

NATuG User Manual

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1 Getting NATuG Running

NATuG is a desktop application supported by Mac, Windows, and Linux. This section covers how to download the latest version of NATuG, the needed libraries, and then compile and run the program. Eventually NATuG will offer pre-compiled and pacakged versions, but that is not currently the case.

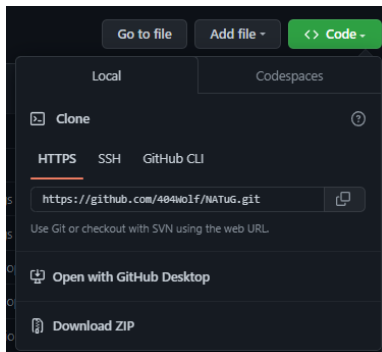


Figure 1: Github code download menu

1. Visit www.python.org/downloads, and then install the most recent version of Python for your operating system. NATuG has been confirmed to work on versions up to Python **3.11.1**.
2. Go to the github.com/404Wolf/NATuG, click the green “code” button, and then click “download ZIP.” See Figure 1.
3. Open your computer’s terminal/console/command prompt. Enter the following commands, in the following order.
 - (a) `cd <filepath>` to enter the directory of the project.
 - (b) `python -m venv venv` to create a virtual environment for the needed libraries to go into.
 - (c) `venv/Scripts/activate` if you are on windows, or “source myenv/bin/activate” if you are on Mac/Linux, to enter into the virtual environment. You will know that you have successfully entered the virtual environment if the current line in terminal begins with “(venv).”
 - (d) `python -m pip install -r requirements.txt` to automatically install all the needed libraries. They may take a while to download.
 - (e) `python -m launcher` to run the program. The first launch may take a bit while the code compiles.
4. You should now be in NATuG! When running the program in the future, simply CD into the folder (step 3a), enter the virtual environment (step 3c), and run the program (step 3e).

2 Quickstart

Constructing a DNA nanotube is a complex, multi-stage process, but NATuG streamlines the steps. However, NATuG also provides a high level of customizability and advanced features that can feel overwhelming at first. Here, you will find a list of things to do that should help you gain a basic level familiarity with NATuG. Each step in this section is designed to provide an exploration opportunity for NATuG’s various a core features, in order of how you would generally go about designing a DNA nanotube.

Disclaimer: The below tasks are by no means comprehensive, and are meant to serve as a simple introduction to the program.

2.1 Running NATuG

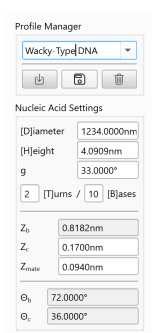
First, go to Section 1 and follow the instructions to get NATuG running. Once NATuG is running, proceed to section 2.2.

2.2 Nucleic Acid Selection

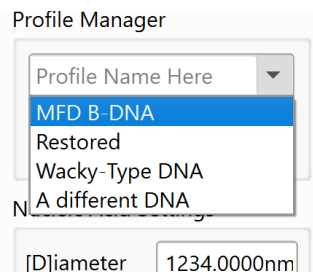
Summary For this step, you will begin to gain familiarity with the Nucleic Acid Tab of the Config Panel (for more information about the Config Panel, see section 4).

Instructions On the right side of the screen, in the config panel, you will find the Nucleic Acid settings tab. This is the area in which settings for the geometry of your DNA. While most of the time you will use NATuG's default provides for DNA settings, now is a good time to experiment with the different inputs. As you change the different settings, also look at the bottom of the NATuG's window—the Status Bar—when hovering over them. It should display a brief explanation of what the different settings actually are. Observe the Side View Plot and Top View Plot change as the settings update.

Figure 2: Experimenting with Nucleic Acid settings



(a) Tinkering With Nucleic Acid Settings



(b) Loading different Nucleic Acid profiles

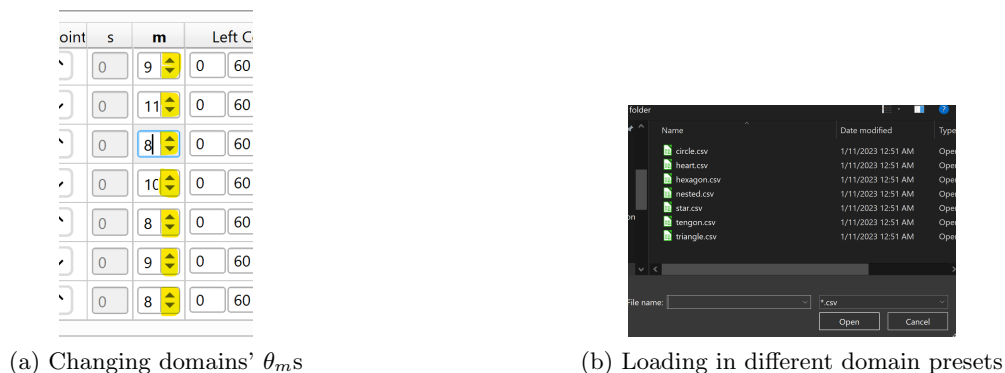
2.3 Domain Adjustment

Summary For this step, you will experiment with adjusting the shape of the nanostructure by tinkering with NATuG's presets.

Instructions In the Config Panel (4) on the right side of the screen, switch to the Domains tab. The panel will pop out because of the required width of the tab. The panel may appear intimidating at first, but here we are just going to focus on changing the interior angles of the domains. Start by clicking the up and down arrow buttons next to the “m” of each domain. As you do, watch the Top View Plot update in real time. By increasing/decreasing the “m” values, the interior angles of domains will change, which will in turn change the shape of the tube. You can type numbers directly into the boxes, but without correcting for changes with other domains' angles, the tube will open up. Notice how when the tube is closed the M/R box in the symmetry section of the tab lights up green.

Loading Presets In the settings area above the domains table, click the load button (the button that has an arrow pointing downwards into a box). Choose a different set of domains, for instance, “nested.csv.” As you play around with this section of NATuG, you can use the save button to save your own designs/your adjustments to the default designs.

Figure 3: Changing up domain settings



2.4 Junction Creation

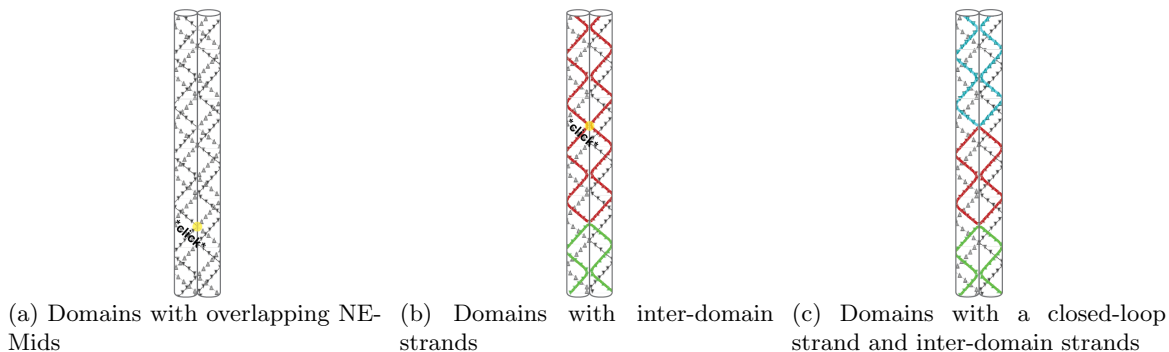
In the Side View Plot—the main area of NATuG—locate two white triangles (which represent the midpoint between two nucleosides, and are called “NEMids”) that are overlapping, and click on them. This will transform two helices of two different domains into two helices that traverse both of the domains. Continuing clicking on overlapping white triangles to weave together strands. See Figure 4 for a visual example.

