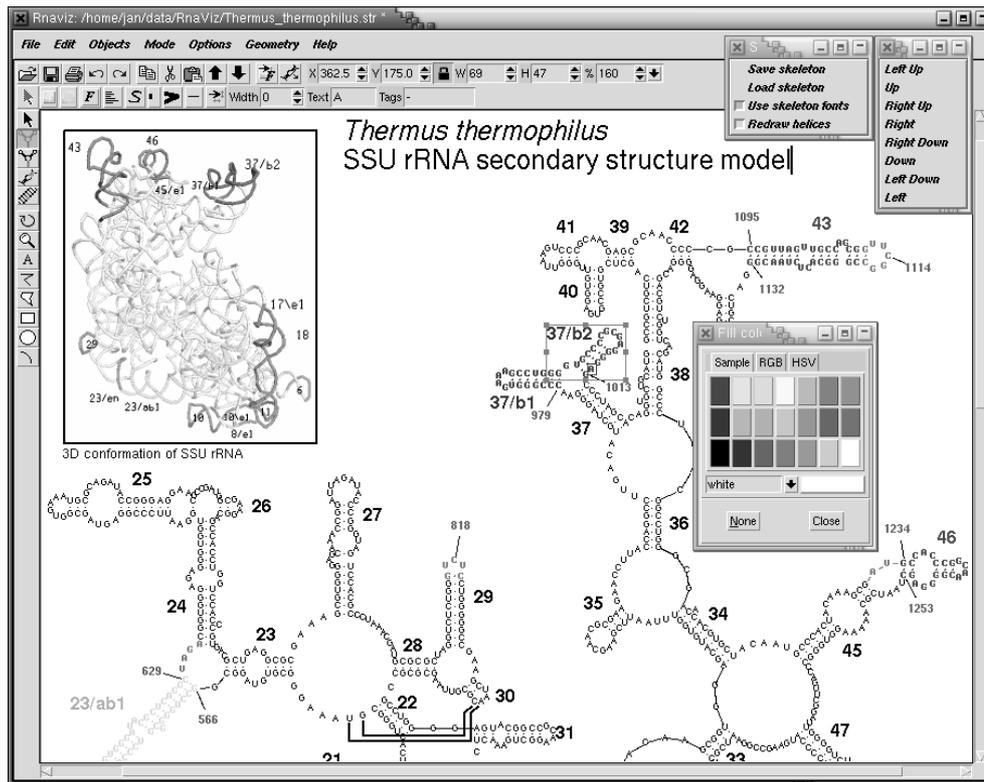
still supported.

Often the user wants to draw several similar structures using the same layout. For this reason, the current layout of a structure can be saved in a skeleton file. This skeleton file can then be applied to other drawings. Several skeletons for typical RNA molecules are included in the distribution. Since this is the preferred method, RnaViz will always present the user with the option of using a skeleton file when opening a new structure. When canceled, the structure will be drawn from scratch. Drawing large structures without a proper skeleton may lead to a layout with considerable overdraw. The layout of the structure drawing can always be readily rearranged using the mouse. Since each nucleotide (or annotation) is a separate object, complex structures such as pseudo knots can be displayed. When moving objects, the connected objects are also automatically rearranged to maintain a proper drawing. Several editing modes allow direct manipulation of trees, helices, helix segments or individual objects.

Figure 1 shows the new interface of RnaViz 2. The new sidebar allows easy access to the different editing modes, zooming and fast creation of annotation objects. The main button bar provides access to filing and printing operations, copy & paste and a fully functional undo/redo feature. It also has added options for direct setting of position, width and height by numbers and the selection of secondary tool bars. A secondary tool bar is available to change the properties such as fonts and colors of currently selected objects. It also has a field where tags can be given to objects, and access to a dialog to change the current selection based on those tags. Another secondary button bar can be chosen for fast rotation of helices in preset directions or for typing in a desired angle.

There are also many usability enhancements in the drawing and annotation facilities: text annotation can be edited in place. Editing of lines has been greatly improved by clearly visualizing points and allowing the addition of new points by double clicking. Other properties besides colors, font, and width, such as cap and join styles, arrowheads, and text justification can now be changed. Annotation objects can be grouped and

\*To whom correspondence should be addressed.



**Fig. 1.** Illustration of the new RnaViz interface. The screen shot shows the editing of a small subunit ribosomal RNA structure with several annotations. The 3D conformation is an inserted bitmap. Also visible are some torn off menus, and the color chooser.

ungrouped. Bitmaps and arcs have been added as new annotation types. Other improvements include zooming in and scaling of structures and objects using the mouse or direct input in the tool bar.

Just like the previous version, RnaViz 2 is developed using a hybrid programming approach combining pieces written in C and in the scripting language Tcl/Tk. However, the internals have changed considerably. RnaViz 2 makes use of an in-house developed object oriented extension to Tcl, that makes the program extremely configurable even using built-in visual tools. It also no longer relies on a patched version of Tcl/Tk, and the dependencies on some harder to port extensions have been dropped. This makes RnaViz 2 very portable. Binaries for Linux and MS Windows are freely available from <http://rna.uia.ac.be/rnaviz/>; porting to other platforms should be easy. Tcl/Tk and the Tcl object system are available under the BSD license. Sources of RnaViz are available under the GPL.

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