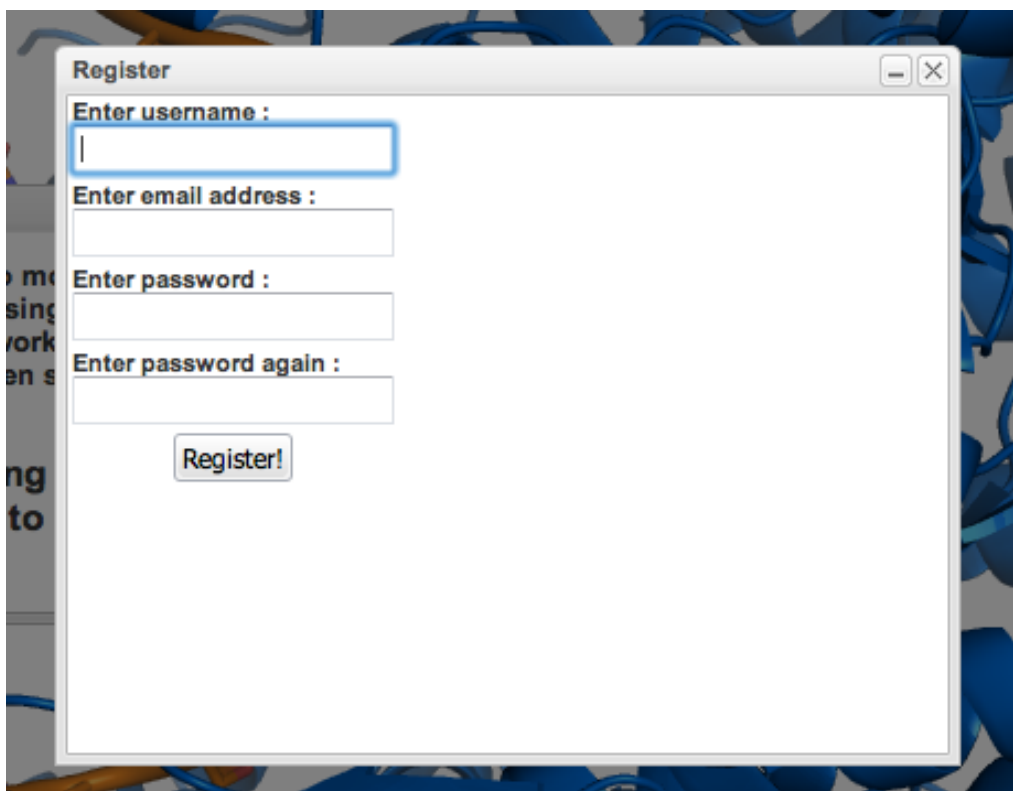


Siliclone User Guide

Version 1.0 — 9 May 2010

Getting Started

To begin using Siliclone, you must register for an account. Registering allows you to save workspaces and DNA sequences, to access workspaces and sequences that have been shared with you, and to share your own with other users and groups of users. To register, click the “Register” button on the right-hand side of the home page. This will bring up the following dialog:

A screenshot of a 'Register' dialog box. The dialog has a title bar with 'Register' and standard window controls. It contains four text input fields with labels: 'Enter username:', 'Enter email address:', 'Enter password:', and 'Enter password again:'. Below the fields is a 'Register!' button. The background of the window shows a blue molecular structure.