2.5 Nicks, Linkages, and More

summary Here, you will begin to experiment with additional Side View Plot modes, and will learn to create nicks in strands, linkages across strands, and more.

Instructions You just experimented with creating junctions, but the Side View Plot mode that creates junctions (“junctor” mode) is one of many modes. The “mode” of the side view plot dictates what happens when you left click points within the side view plot. To try out other modes, go to the top of the window, where you see a list of different buttons (“Informer,” “Junctor,” “Nicker,” etc.), and click on different modes. Then left click on points within the main plot. Below is a list of (very) simplified descriptions of the different modes and how to get started using them.

Figure 4: Creating cross-strand junctions



1. **Informer Mode:** Obtain information about points. To use, click on any point.
2. **Junctor Mode:** Redirect strands across helical domains. To use, click on any two overlapping white triangles.
3. **Nicker Mode:** Split strands in half. To use, click on any point.

Figure 5: Advanced NATuG features

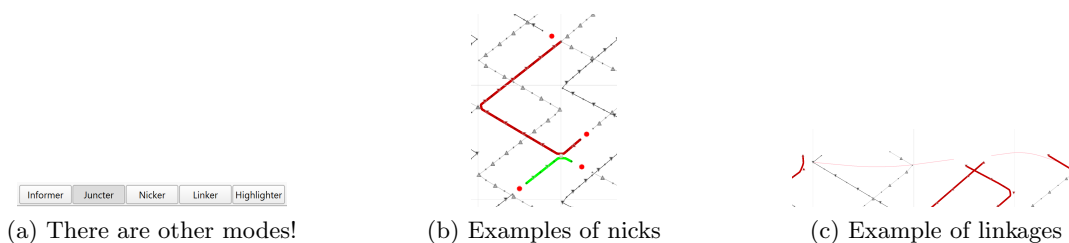
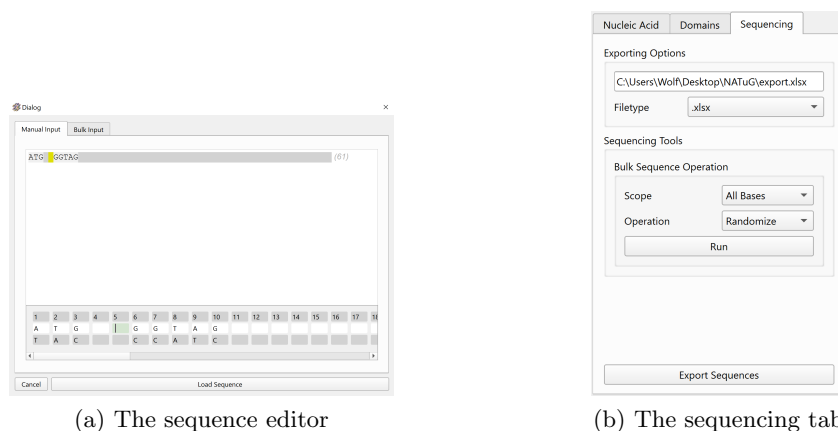


Figure 6: Sequencing capabilities



4. **Linker Mode:** Link the ends of two strands together to make one bigger strand. To use, click on one point that is at the end of a strand, and then another point that is at the end of a strand. Make sure that the arrows do not point towards each other.
5. **Highlighter Mode:** Highlight points. To use, click on any point.

2.6 Sequences

Summary In this step, you will explore NATuG’s sequencing potential by applying sequences to strands and viewing the nucleosides of strands. You will get to use NATuG’s Sequence Selector for the first time, too.

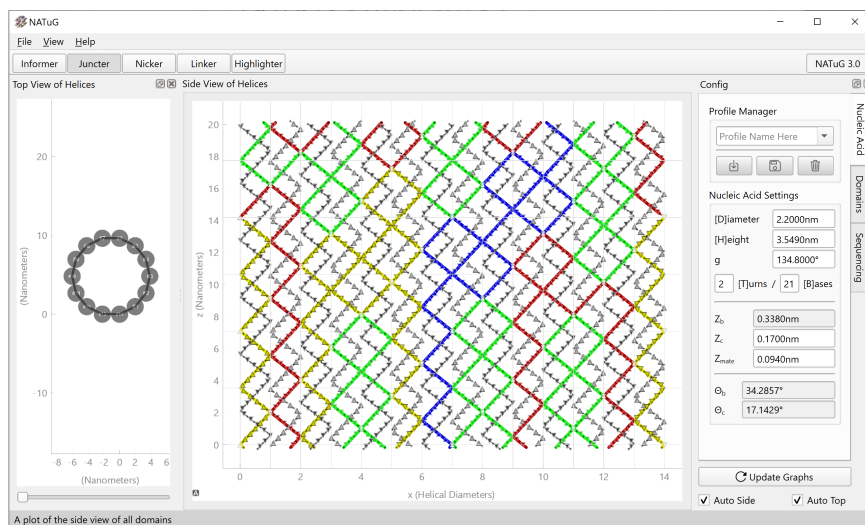
Instructions In the Config Panel, go to the “Sequencing” Tab. When you change to the sequencing tab (figure 6b), the Side View Plot will automatically update to display actual nucleosides instead of the midpoints between the nucleosides. Currently you will only see arrows representing the nucleosides, but this is because you have not yet set the bases of the nucleosides. To set the bases of the nucleosides, click on one of the lines (not a point)—also known as a strand—and a Strand Config dialog should pop up. Click the “load sequence” button, and manually enter random “A”s, “T”s, “G”s, or “C”s to fill up the editor. When you click the “Choose Sequence” button when you are done, the strand will no longer display its points as arrows; rather, there will be letters.

3 Program Layout

Summary In this section, you will learn about the overall layout of NATuG. Various different user-interface elements (such as “panels”) show up in multiple places, and have commonalities in how to interact with them that are expounded in this section.

Breakdown NATuG’s interface consists of a main hub area, surrounded by two panels. There is a status bar at the bottom of NATuG, which provides helpful descriptions of what various buttons and input boxes do as you hover over them, and a file bar at the top of NATuG, which provides access to various cross-program functions.

Figure 7: The overall layout of NATuG



3.1 Panels

NATuG has two panels: the Top View Panel and the Config Panel. Though the contents of panels differ, they do share various important properties, listed below.

