

Structural bioinformatics

# RiboSketch: versatile visualization of multi-stranded RNA and DNA secondary structure

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## Abstract

**Summary:** Creating clear, visually pleasing 2D depictions of RNA and DNA strands and their interactions is important to facilitate and communicate insights related to nucleic acid structure. Here we present RiboSketch, a secondary structure image production application that enables the visualization of multistranded structures via layout algorithms, comprehensive editing capabilities, and a multitude of simulation modes. These interactive features allow RiboSketch to create publication quality diagrams for structures with a wide range of composition, size and complexity. The program may be run in any web browser without the need for installation, or as a standalone Java application.

**Availability and implementation:** <https://rnastructure.cancer.gov/ribosketch>

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## 1 Introduction

The base pairing and sequence information of RNA and DNA is frequently communicated via secondary structure diagrams, in which labeled nodes and lines represent nucleotides and their interactions. These images are valuable for determining and communicating structural hypotheses, conclusions and insights.

Due to the wide variety and complexity of RNA, layout algorithms cannot always generate a clean diagram or anticipate which structural features require emphasis in the context of a particular presentation. This creates the need for manual editing features in conjunction with automatic layout generation. Existing programs (Byun and Han, 2009; Darty *et al.*, 2009; Elias and Hoksza, 2017; Hecker *et al.*, 2013; Kerpedjiev *et al.*, 2015; Wiese *et al.*, 2005) provide varying levels of interactivity, but the ability to exactly position nucleotides and substructures is necessary to produce satisfactory images for the full range of RNA and DNA complexes. Because structures are often composed of multiple strands with interstrand, pseudoknot and non-canonical interactions, a program should both

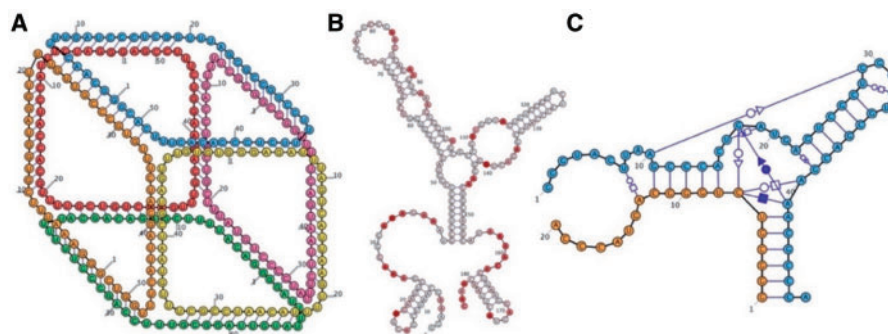
read input that accommodates such elements and facilitate precise editing. It is therefore desirable that a program offer complete control over the display of nucleotides and motifs of complex RNA and DNA, in combination with computational structure optimization features.

## 2 Main features

RiboSketch enables the manipulation of diverse structures through its interactive editing environment, accessible in both online and offline formats. Layouts can be generated automatically, manually (assisted by practical commands), by force simulation, or through any combination of methods.

### 2.1 Input and output

RiboSketch accepts many common secondary structure file formats, such as dot-bracket (Lorenz *et al.*, 2011), MFold connect (Markham *et al.*, 2005) and BPSEQ (Cannone *et al.*, 2002). Many secondary



**Fig. 1.** (A) RiboSketch gives the user complete control over the positions of nucleotides, shown in this 6-stranded RNA cube (Halman *et al.*, 2017). Nucleotide placement and choices of foreground/background layout creating a 3D perspective were performed interactively. (B) SHAPE data coloring of 5S rRNA, *E.coli* (Kladwang *et al.*, 2014). (C) Depiction of Hammerhead Ribozyme including non-canonical interactions (Mir *et al.*, 2016) (Color version of this figure is available at *Bioinformatics* online.)

structure file formats do not contain non-canonical base pairing information, so RiboSketch provides a general solution by enabling the addition of such interactions through direct input into a text field. Alternatively, RiboSketch can read a file format that does contain non-canonical base-pairs derived from the program DSSR (Lu *et al.*, 2015). The state of the program may be saved and stored in a text file format to be later reloaded for continued work. RiboSketch can export rasterized or vector graphics images (PNG or SVG format respectively).

## 2.2 Depiction algorithms

Initial layouts are rendered using a modified version of the Shapiro/NAView approach (Brucoleri *et al.*, 1988; Shapiro *et al.*, 1984), expanded to accommodate multiple strands and pseudoknots (the structure is first rendered based on a maximal subset of nested base pairs, after which the non-nested base pairs are added). For multi-stranded structures, a novel algorithm is applied in which strands are arranged to position related substructures close to one another and to minimize the number of pseudoknots, resulting in a more comprehensible image. RiboSketch can also create circular diagrams, in which nucleotides are positioned in a circle with base pairs drawn as chords.

Customizable display properties include the size, color and labeling of nucleotides. RiboSketch provides an array of color schemes to highlight various structural properties. Additionally, the user may overlay chemical probing data or specify the coloring of individual nucleotides via the input of numerical values (see Fig. 1B). Uniquely, RiboSketch can create depth effects through its ‘bring to front’ and ‘send to back’ commands, allowing diagrams to imply 3D shape (see Fig. 1A). The user may also change the zoom factor. The forced-directed-layout is optionally aided by an algorithm that suggests evenly spaced circular layouts of nucleotides in internal loops and multi-branch junctions.

## 2.3 Interactive editing

RiboSketch enables the user to modify the layout of secondary structure diagrams by clicking, dragging, rotating and utilizing a plethora of commands and features. Operations can be applied to the whole structure, individual nucleotides, or user-defined subsets. Bonds may be interactively added or deleted [in a manner similar to Forna (Kerpedjiev *et al.*, 2015)], and the model dynamically updates. Distances between base-paired nucleotides and the lengths of backbones may be defined and modified. The editing process is made convenient through the ability to undo and redo actions, and to save

and load the state of edited structures. By providing a high level of interactivity, the program is flexible and can process structures ranging from long ribosomal strands to synthetic nanoparticles.

## 2.4 Dynamic simulation

RiboSketch can subject structures to a force simulation in which backbone and base-pair interactions act as springs (similar to Kerpedjiev *et al.*, 2015; Shabash and Wiese, 2017; Wiese *et al.*, 2005), while nucleotides in close proximity undergo repulsion. Helices may be rigidified or left flexible. The user may turn this simulation on or off thus, switching between dynamic and static states to accelerate the editing process. This can be of particular use for processing structures that challenge algorithmic approaches, such as those with many pseudoknots.

## 2.5 Non-canonical interactions

RiboSketch can depict non-canonical interactions using the standard Leontis and Westhof symbol notation (Leontis and Westhof, 2001), as well as hybrid RNA-DNA interactions. Bases can interact with multiple partners (see Fig. 1C).

## 3 Implementation

The implementation for the standalone program utilizes the Java-based Processing environment (<http://processing.org>). In addition to a standalone Java application, we provide a web-based version that can be run within a web browser using JavaScript (without Java). The web version utilizes Processing.js (<http://processingjs.org>).

## 4 Conclusion

With precise editing features and algorithms to accommodate multiple strands and pseudoknots, RiboSketch is valuable for generating images of diverse RNA and DNA secondary structures.

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