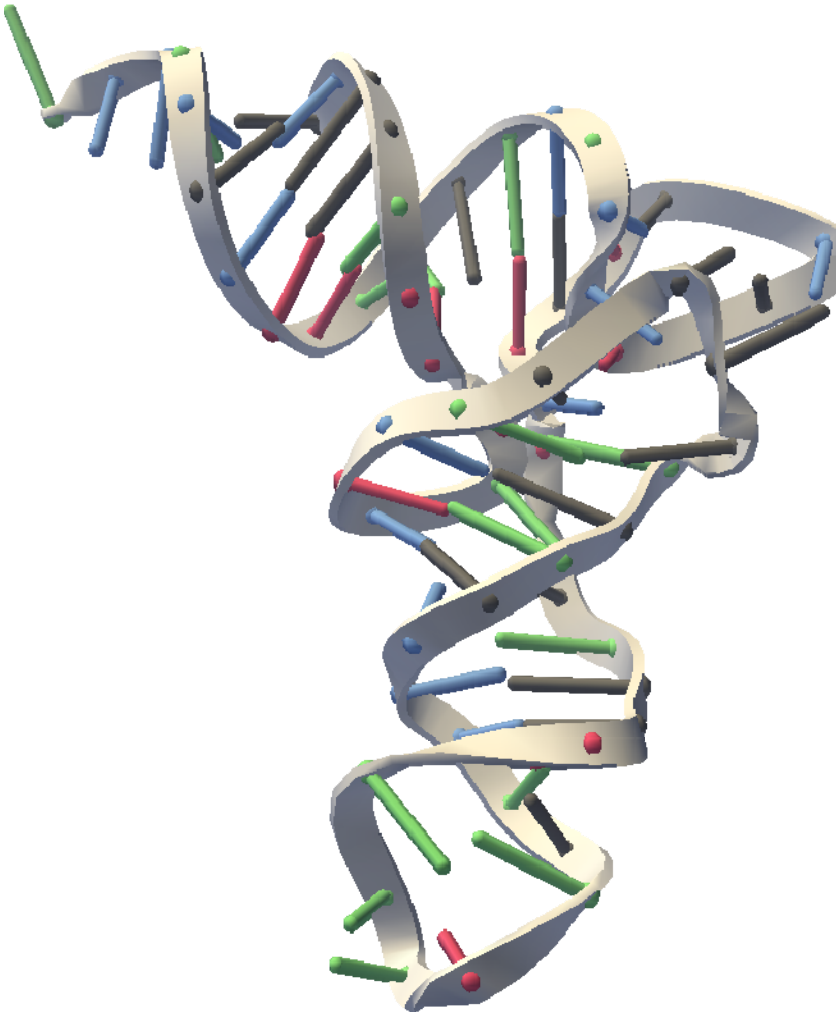
Tornado™



User's Manual

Release 0.10

January 4, 2007

Website: https://simtk.org/home/rna-viz-proto

Copyright and Permission Notice

Table of Contents:

Introduction

This document is a work in progress.

What is Tornado?

SimTK Tornado is a dynamic visualization tool for coarse grain (lumped) representations of RNA and/or protein structure. By shifting the focus from individual atoms to higher order structures, such as double helical duplexes, the scientist's attention is naturally focuses toward a larger scale. Biologists will be able to use their intuition to interactively refold RNA structures and produce morphs from one structure to another.

Purpose

Provides an easy to use application for animating and visualizing RNA and other macromolecular structures.

Audience

Biomedical and computation researchers interested in RNA, molecular motions, and folding pathways.

Installing and Running

System Requirements

Platforms: Windows, Mac, and Linux
Java 1.5 or higher required (http://java.sun.com/)

Java Web Start

Tornado uses Java Web Start to load and run directly from the download page at SimTK.org. The downloaded files are stored in a special area on your computer called the Java Web Start cache, so Tornado should start more quickly on the second and subsequent runs.

Download Application

1. Find the tornado project page at SimTK.org
2. Click on Downloads on the left side menu.
3. Click on Tornado jnlp file on the right side of the screen under Download Links.
4. ToRNAdo will begin to download automatically.
5. If a window saying **Warning – Security,** appears, "The application's digital signature has been verified. Do you want to run the application", click the **Run** button.
6. Wait a few seconds and the **SimTK ToRNAdo** application will appear.