1. Panels are all undockable. By clicking twice on the top area of a panel, or by dragging the panel away from the main window, or by clicking the small middlemost icon in the top right button, one can make a panel become its own window. To redock, click on the top of the panel twice, or drag the panel back into the main window (sometimes the latter can be a bit finicky, but the former should always work).
2. Panels are hideable. By clicking the “x” button in the top corner of a panel, or by going to the file menu, “view,” and then the name of the panel you are trying to hide, you can hide the panel. To unhide a panel, go to the file menu, “view,” and then the name of the panel you are trying to unhide.
3. Some panels are resizable. If a panel is resizable when it is docked, you will see three very small circles in the middle between the panel and the Hub. To increase/decrease the size of the panel, drag from the intersection to/away from the Hub. If a panel is undocked, even if it was not originally resizable it may become resizable when it becomes undocked.

3.2 Hub

NATuG’s main area, the “hub,” is another name for the area of the program where the Side View plot is located.

3.3 Toolbar

Located directly above the Hub is the toolbar, where you can select the current mode of NATuG. Each mode changes what a left click does in the Side View plot. The modes are explained in more detail in section ???. Only one mode can be selected at a time, and one mode will always be active. In some cases, depending on the current tab that the Config Panel is in, certain tabs may be restricted (i.e. you cannot choose them,

and you will be kicked back to “Informer” mode). This is because you cannot perform certain actions on nucleosides, such as junctions; so, the actions are made unavailable.

3.4 File Menu

The file menu contains general, program-wide actions for NATuG, such as accessing this very manual (under “help→manual”). It is essentially an organized list of buttons in a “tree” structure, which are explained in further detail at 3.4.1. On Windows and Linux machines, the File Menu will be on the top of the window itself. On Macs, the File Menu will always be at the very top of the screen.

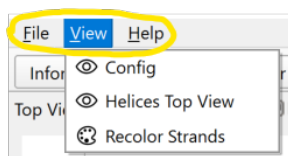


Figure 8: The file menu

(a) In the screenshot view submenu is expanded.

3.4.1 Breakdown

Herein lies a breakdown of what the various buttons of the File Menu do, and their respective keyboard shortcuts (if they have any).

File The file submenu contains functions pertaining to file and save management.

Open (`control+o`) Open a save. This will create a dialog prompting you to choose a file ending with `.nano` that is a save created via the File Menu’s “save” function.

Save (`control+s`) Create a save of the current state of the program. This will create a dialog prompting you to choose a location and a file name to create a save at. If you enter a file name that has an extension of anything other than `.nano`, or you do not specify a file extension, `.nano` will always be the file extension.

View The view submenu contains functions pertaining to the user interface itself.

Config Hide the Config Panel if it is currently being displayed, or display it if it is currently hidden.

Helices Top View Hide the Top View Plot if it is currently being displayed, or display it if it is currently hidden.

Recolor Strands Rerun the strand coloring algorithm. For more information on what this entails, see section ??.

Help The help submenu is for seeking additional information about NATuG.

About Obtain information about NATuG. This creates a popup with text that briefly explains what NATuG is.

Manual (`control+h`) Open the user manual. This will open a web browser that takes you to this very PDF. The web browser will be your system default web browser, and NATuG will simply create a new tab.

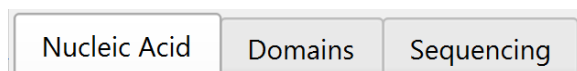
Github Open NATuG’s Github Page. The Github page is where the actual codebase for the program is, and is where the entire history of the development of the program can be found. The web browser will be your system default web browser, and NATuG will simply create a new tab.

4 Config Panel

The Config Panel contains most of the user input areas of NATuG. Within the panel are three primary modes: “Nucleic Acid,” “Domains,” and “Sequencing,” outlined in greater depth on the following pages.

To navigate between panels of the config panel, simply click on one of the tabs. Below are brief descriptions of the various tabs; however, each tab has a dedicated page as well.

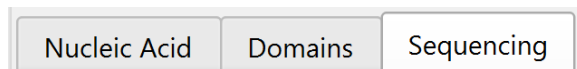
Warning: changing settings within the config panel will reset all current junctions, nicks, links, and highlights. Attempting to change settings when there exist any junctions, links, or highlights will result in a popup dialog that offers to save the current state of the Side View Plot and then refresh the plot, refresh the plot without saving, or cancel the attempted refresh.



The Nucleic Acid Tab is where one can customize the geometrical settings of the nucleic acid that they are creating a nanotube for. This defaults to B type DNA, and generally does not need to be changed.



The Domains Tab is where settings for the interior angles, strand switches, and the number of NEMids to generate are inputted. This section allows the user to actually define the shape of the nanotube.



The Sequencing Tab is where the user can apply bulk sequence actions to all the strands, and export sequences to a spreadsheet for synthesis. This is generally one of the later steps in the nanotube design process.

4.1 Graph Updating

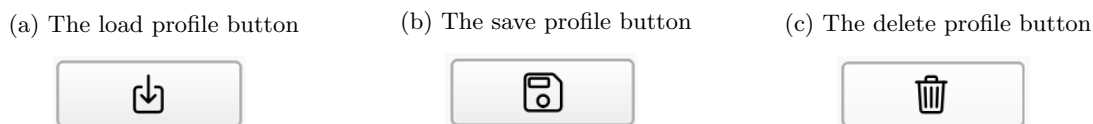
By default, as changes are made within the various tabs of the Config Panel (section 4) the Side View Plot and Top View Plot automatically update. To disable automatic updating for either plot, click either of the “Auto Side” or “Auto Top” buttons on the bottom of the Config panel. When automatic updating is disabled, the “Update Graphs” button must be clicked to refresh the plots, or you can use the keybind **control+u** (“u” for Update). Manual updating can be useful for larger structures that take a long time to load.

The current tab of the Config Panel (section 4) determines what is currently plotted in the Side View Plot. When the current tab is either “Nucleic Acid” or “Domains” NEMids are plotted, and the mode of the Side View Plot is unrestricted. However, when “Sequencing” is active, nucleosides are plotted. When this is the case, only the “highlighter” and “informer” modes are enabled within the Side View Plot’s toolbar.

4.2 Nucleic Acid Tab

The Nucleic Acid Tab is the area in which all geometrical settings for the nucleic acid being used can be entered. All of NATuG’s computations utilize these constants, so only make changes if you know what you are doing. This tab contains a profile manager for easily loading in sets of settings, and has various fields that warrant extended descriptions. When using NATuG, recall that hovering over fields will show additional

Figure 9: Various Profile Actions



information in the Status Bar at the bottom of the window—this feature is particularly useful for the Nucleic Acid Tab because hovering over setting fields shows descriptions in the status bar of what they represent.

4.2.1 Profile Manager

The profile manager lets you easily save and load various sets of nucleic acid settings. Using NATuG’s profile defaults will ensure that all the settings are correct, and you can also create your own profiles for future use.

By default, NATuG includes common profiles, such as one for B type DNA. Profiles are saved internally, and can easily be loaded/retrieved, and .json files containing the profile data can be found within the saves/nucleic_acid folder. These files are loaded when NATuG is booted, and can be modified directly. Additionally, when NATuG is closed, the last used settings are saved, and are automatically retrieved upon the next launch.

To use the profile manager, enter the name of the profile you would like to save/load/delete into the “Profile Name Here” box, and click the respective button. For extended descriptions of what each button does, see below. When a profile manager box is disabled/gray, consult the status bar for information as to why. For irreversible actions warnings will be shown before the action is run. Below is a list of more extended descriptions of the various profile manager actions.

