

PRESENTATION

# VARNAjs: a javascript library for RNA visualization

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Benasque — Aug 01, 2024

- VARNA: Java library for RNA visualization
- Original VARNAjs is not available
- Other js library, such as drawRNAjs, is no longer maintained

## VARNA: Visualization Applet for RNA

A Java lightweight component and applet for drawing the RNA secondary structure

<a href="#">Home</a> <a href="#">Demo</a> <a href="#">User Manual</a> <a href="#">Tutorials</a> <a href="#">Downloads</a> <a href="#">Java Security Fix</a> <a href="#">Links</a>	<p>Recent changes in Java security policy might prevent you from running VARNA. Check out this page for details and ways to solve the problem.</p> <p><b>What VARNA is</b></p> <p><b>Description</b></p> <p>VARNA is Java lightweight Applet dedicated to drawing the secondary structure of RNA. It is also a Swing component that can be very easily included in an existing Java code working with RNA secondary structure to provide a fast and interactive visualization.</p>
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GUI



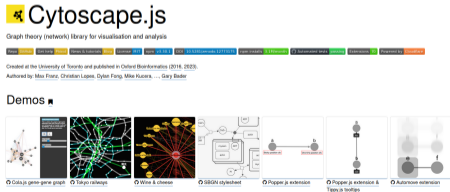
CMD

```
➤ java -cp VARNA-2.9.3.jar fr.orsay.lri.varna.applications.VARNAcmd -sequenceCDD -structureCDD "{(-..2)}" -o e0tf.png -baseMap "#FFFF" -algorithm "xview" -bptyle simple -rotation 180 -auxBPS "(1,7)color=#000000,thickness=1,edgeSwc,edgeSwc,stericity=ct(2,2)color=#000000,thickness=2,edgeSwc,edgeSwc,stericity=ct" -baseStyle1 #11#000000,0,outline#FFFFFF,number#FFFFFF -applyBaseStyleLen 2,0 -baseStyle2 fill#000000,outline#FFFFFF,number#FFFFFF -applyBaseStyleLen 1,1
```

<https://gitlab.com/htyao/varnajs>

<https://github.com/anthonyhtyao/varnajs>

- Conversion/Reimplementation from VARNA
- Current library version: v0.2
- Support most of VARNA library functions, but not all yet
- Live demo: CaRNAval
- Based on Cytoscape.js
  - Thanks to V. Reinharz for the support of non-canonical basepairs



**Cytoscape.js**  
Graph theory (network) library for visualisation and analysis

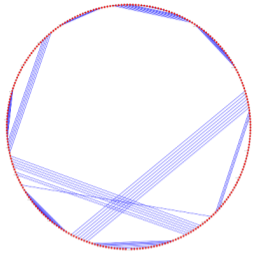
Home | Get Cytoscape.js | Demos | Extensions | Contact | About | [Cytoscape.js on GitHub](#) | [Cytoscape.js on npm](#) | [Cytoscape.js on PyPI](#) | [Cytoscape.js on Docker](#) | [Cytoscape.js on Conda](#) | [Cytoscape.js on Anaconda](#)

Created at the University of Toronto and published in *Cultural Bioinformatics* (2016, SBEB).  
Authored by: Misa Florin, Christian Lopes, Dylan Fong, Mike Kusner, ... - Gary Bader

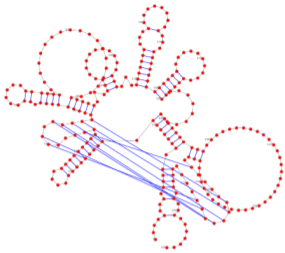
Demos ▾

- 0 Gds.js gene-gene graph
- 0 Large network
- 0 Node & cluster
- 0 iBGN cytoscape
- 0 Popper.js extension
- 0 Popper.js extension & Ego.js toolbar
- 0 Autocore extension