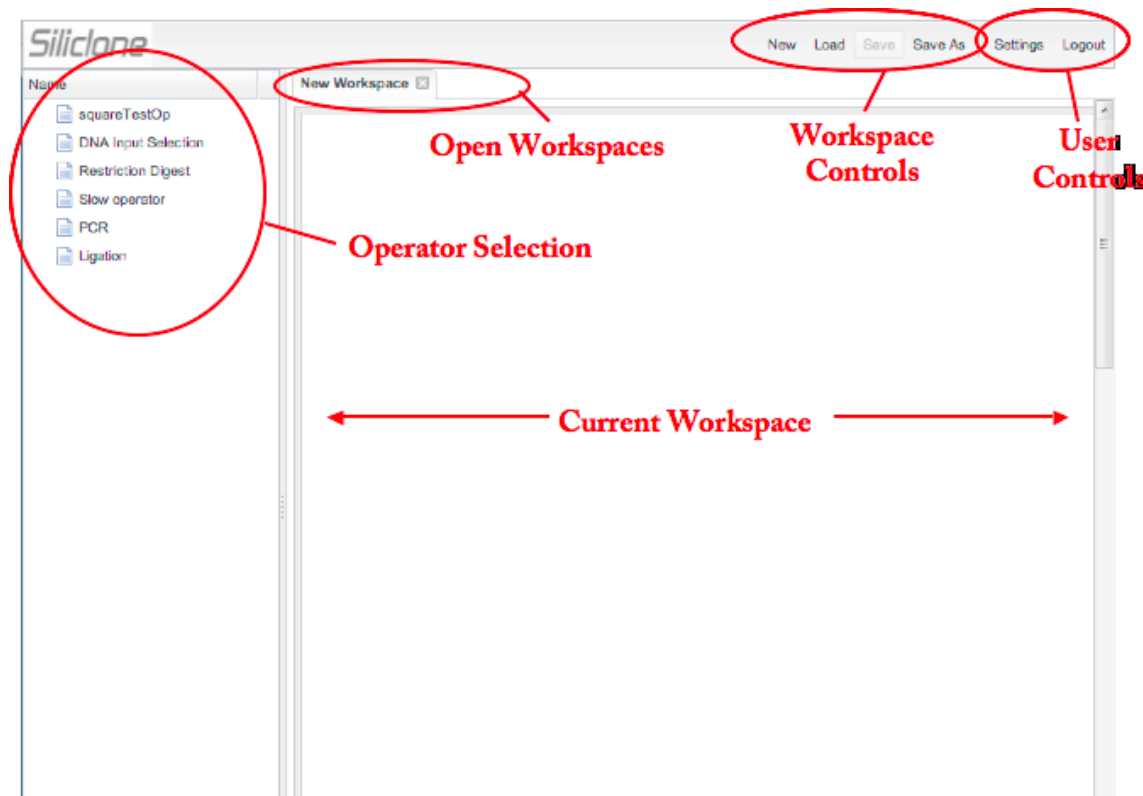
As Siliclone is currently only available to educational users, a .edu email address is required to complete registration.

Once you have registered, you can enter your username and password in the form above the register button to get started using Siliclone!

A screenshot of a login form. It has a light blue background. There are two text input fields with labels 'Username:' and 'Password:'. Below the fields is a 'Login!' button.

The Home Screen

Once you've logged in, you will be greeted by the Home Screen, as shown below. The different parts of the Home Screen are marked on the image below, and each is described in detail.



1. **User Controls**

These buttons provide account and sharing controls. Clicking the “Logout” button will end your current Siliclone session, closing all of your workspaces and returning to the homepage of the website. Clicking on the “Settings” button brings up a dialog with a variety of user controls for changing your account information and sharing settings.

2. **Workspace Controls**

These buttons allow you to control your workspaces. Clicking “New” will open a new workspace, “Load” will open a dialog to allow you to select one of your saved workspaces to open, and the “Save” and “Save As” buttons let you save the currently active workspaces so that you can load it again in another session or share it with other users.

3. **Open Workspaces**

These tabs show the currently open workspaces. The title of each tab is the name of the workspace that tab displays. Click on the different tabs to move between the currently open workspaces.

4. Operator Selection

This section of the screen lists all of the DNA operations that can be used within Siliclone. To add an operator to your current workspace, simply click on its name and drag it to the desired location in the workspace.

5. Current Workspace

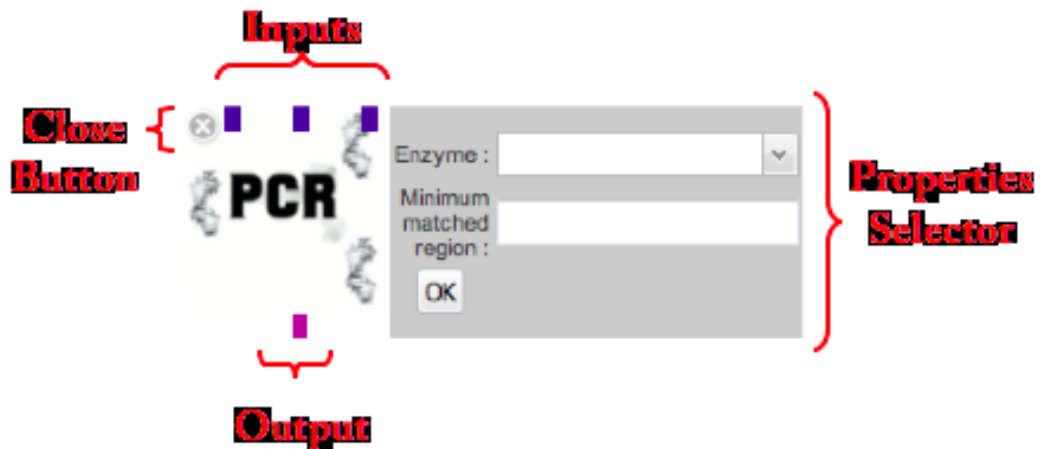
This section is the heart of the Siliclone Home Screen. In the workspace, you can create entire workflows of molecular biology experiments by joining the output of various DNA operations together as the inputs to new operations. More details are described in the following section.