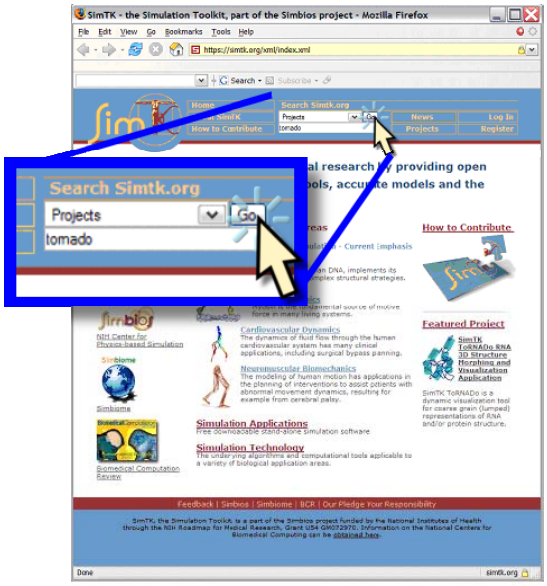


Figure 1 – Find the Tornado project at SimTK.org

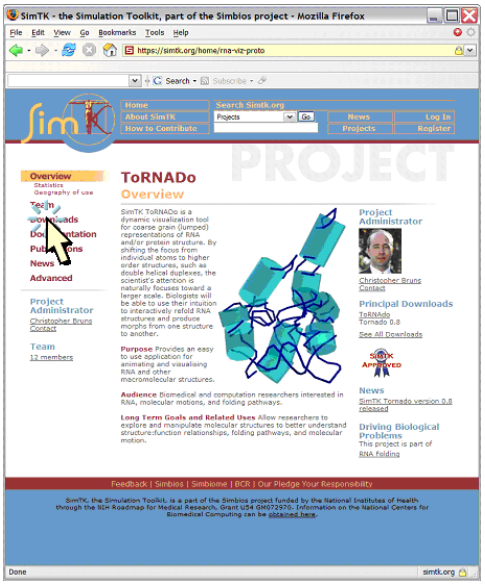


Figure 2 - Find the Tornado download link at the left of the Tornado project page

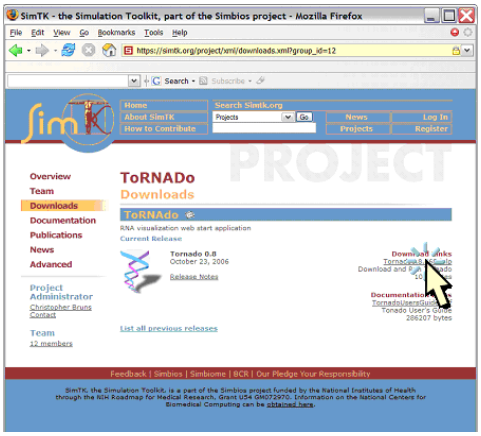


Figure 3 - Select the latest Tornado JNLP file at the right of the Tornado download page

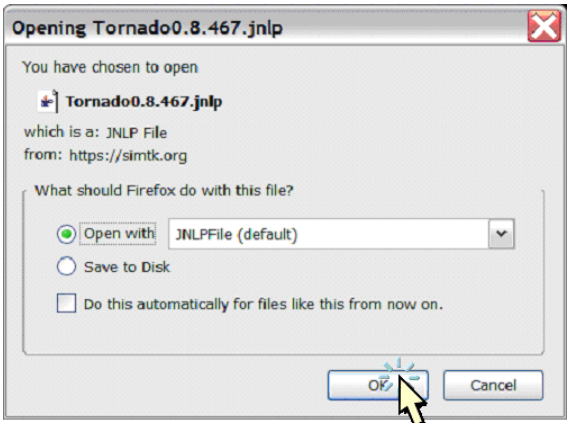


Figure 4 - Open the JNLP file with Java Web Start. If this does not happen automatically, you may need to install a recent release of Java on your computer.