Load Profile Load the profile with the currently chosen profile name. This requires a profile to already exist with the name chosen, and for the current settings to not be the the settings of that profile. (Icon 9a)

Save Profile Save the profile with the currently chosen profile name, or, if there is already a profile with that name, overwrite the existing profile. The profile will be saved to a .json file within saves/nucleic_acid after the program is closed. (Icon 9b)

Delete Profile Delete the profile with the currently chosen profile name. This action is irreversible. Default profiles cannot be deleted. (Icon 9c)

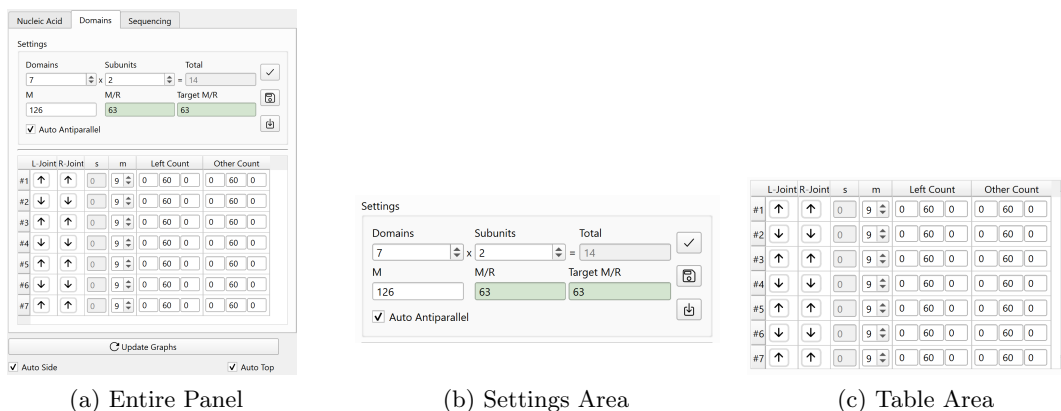
4.2.2 Setting Descriptions

Below lies a list of all of the various Nucleic Acid settings that can be adjusted. Certain settings (the ones that are have an “(a)” in the table) are automatically determined based on other settings and cannot be user set.

Input	Name	Data Type	Description
D	Diameter	number	The diameter of a given domain in nanometers
H	Height	number	The height of one turn of the helical axes
g	Nucleoside-Mate Angle	number between 0 and 360	The angle about the helical axis between a nucleoside and its Watson-Crick mate
T/B	Helical Turns per Bases	integers	There are T turns every B bases
Z_b (a)	Base Height	number	The height between two NEMids on a given helix
Z_c	Characteristic Angle	number	The height a helix climbs as it rotates through the characteristic angle
Z_{mate}	Nucleoside-Mate Height	number	Vertical distance between a NEMid and its mate on the other helix.
θ_c (a)	Characteristic Angle	number between 0 and 360	The smallest angle about the helical axis possible between two NEMids on the same helix.
θ_b (a)	Interbase Angle	number between 0 and 360	The angle that about the helical axis between two NEMids

4.3 Domains

Figure 10: Domains Config Panel



The Domains Tab is the area in which all the settings for each helical domain can be set—such as the interior angles of each domain, or how many NEMids to initially generate. NATuG provides support for symmetrical designs, saving and loading designs, and provides tools for designing closed structures.

4.3.1 Symmetry Settings

For larger, more complex nanostructures, it is often helpful to take advantage of symmetries. This means repeating the settings of a set, or “subunit,” of domains a certain number of times. To this end, the Subunit Table (4.3.2) is not a place to enter settings for every single domain, but rather contains the domains of a single subunit; single subunit structures are a special case in the Subunit Table does showcase the settings of all domains. Within the Symmetry Settings area of the Domains Tab (Figure ??) you can change the number of copies of the domains listed in Subunit Table, along with more advanced settings, listed below. After you have made changes within this area, click the check icon, the top right button, to confirm your choices.

Name	Data Type	Description
Domains	integer	The number of domains per subunit. This dictates how many domains show up in the Subunit Table. This is also known as the domain count, or N
Subunits	integer	How many times to copy the current subunit. This is also known as the symmetry factor, or " R ."
Total	integer	The total number of domains within all subunits. This is equivalent to subunits·domains.
M	integer	The sum of all the ms for all the domains within all the subunits.
M/R	number	The sum of all the ms for a given subunit. This is equivalent to, as the name implies, M/R .
Target M/R	number	This is equivalent to $B^{\frac{N-2}{2R}}$, where B is a parameter of the specific nucleic acid (which can be adjusted within the Nucleic Acid Tab, discussed in more detail in section 4.2), N is number of domains, and R is the symmetry factor.
Antiparallel	boolean	Whether the domains' L/R-Joints automatically alternate (up-up, down-down, up-up, etc.) across all domains of all subunits. In most cases this should be checked, and this is the default. If this is unchecked, the helical joints will not be copied, and will be blindly cycled across all domains.

4.3.2 Subunit Table

The Subunit Table (Figure ??) is the place where you actually enters settings for all of the domains in a given subunit. As discussed in section 4.3.1, all of the domains that get plotted are a specific number of copies of the current domain settings in this table. Each domain possess various different settings, which are listed in greater detail below.

Column	Data Type	Description
L-Joint	up or down	Whether the up helix or the down helix is the helix that lines up to the R-Joint direction helix of the previous domain.
R-Joint	up or down	Whether the up helix or the down helix is the helix that lines up to the L-Joint direction helix of the next domain.
s	integer	θ_{switch} multiple. This is automatically determined based off of L-Joint and R-Joint. If the joints are the same direction, this is 0; if they go from up to down, this is -1; and, if they go from down to up, this is 1.
m	integer	The angle between the domain's center and the next domain's center. This is a multiple of θ_c , (which can be set in the Nucleic Acid Tab, discussed in section 4.2). While you can manually enter an integer into this box, if you increase the angle of a single domain without compensating elsewhere, the tube will no longer be closed. Clicking the buttons will automatically adjust the interior angle of the surrounding domains, so that this one increases by 2, and the next and previous ones decrease by 1, and vice versa.
Left Count	integer (x3)	<p>A set of three integers representing how many NEMids to generate for the left-helical-joint direction helix—the helix that is lined up to the right-helical-joint of the previous domain. For each NEMid generated, a nucleoside will also be generated, but these boxes indicate only how many NEMids to generate. They represent the following, in the following order:</p> <ol style="list-style-type: none"> 1. After generating the initial number of NEMids (integer 2), this is how many additional NEMids to generate on the bottom of the strand. This can be negative to trim NEMids. 2. The initial number of NEMids to generate. The first NEMid is lined up to a NEMid on the line of tangency between the previous and this domain. 3. After generating the initial number of NEMids (integer 2), this is how many additional NEMids to generate on the top of the strand. This can be negative to trim NEMids. <p>Note that adjusting box 1 and 3 is particularly useful for creating sticky ends, since you can tell NATuG to generate nucleosides without mates.</p>
Right Count	integer (x3)	A set of three integers representing how many NEMids to generate for the other helix in the double helix. See above for further descriptions of the boxes.

4.3.3 Presets

The Domains Tab allows you to export and sets of domain settings, along with the complementary symmetry settings, in a matter of clicks. This section covers how to save and import collections of domains.