The Basic Pieces

The Siliclone user interface is designed to be intuitive, but there are a few things you need to know to get started. Siliclone is centered around the idea of user **workspaces**. Each workspace is intended to represent a workflow of simulated molecular biology operations that can together constitute a complete experiment. The workspace consists of **operators**, **DNA sequences**, and **visualizations**.

1. Operators

Operators are used to perform simulations of biological operations, such as running a PCR or a restriction digest. Each operator has a number of *input slots* that accept DNA sequences output from other operators and an *output slot* that holds the result of running the operation on the given input. Clicking on an operator brings up a **Properties Selector** (which will also open by default when an operator is added to the workspace), where you can enter various parameters to control the simulation. The simulation will start running immediately once all inputs to the operator have been connected, and the simulation will be started again whenever a change is made to one of the parameters using the properties selector or when one of the input sequences changes. Clicking on the close button on the top-left corner of each operator will remove that operator from the workspace.



The most basic operator is the **DNA Input Operator**, which will be needed to get the initial DNA sequences used as input for other operators. It is unique among operators in that it has no input slots. Using the DNA Input Operator, you can add sequences to Siliclone by manually entering a nucleotide sequence, uploading a file in a supported format (currently only FASTA files, but more formats will be added soon), or loading a previously saved sequence. When you click the OK button, the chosen sequence is set as the output of the selected DNA Input Operator, meaning that it is ready to be used as input to other operators you add to your workspace!

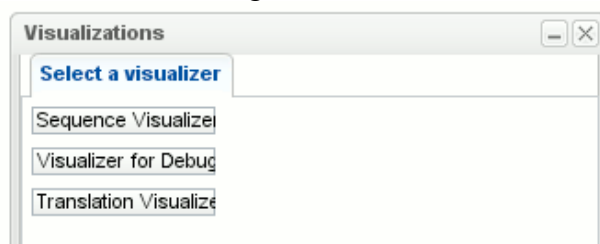
A screenshot of the DNA Input Operator dialog box. It has a gray header bar with three tabs: "Manual Entry" (selected), "Upload", and "Saved Sequence". Below the tabs, there is a "Name :" label followed by a text input field. Below that is a "Sequence :" label followed by a larger text area. At the bottom, there is a checkbox labeled "Circular?" and an "OK" button.

2. DNA Sequences

DNA sequences have three related representations in the Siliclone workspace: as a small gray rectangle at the top of an operator, representing input to that operator; as a small purple rectangle at the bottom of an operator, representing output from that operator; and as black “wires” between operators, representing a sequence traveling from the output of one operator to the input of another.

3. Visualizations

You can choose to visualize any DNA sequence in Siliclone in a number of ways. When you click on any sequence, the visualization selection window will appear, as shown in the image below.



This window shows the available visualization options. Clicking on one of the buttons in this window will open up the selected visualizer in a new tab. At present, two main visualizations are available. The **Sequence Visualizer** simply shows the nucleotides of the selected DNA sequence:



The **Translation Visualizer** shows the results of translating the nucleotide sequence into amino acids. Translation is performed for all six possible reading frames.



More visualization options will be added over the next several weeks and months.

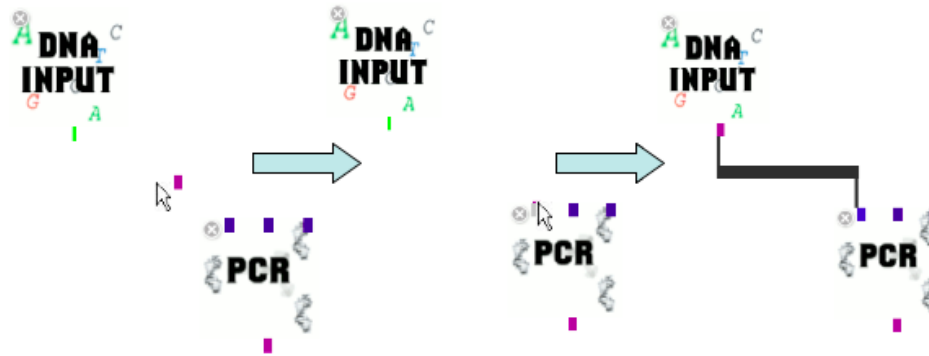
You can close the visualizer window for a particular sequence, and your selected visualizations will still be available when later you click on that sequence to re-open its visualization window. In addition, visualizations automatically update when their underlying sequences change.

Creating Workflows

Indeed, the true power of Siliclone lies in its ability to combine multiple operators to create entire workflows. Siliclone doesn't just provide convenient simulation tools that allow you to predict the result of molecular biology experiments; it also allows you to take the results and use them for further operations—just as you would in the lab!