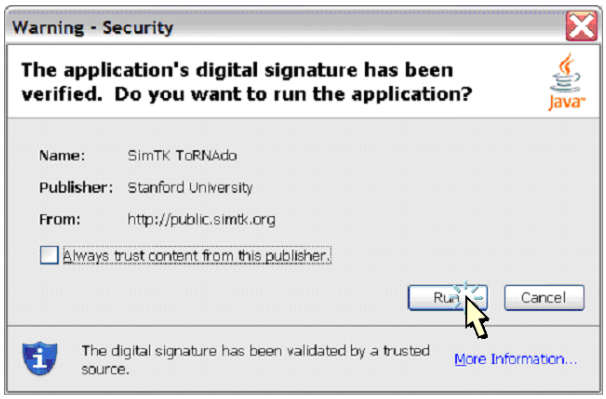


Figure 5 - Acknowledge the trusted digital signature on the Tornado application

Figure 6 - Acknowledge digital signatures on third party components

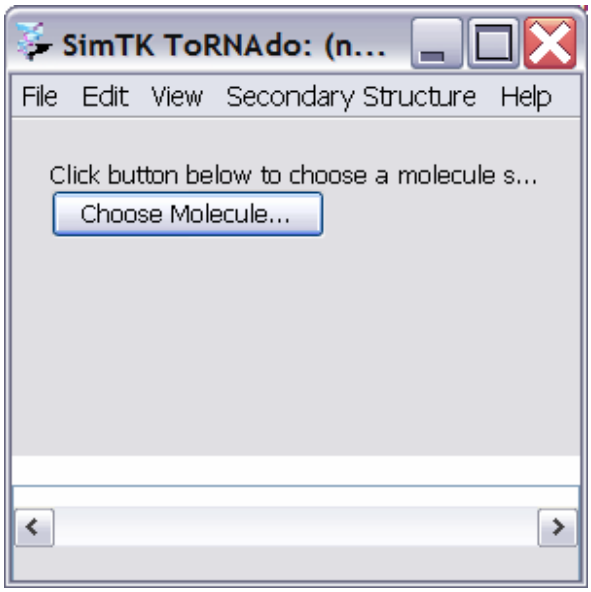
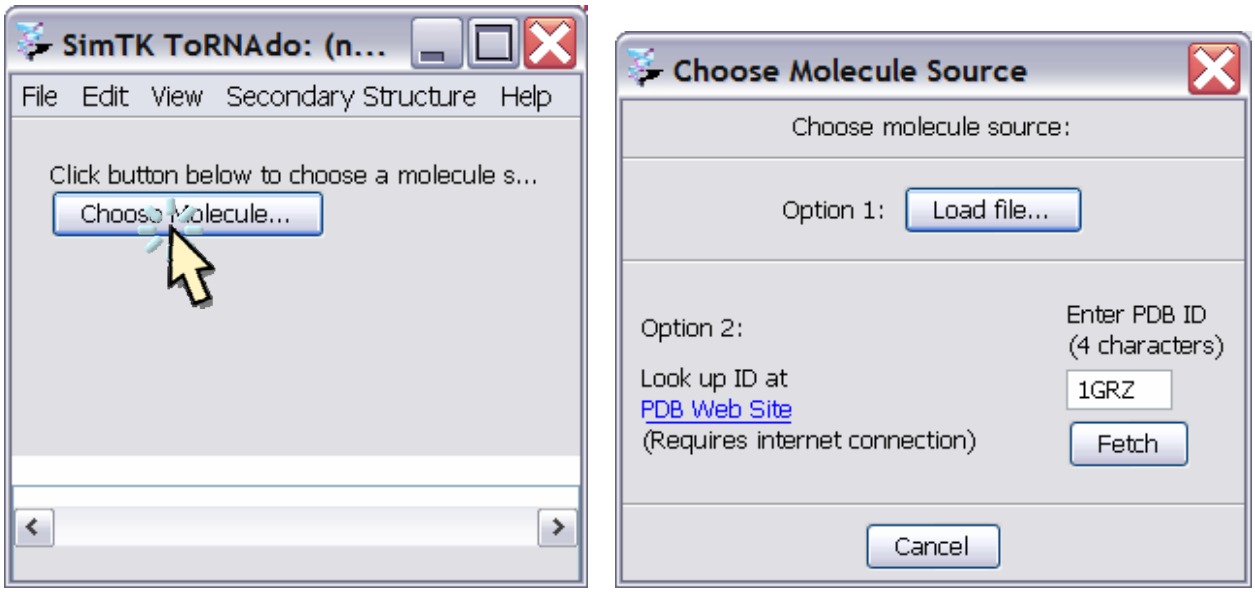


Figure 7 - The tornado application is now running on your computer.

Note: If you do not see the window in Figure 7, please consult the section "Troubleshooting Java Web Start" on page 9.

Tutorial

After downloading and running Tornado as described in the previous section of this document, you should see the Tornado application window, as shown below:



Loading Molecules

- Click on **Choose Molecule** button to choose a molecule structure.
- Option 1: click on the **Load file** button to choose a molecule saved locally.
- Option 2: enter the molecule ID (PDB ID) and click the **Fetch** button to load molecule from the PDB Web Site (requires internet connection).
- Molecule will appear on the screen with default view **Residue Balls**.
- To load a new molecule, go to the **File** menu and click **Load PDB Molecule** and choose option 1 or 2.

Change Molecule Views

- Go to the **View** menu, click on **Molecule Style**.
- A menu of various view styles will come up.
- Choose desired style. See the subsection “representations” under Molecular Visualization for more information.

Save Current Molecule View as an Image

- Go to the **File** menu, click on **Save PNG Image**.
- Under **File Name**, choose a desired name followed by **.png**
- Save the file in the desired location.

Rotating, Zoom In/Out Molecules

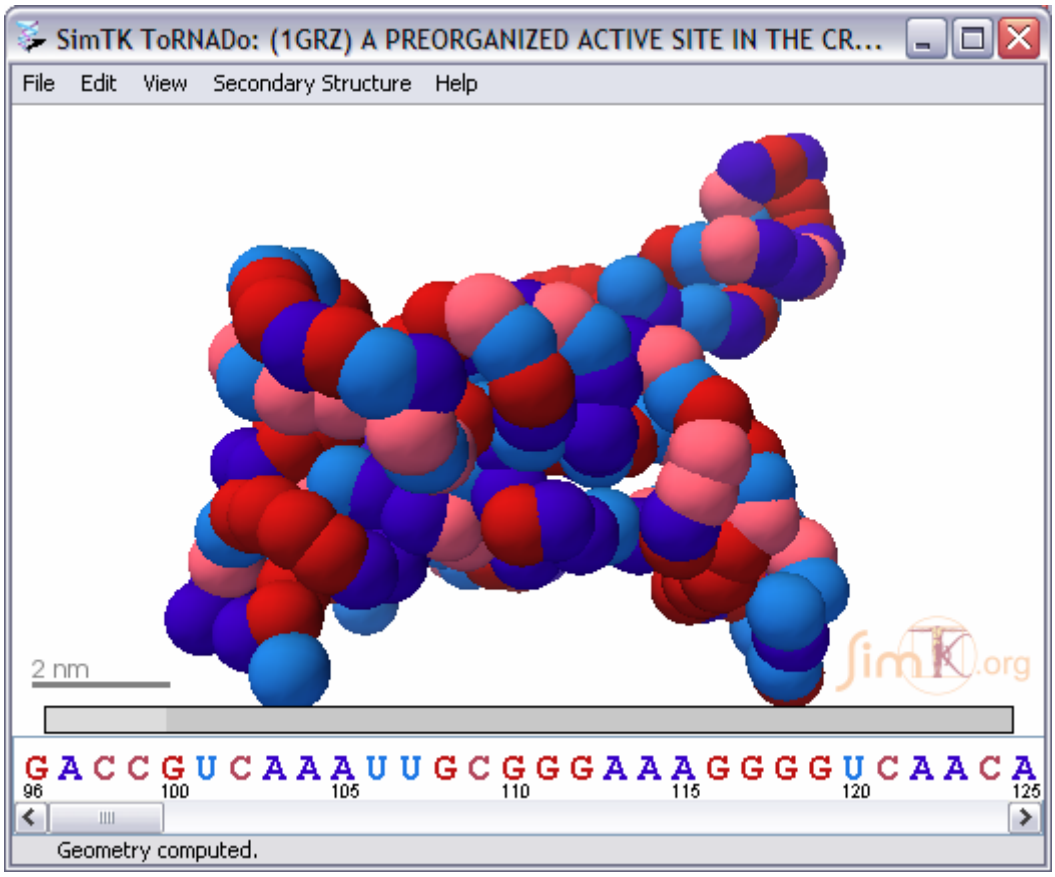
- Go to the **View** menu, click on **Rotation**.
- A menu of various rotation styles will come up.
- Choose desired rotation.

