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)

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

3.) 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).

4.) 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

5.) 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.

6.) 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   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).

<u>Export Figures:</u>

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.

<u>Comp panel</u>:   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.

<u>TopoICE in KnotPlot: Solves tangle equations</u>

<u>TopoICE-X</u> 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

<u>TopoICE-R</u> 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

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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