To set the output sequence of one operator—for example, a DNA Input Operator—as an input sequence of another operator—say, a PCR Operator—simply click on the output node of the first operator and drag it to one of the input nodes of the second operator. As shown in the image below, the input node will change to a light gray color when it another node is held on top of it to indicate the potential connection. When you release the mouse, a black “wire” will form between the two operators, indicating the DNA sequence flowing between the two operators. Now, the second operator will recompute its own output sequence whenever the output sequence flowing into one of its input slots changes.

To remove a DNA sequence from another operator as the source for an input node of a different operator, simply click on the input node. The black wire connecting the two operators will vanish, indicating that they are no longer connected.



Sharing & Other Settings

In addition to allowing you to simulate molecular biology workflows and access them from anywhere, Siliclone also allows you to share your work with as many (or as few) other users or groups of users as you like! To manage groups and sharing, click the “Settings” button in the top-right corner of the screen (next to the “Logout” button). This will bring up a screen with several tabs for controlling different settings.

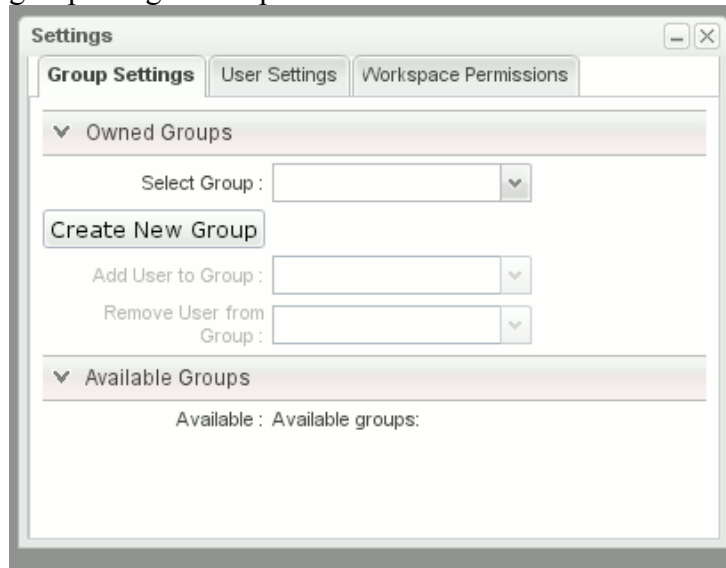
1. User Settings

The first settings tab allows you to control settings related to your own account. From here, you can change your password or delete your account. Note that deleting your account will not delete your saved workspaces or sequences so that other users granted access to them will still be able to use them.

2. Group Settings

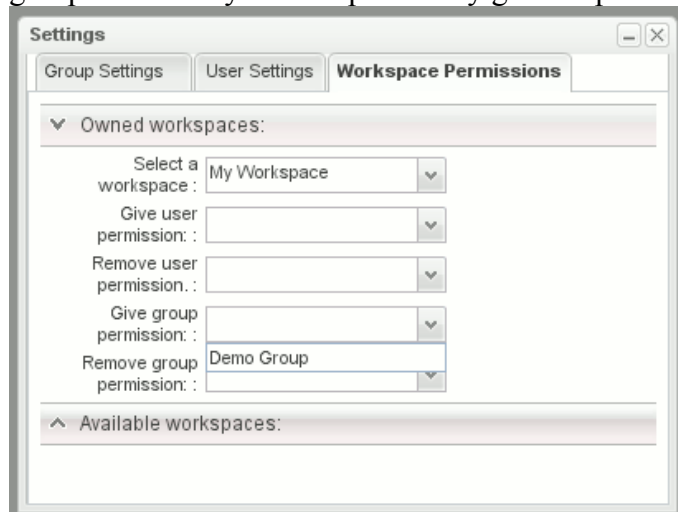
This tab lets you manage groups. Groups are a convenient way to control access to different workspaces and sequences for a number of users at once. For example, you may wish to provide all members of your lab with access to a particular workspace that you own. Instead of granting access to each member individually, you can add all the members to a group and then grant access to that group.

From the group settings page, you can click the “Create New Group” button to create a new group of users, or you can select one of your existing groups from the “Select Group” dropdown menu and add or remove users to that selected group using the dropdown menus below.



3. **Workspace Permissions**

This tab allows you to control which users and groups have access to each of your workspaces. When you create and save a new workspace, it by default can be seen and used only by you. To grant permissions to others, first select the workspace from the top dropdown menu. Then, use the additional dropdown lists to add permissions to other users or groups, or to remove permissions for users or groups to which you have previously granted permissions.



Conclusion

We hope you enjoy using Siliclone! This program is still very much under development, so please [email us](#) with any feedback or error reports!