  Manual Rotation

  - Left click and hold the mouse on current screen.
  - Move up, down, left, right to rotate as desired.

  Zoom In/Out

  - Right click and hold mouse on current screen.
  - Move up or down to zoom in and out.



Molecular Visualization

Selecting residues

Select one or more residues to highlight those residues in the display.

The following mouse gestures apply to all molecule displays in Tornado, including the linear sequence display, 3D structure display, and secondary structure display.

- Click on a residue to select that residue
- Ctrl-click on a residue to add that residue to the list of selected residues.
- Double-click on a residue to center the display on that residue.
- Shift-click to add all residues between the most recently selected residue and the current residue to the list of selected residues.

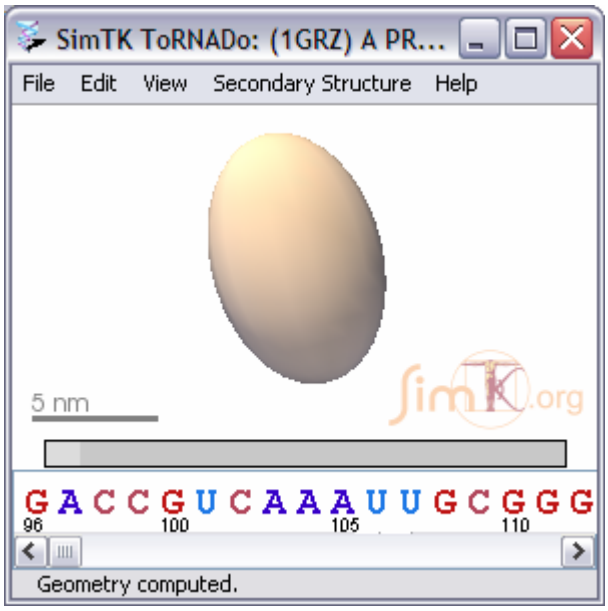
Representations

	RNA/DNA	Protein	Ligands	Water
Molecule Ellipsoids	ellipsoid	ellipsoid	ellipsoid	not shown
Molecule Blobs	blob	blob	blob	not shown
Secondary Structure ★	rope and cylinder	backbone	space filling	not shown
Residue Spheres	residue spheres	residue spheres	ball and stick	not shown
Ribbons	ribbon	ribbon	ball and stick	not shown
Bond Lines	lines	lines	lines	not shown
Atom Balls	atom balls	atom balls	atom balls	not shown
Bonds and Atoms	bonds and Atoms	bonds and Atoms	bonds and Atoms	bonds and Atoms

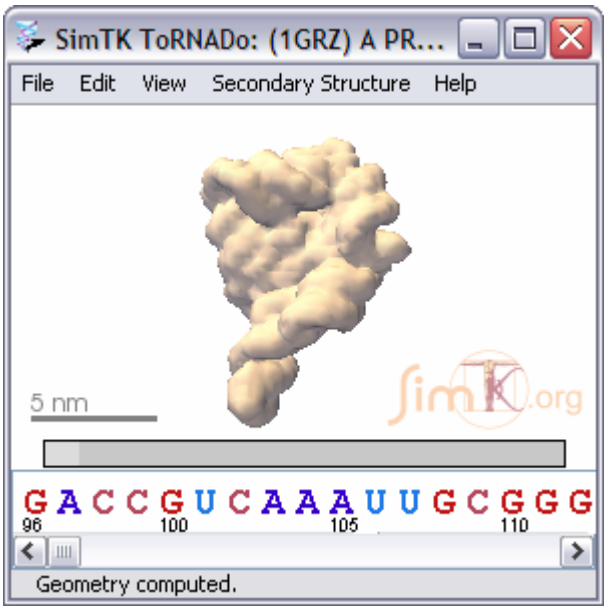
★ **Note: For the secondary structure representation to be shown – as seen below — you need to first select Secondary Structure > Compute Secondary Structure from the top menu**

