**KnotPlot**

KnotPlot web page: <http://knotplot.com>

Knotplot download page: <http://knotplot.com/download/>

KnotPlot Bulletin Board: <http://knotplot.com/phpBB/>

Note: Commands listed below in bold can be used in the KnotPlot command window. Other commands use the KnotPlot Control Panel.

Entering knots/links/tangles into KnotPlot:

1. Load knot

Use second row (A – F) to load link from a zoo of knots/links.

Use Command Window.

Ex: **load 3.1** (not 3\_1)

Ex: **load 3.1\*** (for mirror image of 3.1)

1. Sketch it (Sketch Panel).
   1. Sketch beads one at a time. Left click for under, right click for over.
   2. Sketch continuously by clicking and dragging a path for alternating knot.
   3. Use edit panel to change crossings and other modifications.
2. Use Dowker-Thistlethwaite code

Ex: **diagram 4 6 2**

Note the Dowker code is the SAME for a knot and its mirror image.

Can use the sketch panel to get the mirror image by reflecting in the x, y, or z direction or

In command window: **reflect x reflect y reflect z**  
reflections can be concatenated: **reflect xz**.

Ex: **diagram -10 16 28 20 18 -30 22 -6 2 8 24 14 12 4 26**

Note the DT code demo listed under the Demo A panel-- see last (i.e 5th) row, last column, under Knot Theory.

DT code: Travel around knot numbering each crossing as you encounter it. Thus each crossing will receive two numbers. Note that at each crossing an even number is paired with an odd number (why?). If the knot has n crossings, we obtain a bijection f: {1, 3, …, 2n-1} 🡪 {2, 4, …, 2n}. To obtain the DT code of the knot take the sequence f(1) f(3) … f(2n-1) and add negative signs to f(i) if f(i) corresponds to an undercrossing (ie, the undercrossing is even).

1. Load file containing coordinates.

Ex: **load file.txt**

Note the above file was created by taking the protein coordinates for 1FLO (Flp recombinase) from <http://www.ncbi.nlm.nih.gov/protein>

1. For tangles, use tangle calculator under TopoICE Panel or use command window.

To delete a tangle from the stack use stack operator **~**

Ex: **tangle 321o.**

For a rational knot: tangle 321oN

Note the rat tang demo listed under the Demo A panel -- see 3rd row, last column, under Knot Theory.

1. Cons panel can be used to create torus knots, Lissajous knots, chains, and braids.

Click on help for more information. Note the help button is very useful in most panels.

You can also type in braid words to the KnotPlot Command Window, a tutorial is in the PDF file [http://knotplot.com/software/ex2.pdf](http://knotplot.com/software/ex2.pdf" \t "_blank) The PDF refers to a demo that no longer exists (or is different), but the info on typing in a braid word is still valid.

To save a knot:

**save filename** saves in KnotPlot format

**save filename ascii** or **save filename raw** saves readable file of coordinates

Note KnotPlot files are saved in the KnotPlot folder.

In Windows 7, there are two KnotPlot folders: C:\Program Files (x86)\KnotPlot,

C:\Users\your user name\AppData\Local\VirtualStore\Program Files (x86)\KnotPlot

KnotPlot saves files into the second KnotPlot folder.

Simplifying diagrams (Dynamics panel and Main panel)

Click go.

Select no collide if you want to preserve knot type.

To make small changes:

Use anchors.

In command window : **ago n** where n is the number of steps.

Ex: **ago 200**

If knot becomes stuck, change stusplit to nonzero value (slider near bottom of Main panel—check out smooth tubes vs beads and cyls buttons near middle of Main panel).

Export Figures:

Use Export Panel or see Postscript examples at <http://knotplot.com/postscript/>

To view the postscript file on a PC, you may need ghostview

<http://pages.cs.wisc.edu/~ghost/doc/GPL/gpl864.htm> (near end of page)

and GSview: <http://pages.cs.wisc.edu/~ghost/gsview/get49.htm>

**Alternatively, you can copy it into a power point slide.**

Comp panel: This panel will allow you to calculate several knot invariants as well as diagram invariants. The HOMFLY polynomial calculator in KnotPlot using the **homfly** command is buggy, it may crash for knots with nugatory crossings.

Note there is a non-graphics version of KnotPlot. One can write programs which call KnotPlot. A tutorial for this will be available this Spring.

TopoICE in KnotPlot: Solves tangle equations

TopoICE-X models topoisomerase action. In addition to solving tangle equations, TopoICE-X also finds distances between knots.

References: 3D visualization software to analyze topological outcomes of topoisomerase reactions, I. K. Darcy, R. G. Scharein, and A. Stasiak, Nucleic Acids Res. 2008 June; 36(11): 3515–3521.

Manual: <http://nar.oxfordjournals.org/cgi/content/full/gkn192/DC1>

TopoICE-R models recombinase action.

Reference: TopoICE-R: 3D visualization modeling the topology of DNA

recombination, Isabel K. Darcy, Robert G. Scharein, Bioinformatics, Vol. 22

no. 14 2006,1790–1791

<http://bioinformatics.oxfordjournals.org/cgi/reprint/22/14/1790>

Manual: <http://www.knotplot.com/download/TopoICE-Rmanual.pdf>

Examples: <http://www.knotplot.com/download/TopoICE-Rexamples.pdf>

**TangleSolve:** Solves tangle equations modeling recombinase action. <http://bio.math.berkeley.edu/TangleSolve/>

Reference: TangleSolve: topological analysis of site-specific recombination. Saka Y, Vázquez M, Bioinformatics. 2002 Jul;18(7):1011-2. <http://bioinformatics.oxfordjournals.org/cgi/reprint/18/7/1011>

Tangle Model : <http://bio.math.berkeley.edu/TangleSolve/tmodel/frames2.htm>

Tutorial: <http://bio.math.berkeley.edu/TangleSolve/tutorial.html>