



User's Manual

Release 0.8

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Website: <https://simtk.org/home/rna-viz-PROTO>

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Table of Contents:

Table of Contents:.....	3
Introduction.....	4
What is Tornado?.....	4
Purpose.....	4
Installation.....	4
System Requirements.....	4
Troubleshooting Java Web Start.....	4
Molecular Visualization.....	5
Representations	5
Coarseness (Fineness) of representation	6
Molecule ellipsoids.....	6
Molecule blobs.....	6
Secondary structure	6
Residue spheres.....	6
Ribbons.....	6
Line Drawing.....	6
Space-filling atoms.....	6
Ball and Stick.....	6
Nucleic Acid Secondary Structure – RNAML files.....	6

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.

Installation

System Requirements

Platforms: Windows, Mac, and Linux

Java 1.5 or higher required (<http://java.sun.com/>)

Troubleshooting Java Web Start

If downloading stalls, try the following:

1. Click "Cancel", and reopen the jnlp file.
2. If it still fails, clear the Java Web Start cache, and try opening the jnlp file again.

Molecular Visualization

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
Ball and Stick	ball and stick	ball and stick	ball and stick	ball and stick

Coarseness (Fineness) of representation

Molecule ellipsoids

Molecule blobs

Secondary structure

Residue spheres

Ribbons

Line Drawing

Space-filling atoms

Ball and Stick

Nucleic Acid Secondary Structure – RNAML files