Exporting To save the current state of the Domains Tab, including the Subunit Domains and symmetry settings, click the save button (the floppy disk icon), and choose a location to save. A file dialog will

prompt you to choose an output filepath and file name for the save, and will open by default to the filepath `saves/domains/presets`. The output file is a .csv file with a format outlined in section 4.3.3.

Importing To import the current state of the Domains Tab, including the Subunit Domains and symmetry settings, click the load button (the arrow pointing down into a box). A file dialog will prompt you to choose an output filepath and file name for the profile that you are trying to import, and will open by default to the filepath `saves/domains/presets`. If the file is of the wrong format, an error will be raised.

NATuG includes, by default, within the `saves/domains/presets` folder, various different profiles, listed below. For the most part, the names are an indication of the top view nanotube shape.

- circle.csv
- heart.csv
- hexagon.csv
- nested.csv
- start.csv
- tengon.csv
- triangle.csv

CSV Format When you import/export a collection of domains, the file must be a .CSV file with the format found in the table below. For the table below, column is the CSV column, and description is what the entries should take the form of for that column. The formatting here is very strict, and anything other than the below listed formatting will likely raise an error when importing/exporting.

Column	Description
Left Helix Joints	Either <code>UP</code> or <code>DOWN</code> for each row. Each row represents a domain.
Right Helix Joints	Either <code>UP</code> or <code>DOWN</code> for each domain. Each row represents a domain.
Left Helix Count	A set of the three left helical counts, in the format <code>bottomCount-baseCount-topCount</code> (separated with dashes), for each row. Each row represents a domain. See the Settings Descriptions chart (4.3.2) for further explanation of what these represent.
Other Helix Count	The same as the left helical count, but for the other helix.
Symmetry	The first row should be an integer indicating how many subunits to use. There will be no symmetry if the first row is set to 1.
Antiparallel	The first row should either be <code>True</code> or <code>False</code> . If <code>True</code> the <code>Left Helix Joints</code> and <code>Right Helix Joints</code> will be ignored upon loading.

4.4 Sequencing

This tab allows for bulk sequence operations, and for exporting sequences to a spreadsheet for synthesis. Because sequencing is such a critical part of NATuG, it has a section that goes into greater depth about how it works. It is also important to note that this is not the only place where sequences can be set. For more information about sequencing, consult section 7.3.

4.4.1 Bulk Sequence Operations

Bulk sequence operations let you set the sequence of many nucleosides at once. In order to run a bulk sequence operation, select a “Scope,” then an “Operation,” and then click “Run.”

Figure 11: Sequencing Tab

Scopes The scope is which nucleosides the operation should run on.

- **All bases:** All the nucleosides of all the strands.
- **Unset bases:** All the nucleosides of all the strands that do not currently have a base set.

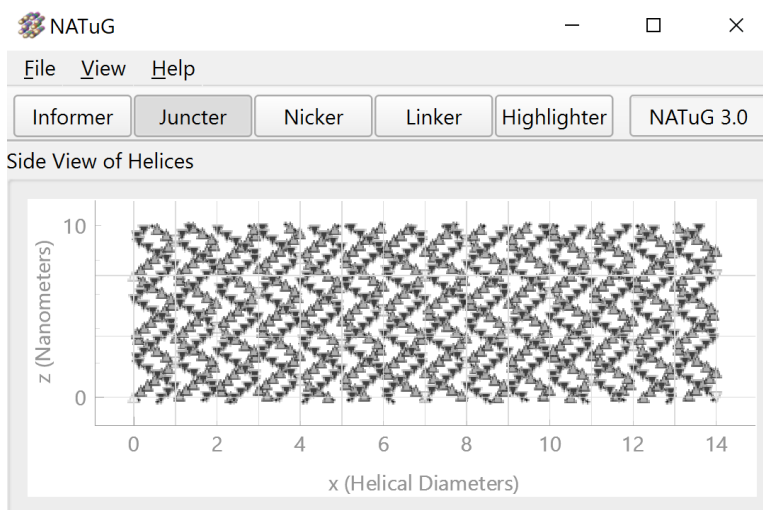
Operations The operation is what to do to the nucleosides within the scope.

- **Randomize:** Select random bases.
- **Clear:** Unset the bases.

5 Side View Plot

The Side View Plot is the heart of NATuG. It allows you to directly interact with strands that have been created as a result of user inputs set elsewhere. The plot can be broken into a few distinct parts that function together to allow for a high degree of interactivity.

Figure 12: The Side View Plot & toolbar



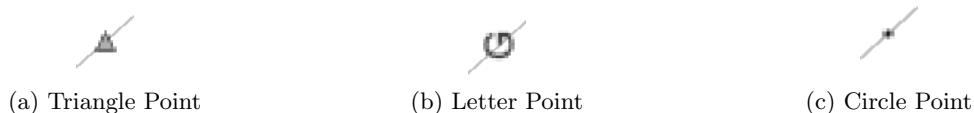
5.1 Graphics

Before diving into how to actually interact with the Side View Plot, it is important to understand what the contents of the plot actually represent. The Side View Plot is not, as its name implies, a direct side view of the double helices. Rather, it is more of an “unrolled” plot, since it is distorted in such a way as to neatly lay out the double helices next to one another.

Importantly, the plot consists of various artifacts, which represent physical nucleosides, or abstract areas between physical nucleosides. Below lies further descriptions of what these artifacts are.

5.1.1 Points

Figure 13: Side View Plot Point Graphics



If the Config Panel’s (4) current tab is set to either “Nucleic Acid” or “Domains”:

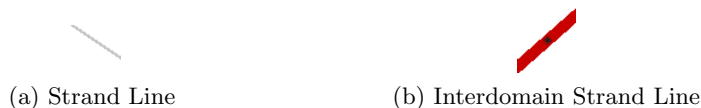
- The triangles represent NEMids. The direction the triangles point (up/down) indicates the direction of the strand. White triangles represent two overlapping NEMids that are clickable, and, when clicked, can form a cross-strand exchange.
- The dots represent nucleosides, and cannot be interacted with.

If the Config Panel’s (4) current tab is set to “Sequencing”:

- The triangles represent nucleosides with unset bases. The directions the triangles point (up/down) indicates the direction of the strand.
- The letters represent nucleosides that have bases set. The letter indicates what the base of the nucleoside is.
- The dots represent NEMids, and cannot be interacted with.

5.1.2 Lines

Figure 14: Side View Plot Line Graphics



The lines connecting dots together are not a literal representation of the location of the phosphate backbone of the DNA, but rather serve as a visual aid to see which strands are which. To this end, by default “interdomain” strands (strands that traverse multiple domains) are automatically styled to be thicker and more colorful to stand out—however, the styles of lines are completely customizable.

Additionally, for interdomain strands, the lines are curved (with Chaikin’s Corner Cutting Algorithm). This is so that it is clear which strand is which, and because with the thicker lines that interdomain strands possess appear to merge with themselves without rounding of corners. At this time, this setting cannot be disabled.

5.2 Interaction

NATuG utilizes the pyqtgraph framework for its plots. Below lies a general description of the means of interaction for the plot, but, for a more direct and comprehensive breakdown, visit pyqtgraph’s website (pyqtgraph.readthedocs.io).