Coarseness (Fineness) of representation

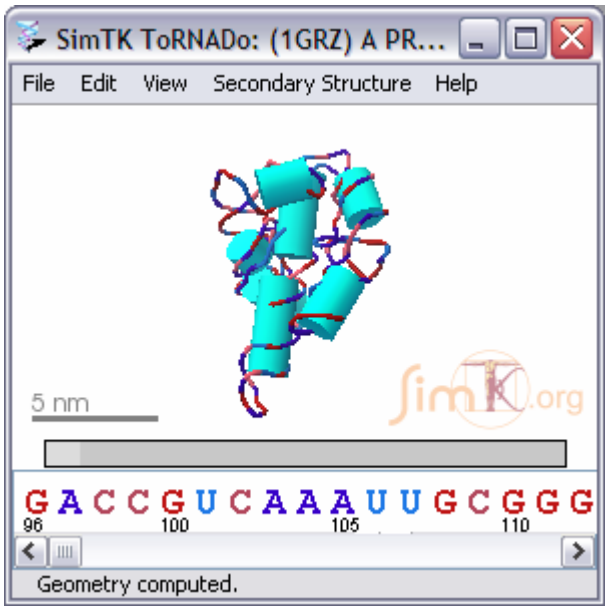
Molecule Ellipsoids



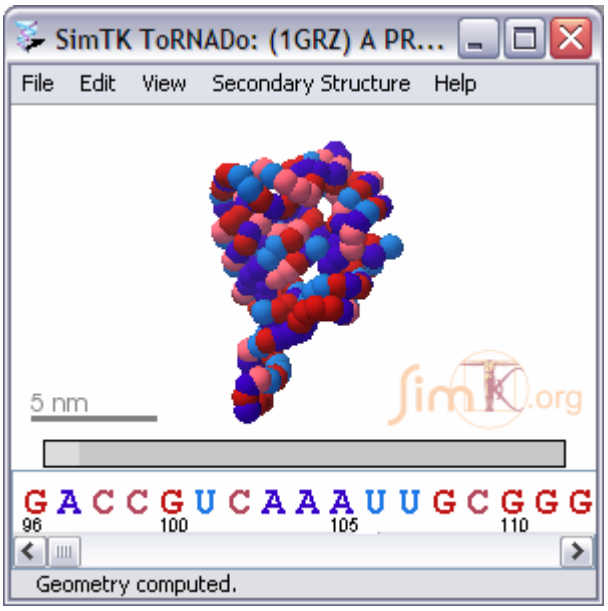
Molecule Blobs



Secondary Structure★

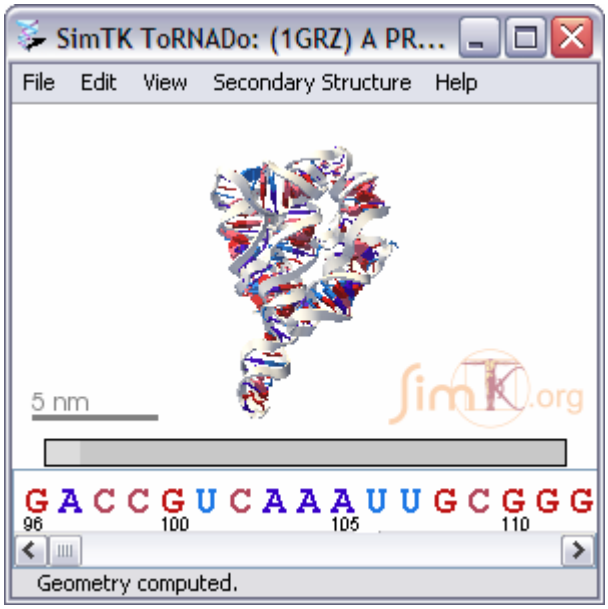


Residue Balls

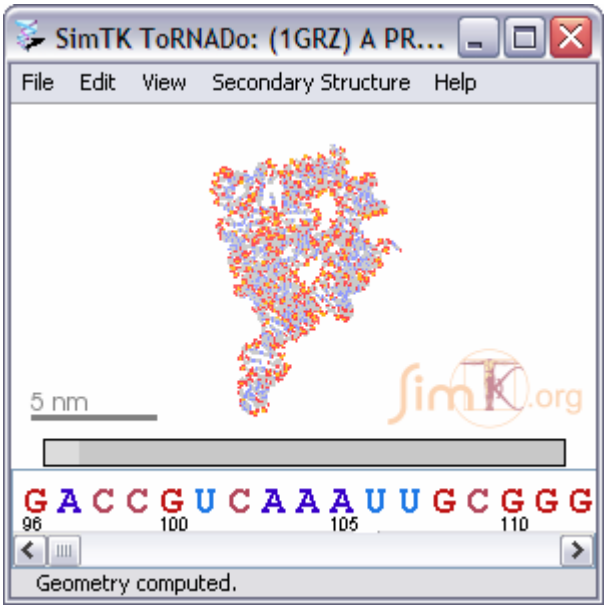


★ **Note: For the secondary structure representation to be shown – as seen above — you need to first select Secondary Structure > Compute Secondary Structure from the top menu**

