# StatAlign Tutorial

November 16, 2012

This is a beginners tutorial on how to align RNA (or DNA) sequences and determine the consensus structure. First you have to download StatAlign. The current snapshot version is available from our download page as a zip archive. To run StatAlign, extract the archive, then double-click StatAlign.jar, or use the following command line syntax to get options:

```
java -jar StatAlign.jar -help
```

Once you start StatAlign, a window similar to this one should appear. If it doesn't you probably have to install java.
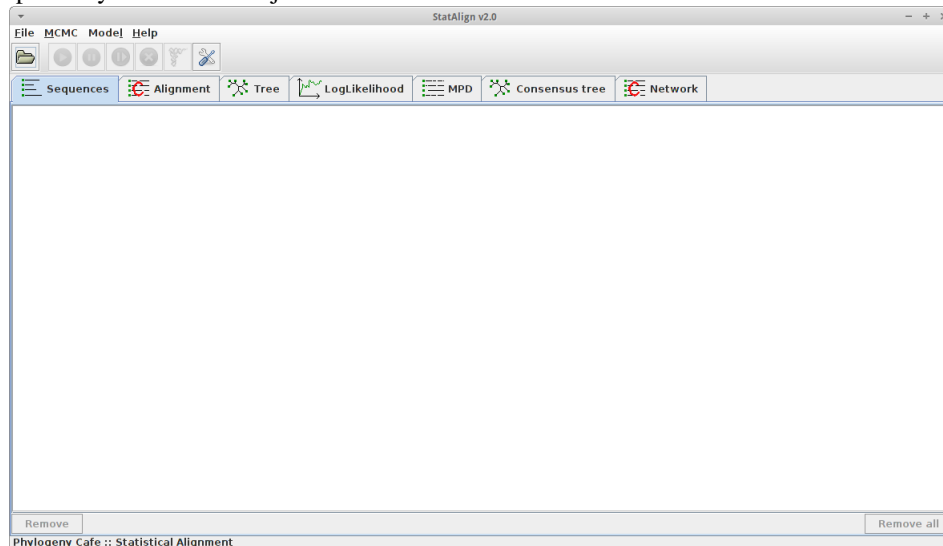
You start by opening a file which includes RNA sequences in a format similar to this one:

```
>gi|seq1
GCCTACGGCCATACCACCCTGAAAGCGCCCGATCTCGTCTGATCTCGGAAGCTAAGCAGGGACGGGCCTG
GTTAGTACTTGGATGGGAGACCGCCTGGGAATACCTGGTGCTGTAGGCTTT

>gi|seq2
GCCTACGGCCATAGGGCCCTGAAAGCGCCCGATCTCGTCTGATCTCGGAAGCTAAGCAGGGACGGGCCTG
GTTAGTAAATGGATGGGAGACCGCCTGGGAATACCTGGTGCTGTAGGCTTT

>gi|seq3
GCCGCGGGCCATACCACCCTGAAAGCGCCCGATGCTGTCTGATCTCGGAAGCTAAGCAGGGACGGGCCTG
GTTAGTACTTGGATGGCGAACCGCCTGGGAATCCATGGTGCTGTAGGCTTT
```
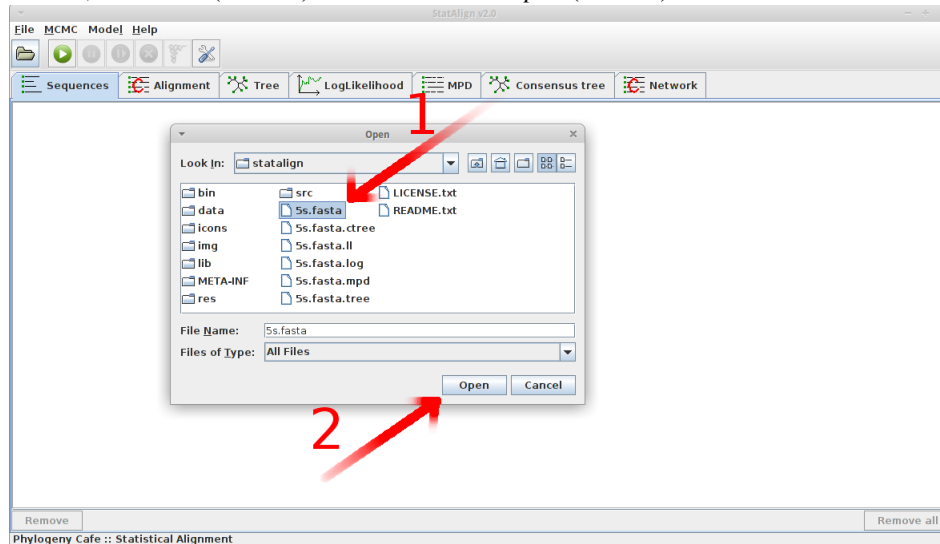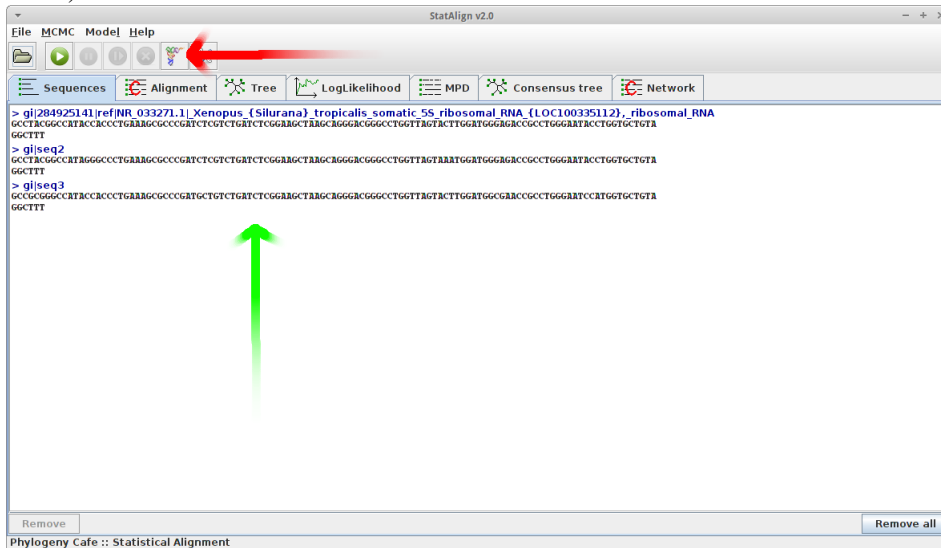
That can be done by clicking the folder icon which the red arrow points to.
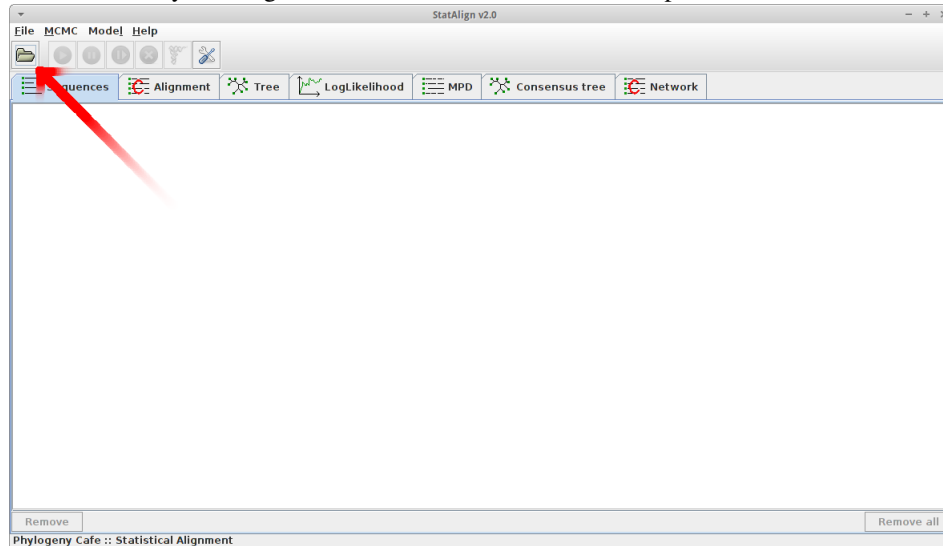
Then you get a pop-up window similar to this one. First you browse for the sequence file, click on it (arrow 1) and then click on *Open* (arrow 2).