5.2.1 Panning

To pan from left to right within the side view plot, left click, and then drag your cursor away from the area that you want to pan to. You can think of this as “pulling” the graph towards the cursor. Alternatively, if you have a mouse, you also have the option of clicking the scroll wheel and dragging in the direction that you would like to move the plot in.

5.2.2 Zooming

To have the plot automatically zoom in out to showcase all of the items currently plotted, click the small “A” symbol in the bottom left of the plot. This is called the “Auto Range” button. For zooming in on specific areas of the plot, see below.

- If you have a mouse:
 - To zoom while maintaining the aspect ratio of the plot, use the scroll wheel.
 - To zoom without regard for the aspect ratio of the plot, right click, and then drag in the direction that you would like to stretch the plot in. The axes will automatically update.
- If you have a trackpad:
 - To zoom while maintaining the aspect ratio of the plot, pinch inwards to outwards to zoom in, and outwards to inwards to zoom out.
 - To zoom without regard for the aspect ratio of the plot, pinch and right click simultaneously.

5.2.3 Configuration

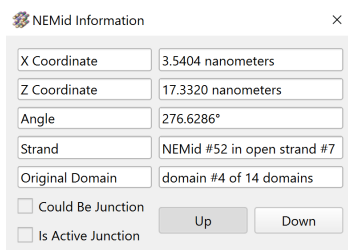
For additional options for the plot, right click. Upon right clicking, a small dialog showing additional plot options will show up. This allows for more advanced configuration of how the plot appears.

5.3 Modes

The currently chosen mode dictates what left clicks on non-dot points in the Side View Plot does. To change the mode, simply click on the mode that you would like to change to. Only one mode can be chosen at a time, and the currently chosen mode is indicated in a slightly darker gray than the others.

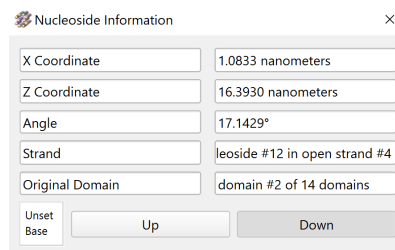
5.3.1 Informer Mode

Figure 15: Informer Dialogs



The NEMid Informer Dialog is a window titled "NEMid Information" with a close button (X) in the top right corner. It contains several input fields and checkboxes. The fields are: X Coordinate (3.5404 nanometers), Z Coordinate (17.3320 nanometers), Angle (276.6286°), Strand (NEMid #52 in open strand #7), and Original Domain (domain #4 of 14 domains). There are two checkboxes: "Could Be Junction" and "Is Active Junction", both of which are currently unchecked. At the bottom, there are "Up" and "Down" buttons.

(a) NEMid Informer Dialog



The Nucleoside Informer Dialog is a window titled "Nucleoside Information" with a close button (X) in the top right corner. It contains several input fields and checkboxes. The fields are: X Coordinate (1.0833 nanometers), Z Coordinate (16.3930 nanometers), Angle (17.1429°), Strand (leoside #12 in open strand #4), and Original Domain (domain #2 of 14 domains). There are two checkboxes: "Unset Base" and "Is Active Junction", both of which are currently unchecked. At the bottom, there are "Up" and "Down" buttons.

(b) Nucleoside Informer Dialog

The “Informer” mode is for obtaining additional information about given points. It provides a dialog that shows various attributes of the point(s) that were clicked on.

The informer mode is for obtaining additional information about given points. When the informer mode is active, clicking on any point within the main plot will create a dialog that provides additional information about the point. If you click on a NEMid that could be made into a junction, two informers will appear—one for the NEMid that was clicked, and one for the NEMid that that NEMid could potentially be made into a junction with. There are two different types of dialogs: the NEMid Dialog 15a and the Nucleoside Dialog 15b.

Nucleoside Informer Descriptions of the various properties that the Nucleoside Informer displays:

1. **X Coordinate:** The x coordinate of the nucleoside.
2. **Z Coordinate:** The z coordinate of the nucleoside.
3. **Angle:** The angle of the nucleoside. The line of tangency between the previous domain and this domain marks the zero degree mark. This is automatically moduloed by 360.
4. **Strand:** The index of the nucleoside within its parent strand, and the index of the parent strand within the list of all strands. Indexes begin at #1. This is the nucleoside index, not the item index, so even though it is true that strands progress nucleoside, NEMid, nucleoside, etc., this index only takes into account nucleosides.
5. **Original Domain:** The domain that this nucleoside belongs to.
6. **Base:** The base that this nucleoside is currently set to. If the nucleoside does not have a base set, this box will read “Unset Base.”
7. **Direction:** The direction of the strand. The darker box is the direction that the strand is going in.

NEMid Informer Descriptions of the various properties that the NEMid Informer displays:

1. **X Coordinate:** Same as Nucleoside Informer #1
2. **Z Coordinate:** Same as Nucleoside Informer #2
3. **Angle:** Same as Nucleoside Informer #3
4. **Strand:** Same as Nucleoside Informer #4
5. **Original Domain:** Same as Nucleoside Informer #5
6. **Could Be Junction:** Whether this NEMid could be conjuncted with another NEMid. If this is set to true then clicking on this NEMid in Juncter Mode (5.3.2) will be allowed, otherwise an error will be displayed.
7. **Is Active Junction:** Whether this NEMid is currently conjuncted with another NEMid.
8. **Direction:** Same as Nucleoside Informer #7

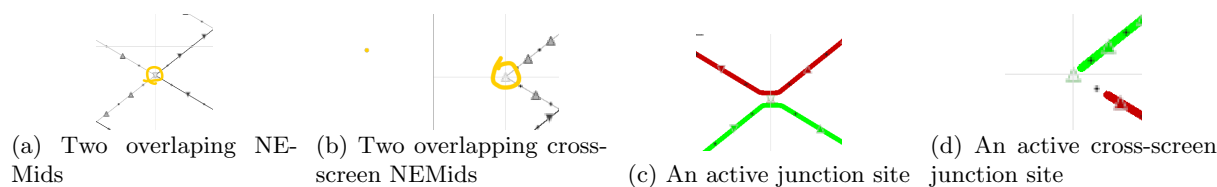
5.3.2 Juncter Mode

The “Juncter” mode allows for the creation of cross-strand exchanges. It lets you left click on overlapping NEMids to create junctions.

There are two ways to create a junction:

- Clicking on two overlapping NEMids (indicated by white triangles that are on top of each other as shown in figure 16a). This is the typical type of junction, and is highly versatile—it can split closed loops, form closed loops, allow a strand to go across many domains, and more. See figure 16c for an example of what a junction will look like after a left click.

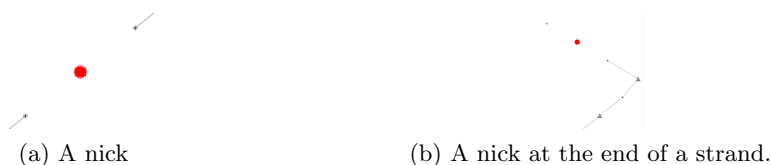
Figure 16: Junction Sites and Junctable Regions



- Clicking on a single NEMid that overlaps a NEMid on the other side of the screen (see figure 16b). This type of junction is called a “cross-screen” junction, and can be seen in figure 16d. Since the Side View Plot is really an unrolled view of all of the helical domains, the very left for closed structures will sometimes have NEMid overlaps with the very right.