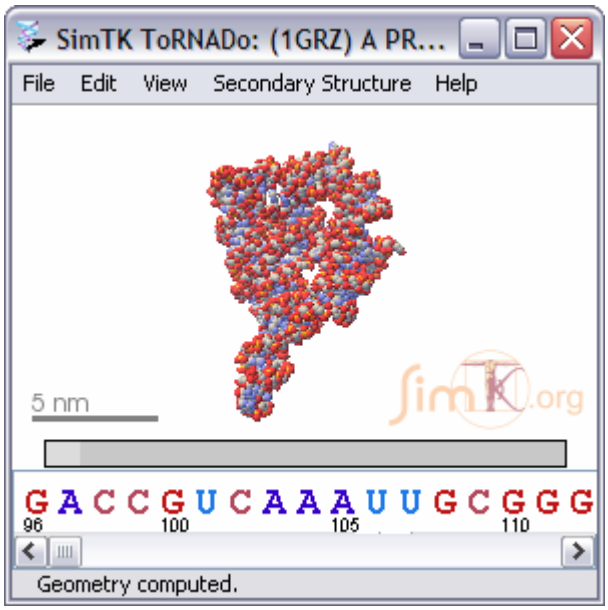
Ribbons



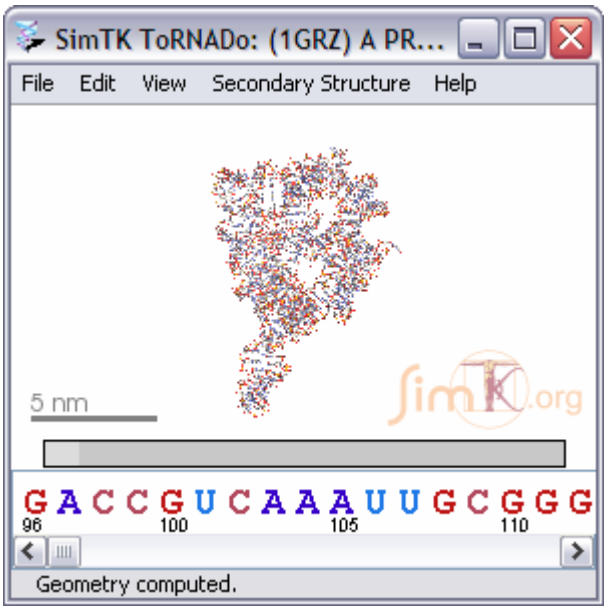
Bond Lines



Atom Balls



Bonds and Atoms



Nucleic Acid Secondary Structure – RNAML files

RNAML is an xml file format for descriptions of RNA structure. Examples of other applications that use RNAML format are RNAVIEW and MFOLD.

You can load an RNAML file for your structure and display the corresponding secondary structure. Select: "Secondary Structure > Load Secondary Structure File". You can leave "Secondary Structure > Secondary Structure Source > All" or switch to the choice corresponding to your RNAML file.
To view the secondary structure select: "View > Molecule Style > Secondary Structures".

To view the secondary structure computed by Tornado select: "Secondary Structure > Compute Secondary Structure", then "Secondary Structure > Secondary Structure Source > Tornado". Make sure "View > Molecule Style > Secondary Structures" is selected.

Saving An Image File of the 3D structure

From the menu bar, select "File"->"Save PNG Image".
At the right side of the file save dialog, you can adjust the image magnification, which permits you to save images at a higher resolution than you monitor can display.

Troubleshooting Java Web Start

If downloading stalls, it is possible that a problem is Java Webstart occurred.

Webstart is supposed to fetch the latest version of the program from the simtk server, but sometimes it does not update to the latest version. In this situation, you can get the latest version the next time you run by clearing the webstart cache.

PC Instructions --

Run Java Web Start by itself by typing "javaws" at the command line, or by finding and clicking Java Web Start on your system.