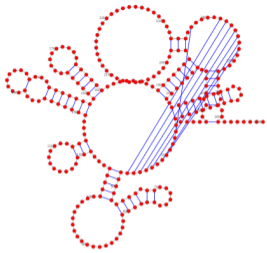
Circle



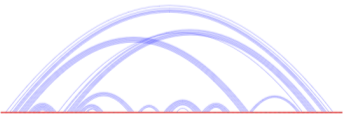
NAView



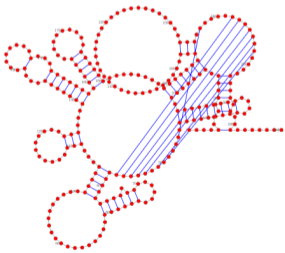
Radiate



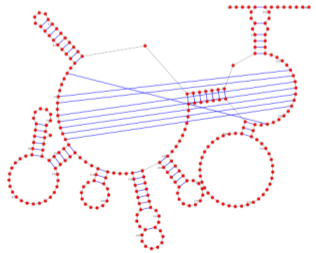
Line



Turtle

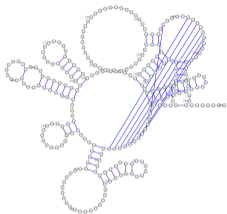


Puzzler

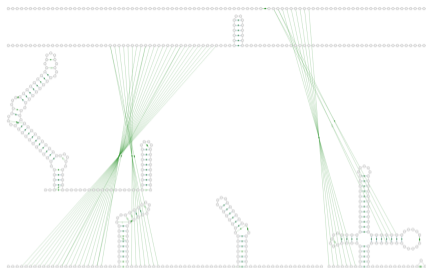


Cytoscape.js supports user-defined layouts

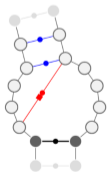
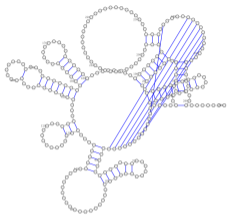
**RNA**



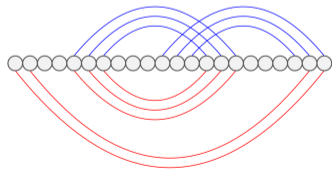
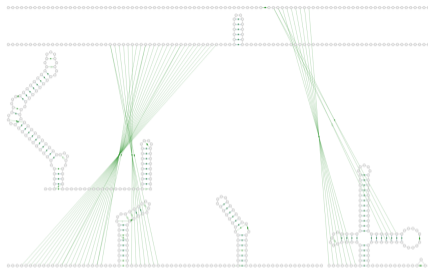
**Panel**



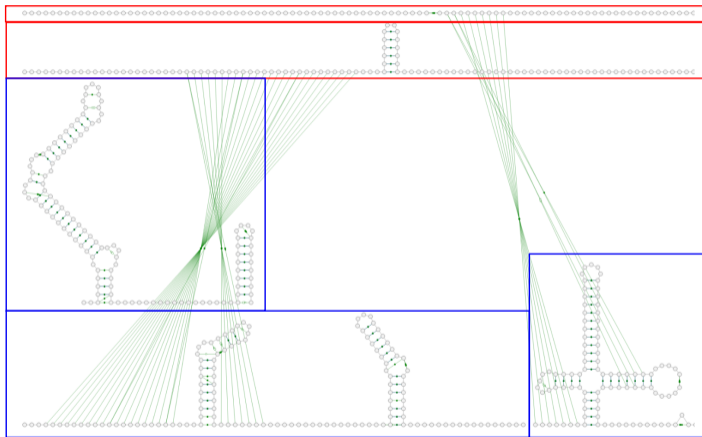
## RNA

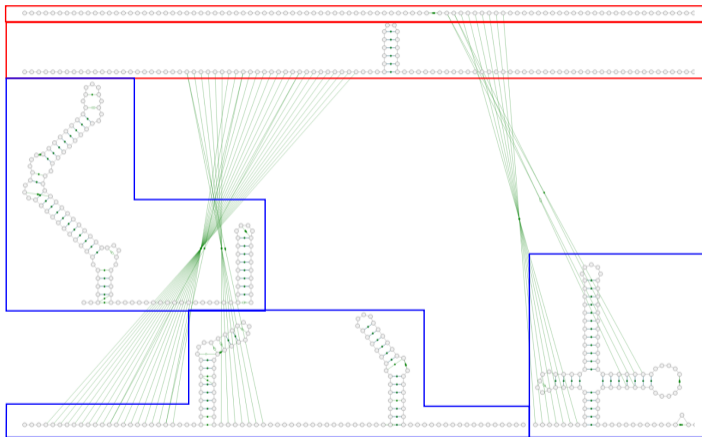


## Panel



# Multi RNAs drawing problem





## RNATETRIS

**Input:**  $N$  RNAs of different bounding box shapes (tetrominoes)

**Output:** Non-overlapped position of RNAs while minimizing

- 1 size of occupied area
- 2 inter-RNAs interactions distance