5.3.3 Nicker Mode

Figure 17: Nick examples



The “Nicker” mode is how you can create nicks within the strand. Nicks are essentially gaps that split a strand into two different strands.

To create a nick, click on any NEMid, and the NEMid will convert into a red circle. There will then be two strands: one consisting of all of the NEMids and nucleosides that were above the NEMid, and one consisting of all the NEMids and nucleosides below the NEMid. The NEMid itself will be removed.

Notes about nicking:

- When you create a nick the data of the original strand is saved, so, to remove a nick, click on the nick a second time and the original strand will return.
- Creating a nick at the end of a strand is unadvised because, as can be seen in figure ??, you will likely inadvertently create a strand that consists of a single nucleoside.
- The nitrogenous bases of all the nucleosides in the two new strands will be preserved.

5.3.4 Linker Mode

The “Linker” mode allows you to connect the end of one strand to the beginning of another strand, and vice versa.

Linkages A linkage is a single-stranded region that connects two formerly distinct strands. In this single-stranded region nucleosides can be added, and bases for those nucleosides can be set. To customize a linkage click on the linkage, and the linkage editor should pop up. The Linkage Editor (see figure 18) is a dialog that allows you to add nucleosides to the linkage, and to set the sequence of the items in the linkage. To increase or decrease the number of items within the linkage, simply increase the “Nucleosides in Linkage” spinbox, and click tab or enter. Note that the nucleosides in the linkage will show up in the regular strand config sequence editor, but this window only shows the sequence of the items within the linkage.

To create a linkage:

Figure 18: The linkage editor

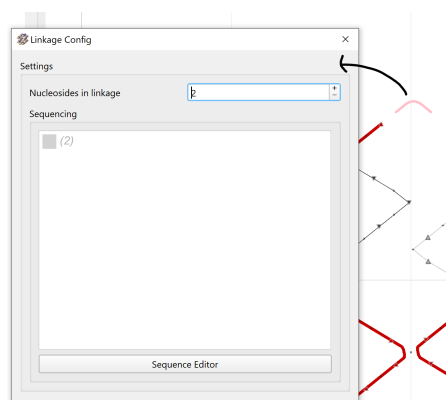
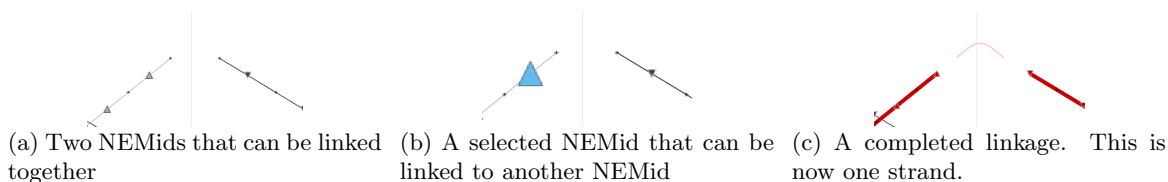


Figure 19: Linkage creation process



1. Locate two NEMIds that can be made into a linkage. Consult the following list of prerequisites for determining if two NEMIds can be linked together—if the following conditions are not met a warning will be displayed.
 - (a) Both NEMIds must be endpoints of their respective strands. This means the second to last or second item in their strands (with the nucleoside that follows them being the very last or very first item).
 - (b) One NEMId is at the 5' end of its strand and the other NEMId is at the 3' end of its strand.
 - (c) Both strands consist of >1 NEMIds.
2. Left click on one of the NEMIds that you would like to link with the other NEMId. The order in which you click the NEMIds does not matter. After clicking on a NEMId in linker mode, the NEMId should turn blue and grow larger. This indicates that it is selected.
3. Left click on the other NEMId that you would like to link it to. A linkage should be created upon releasing left click.

5.3.5 Highlighter Mode

The “Highlighter” mode lets you highlight points. It makes them larger and yellow, which can be useful for presentations (see figure 20). To highlight a NEMId or nucleoside, simply click on it. To unhighlight a NEMId or nucleoside, click on the highlighted NEMId or nucleoside a second time.

Notes about highlighting:

- Items will stay highlighted even when you leave highlighter mode. This means that there are actually multiple ways to unhighlight items, including, but not limited to the following.
 - Click the highlighted point while in highlighter mode



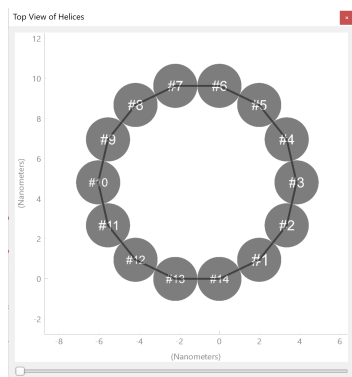
Figure 20: A highlighted NEMId

- Create a nick to split the strand in two, or create junction
- Click the “Update Graphs” button to refresh the plots
- At this time NATuG’s highlighting is uncustomizable, so all highlighted items will be large and yellow versions of their past selves.

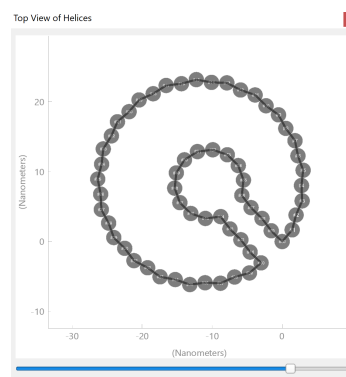
6 Top View Plot

The Top View Plot presents an overhead view of the nanostructure that is currently being created. It allows you to visualize the actual tube shape, and see the interior angles of all the domains. The Top View Plot is a panel, which means that it can be undocked, among other things. For information on panels, see 3.1.

Figure 21: Top View Plot Panel



(a) Top View Plot Example 1



(b) Top View Plot Example 2

6.1 Graphics

In the Top View Plot, each circle represents a helical domain, which is the region in which the double helices exist. The circles are numbered, and the numbers represent the domains’ respective indexes. The units of the axes are in nanometers, and depend on the diameter of domains, which can be set in the Nucleic Acid Tab (4.2). An imaginary 0th domain is drawn as well to show the last domain’s interior angle, but this domain does not actually exist. Additionally, to make it easier to see the interior angles of the domains, a thin line is drawn atop all of the domains’ circles.

6.2 Interaction

For the most part, interacting with the Top View Plot is the same as interacting with the Side View Plot (documentation for interaction with the side view plot can be found at 5.2). However, there are a few important differences:

- The aspect ratio of the Top View Plot is locked at 1:1. This means that you cannot stretch the plot.
- The Top View Plot is rotatable. To rotate the top view plot, drag the handlebar beneath the plot to the right. The left edge of the bar represents a 0° rotation, and the right edge of the bar represents a 360° rotation. The plot is rotated after coordinates for all of the domains are computed, and the pivot point of rotation is the middle point of all the domains.
- Clicking on a number (not a circle, but rather on a number) will navigate the Side View Plot to the specific domain that was clicked on. Clicking on the same number a second time will restore the full view of the plot.