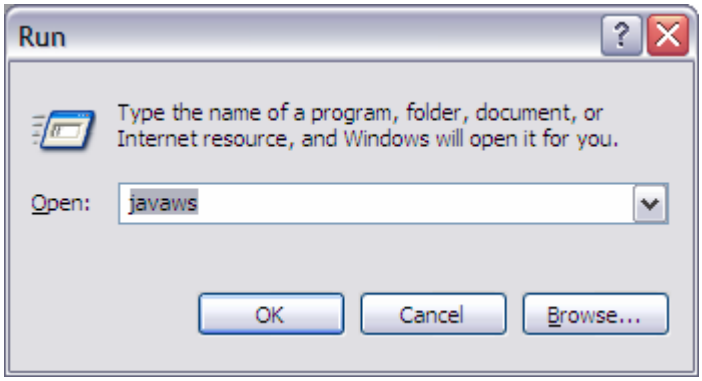


Figure 8: Command line window

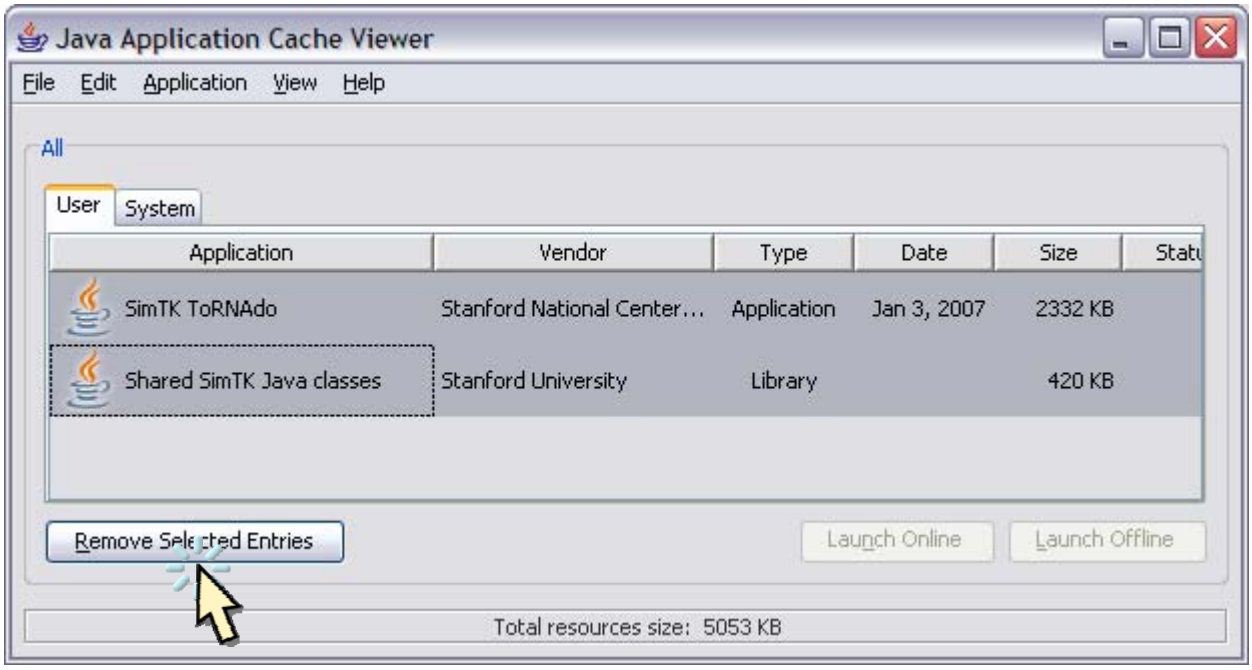


Figure 9: To force an update to the latest version of the program, run Java Web Start by itself, then remove the ToRNADo application and any Shared SimTK Java Classes from the application cache.

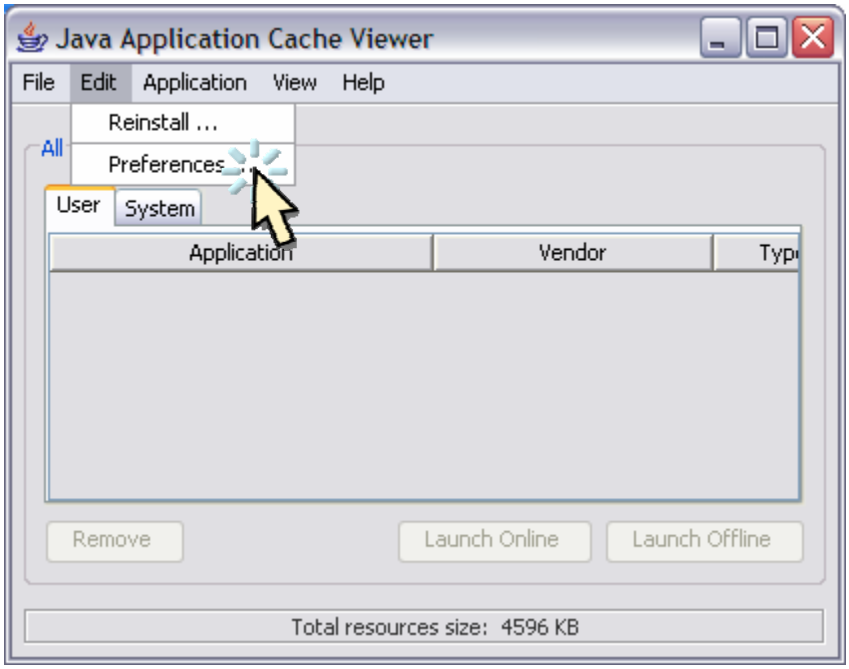


Figure 10: If the ToRNADo application is not shown in the Java Web Start Application Manager, you will be unable to remove just the ToRNADo application from the application cache. In this case, clear the entire application cache using the Preferences menu.

MAC Instructions –

Run Java Cache Viewer by typing "javaws" in a terminal window, or by finding and clicking Java Cache Viewer on your system, located in the Utilities > Java > J2SE folder which you can find as follows:

- Find the "Utilities" folder by going to the "File" menu, click on "Find" and type "utilities" on the search area.
- In the "Utilities" folder find the "Java" folder and expand it.
- In the Java folder select the J2SE folder
- Double Click on "Java Cache Viewer" to run the application.
- The "Java Web Start Application Cache Viewer" window will come up.