7 Strands

Whereas a “helix” is specifically a strand that stays within one domain, a “strand” can traverse many domains. When a strand crosses through many domains, it weaves the nanotube together. But, equally important to choosing where the strand goes is determining the base sequence. And, being able to choose styles to represent strands in publications is also critical. This section covers how to customize the properties of a strand.

7.1 Selecting a Strand



Figure 22: A selected strand

To select a strand, left click on the line between two NEMids/nucleosides within the Side View Plot. The Strand Config Dialog should pop up, and the NEMids/nucleosides of the strand should grow larger (this is because the width/color of the strand is customizable, so it would be annoying if the strand’s color/width changed when highlighting). Only one strand can be selected at a time. Multiple strands can be selected at a time, and the name of the window indicates the strand that the Strand Config Dialog is for.

7.2 Configuration

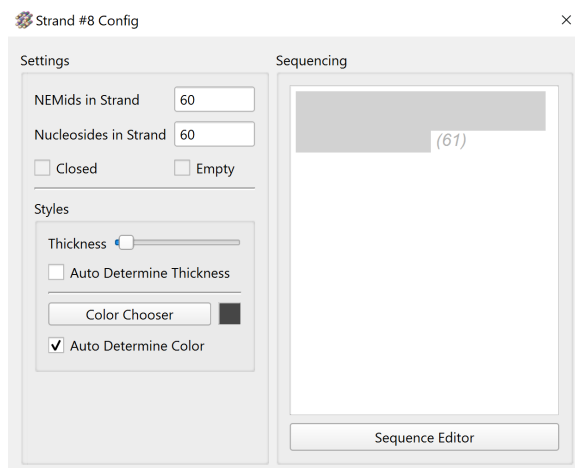


Figure 23: Strand Config Dialog

The Strand Config Dialog is the place where you can configure strand styles, obtain additional information about a given strand, and set a strand’s sequence. Below there is a detailed description of the three main parts of the strand config dialog:

Settings The settings area of the Strand Config Dialog encompasses the entire left side of the dialog. Within this area, information about the strand can be found, and various styles can be customized.

Information The information area of the Strand Config Dialog provides the following information about the strand:

- **NEMids in Strand:** The number of NEMids that are in the strand.
- **Nucleosides in Strand:** The number of nucleosides that are in the strand.
- **Closed:** Whether the strand is a closed loop strand.
- **Empty:** Whether the strand has no items in it. In general, this will be false.

In addition, the strand's index in regards to all the other strands (its "id") can be found as the title of the window (see the top of figure 14a)

Styling The style area of the Strand Config Dialog lets you customize styles of the strand. The styles update in real time, with the exception of the "Automatic" style checkboxes. The "Auto" checkboxes next to the different strand styles tell NATuG whether or not to override the user-set strand style when refreshing/recoloring the plot. If you want to reset a style of a strand back to the default, select the "Auto" checkbox for the style, and then in the file menu choose "View," and "Restyle Strands."

Below lies a list of the various styles that can be customized, and the default settings of the given styles.

- **Thickness:** The width of the strand. This is a handlebar that represents the width of the strand in pixels. The very left of the bar represents 1 pixel of thickness, and the very right of the bar represents 50 pixels of thickness. By default, strands that stay in their own domain are 2 pixels thick, and strands that traverse multiple domains are 9.5 pixels thick.
- **Color:** The color of the strand. The "Color Chooser" button creates a Color Chooser Dialog that allows you to select the color of your choosing. Within the dialog, you can enter parameters for your color in RGB/CMYK, choose a screen color, or choose from a preset. By default, strands that stay in their own domain are either light or dark gray, and strands that traverse multiple domains are automatically assigned colors as to keep them distinct from other strands that traverse multiple domains.

7.3 Sequence Selector

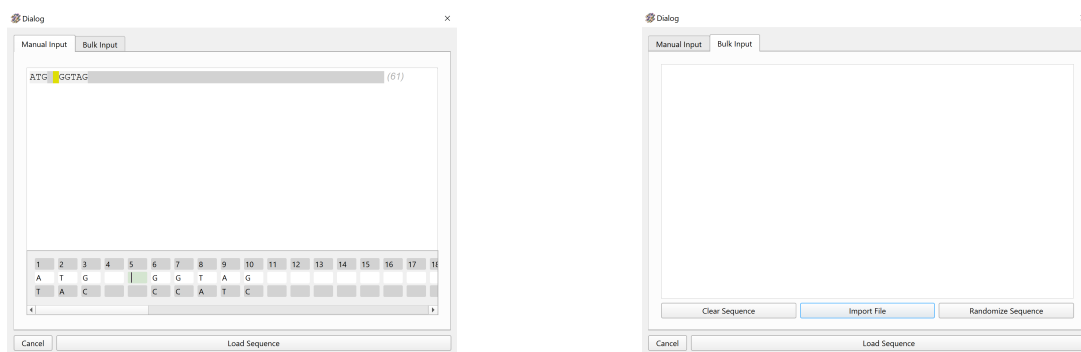
The purpose of the Sequence Selector is to provide a user-friendly way to obtain a valid sequence for a given strand/portion of a strand. Generally, this will pop up when you click a button along the lines of "Choose a Sequence." To use the Sequence Selector, you can either choose to use the Bulk Sequence Input tab, or, if the length of the sequence you are being prompted to choose is under 1,000 bases, the Manual Input Tab. Once you have made your selection of sequence, click the "Load Sequence" button, or click the "Cancel" button to exit the Sequence Selector and cancel the sequence choosing operation. Below, more information about the two areas of the Sequence Selector can be found.

7.3.1 Manual Input Tab

The Manual Input Tab of the Sequence Selector is like a text editor for a DNA sequence, and makes entering a sequence manually super-simple and convenient. Because of how the Manual Input Tab is implemented, it becomes particularly slow after displaying more than 1,000 bases, so, when more than 1,000 bases need to be set you must use the Bulk Input Tab. The Manual Input tab consists of two main areas, the bottom Sequence Entry Area and the top Sequence Display Area.

Sequence Entry Area The Sequence Entry Area is a horizontally scrollable area that showcases all of the bases currently chosen as editable text boxes. Each white rounded box, also called an Entry Box, represents a single nitrogenous base. The box above each Entry Box is the index of that base. The box below each Entry Box is the complementary base. NATuG uses Watson-Crick base pairing, so the complement of A is T, the complement of T is A, the complement of G is C, the complement of C is G, and the complement of None is None.

Figure 24: Sequence Selector Dialog



(a) Manual Input Tab

(b) Bulk Input Tab

When you are using the Sequence Entry Area, you can type into one box at a time either the letter “A,” “G,” “C,” or “T,” or you can click the delete key. What you type will automatically be capitalized, and after you enter the letter of a base you will automatically be shifted to the next Entry Box to the right, or, if you enter a base into the last box, you will be shifted to the first Entry Box. As you enter bases into the various Entry Boxes, the Sequence Entry Area will automatically scroll to keep the currently selected box in view.

Sequence Display Area The Sequence Display Area is a larger area that displays the entire current sequence. This area is read only, and highlights the currently selected Entry Box of the Sequence Entry Area. You can select and copy the text of this box, but you cannot edit this box.