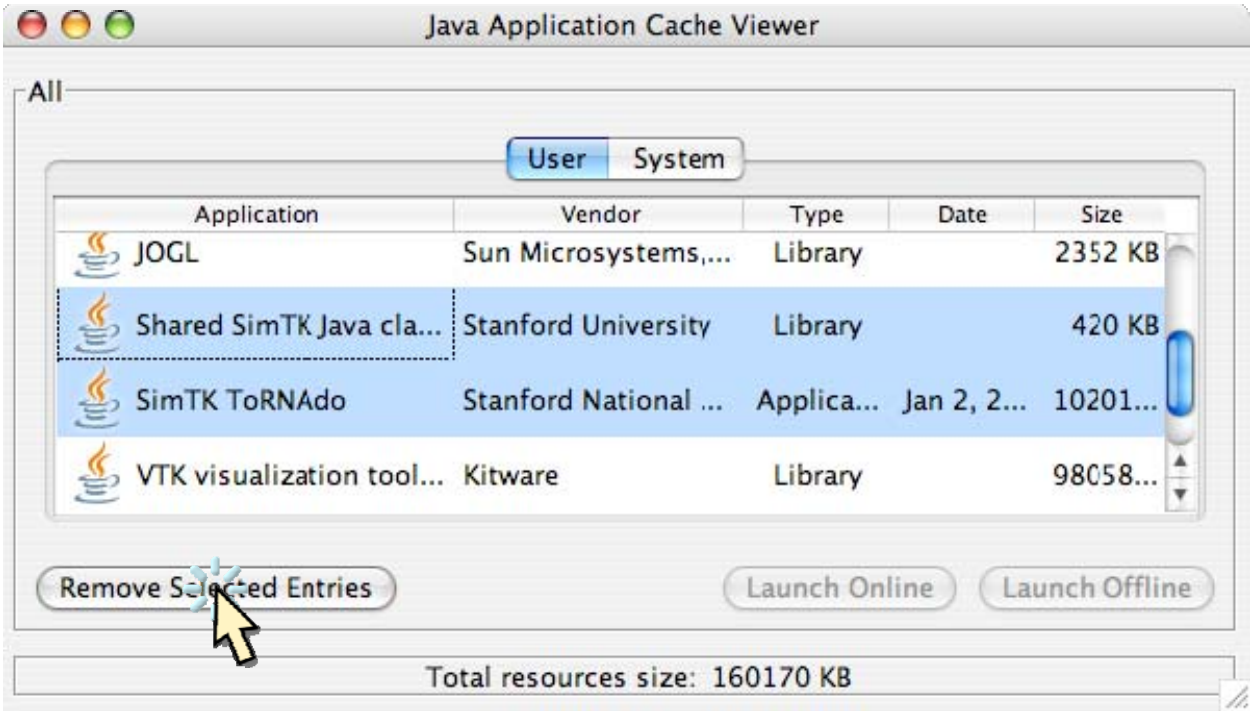


Figure 11: To force an update to the latest version of the program, bring up the Java Cache Viewer, and remove the ToRNADo application and any Shared SimTK Java Classes from the application cache.

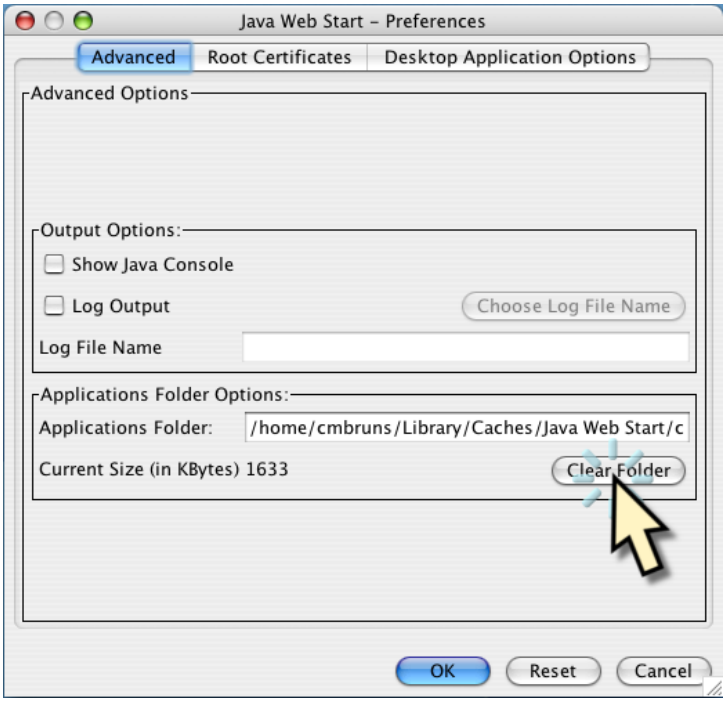


Figure 12: If you cannot find the ToRNADo application, you can clear all applications by running Java Web Start in Utilities > Java > Java Web Start and selecting Preferences from the top menu.

After Clearing the Java Cache reopen the jnpl file.

Submitting Problem Reports and Enhancement Requests

If you observe a problem with the Tornado program, or if you would like to request a new behavior in future versions of Tornado, please file a bug or feature report at SimTK.org. You can do this by selecting "Help > Report a program Problem (bug" or "Help > Request a new program feature" directly from the application.

You can also file a bug or request a feature from the Simtk.org site:

- Go to the ToRNADo project page (https://simtk.org/home/ rna-viz-proto), and select Advanced->"Features & Bugs". Then select "Bugs" or "Features" on the main screen and then select "Submit New" from the left menu.
- Fill in the report and click "Submit".

Thank you for helping us to improve Tornado.

References

[RNAVIEW] Yang, H., Jossinet, F., Leontis, N., Chen, L., Westbrook, J., Berman, H.M., Westhof, E. (2003). Tools for the automatic identification and classification of RNA base pairs. *Nucleic Acids Research* **31** (13): 3450-3460.

[MFOLD] M. Zuker, D.H. Mathews and D.H. Turner Algorithms and Thermodynamics for RNA Secondary Structure Prediction: A Practical Guide in RNA Biochemistry and Biotechnology, J. Barciszewski and B.F.C. Clark, eds., NATO ASI Series, Kluwer Academic Publishers, (1999)