If everything went well you should now see your RNA sequences (green arrow). Next step is to enable the RNA mode. That can be done by clicking the RNA icon (red arrow).

You should now see a pop-up window where you can choose between folding methods. In this tutorial we are just going to use PPFold so you can simply click the *OK* button.
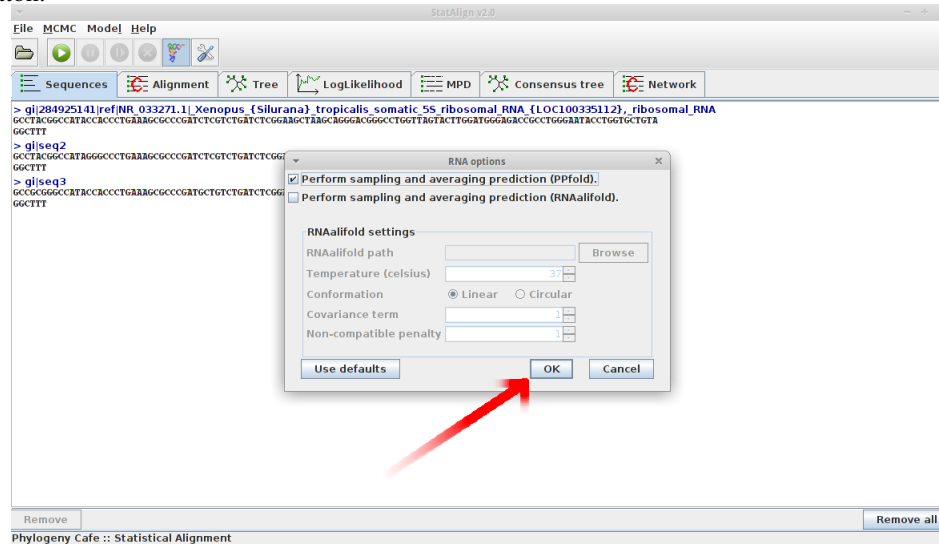

Now you should see 4 new tabs which indicate that RNA mode has been activated. To align and fold the sequences you press the play button which the red arrow points to.
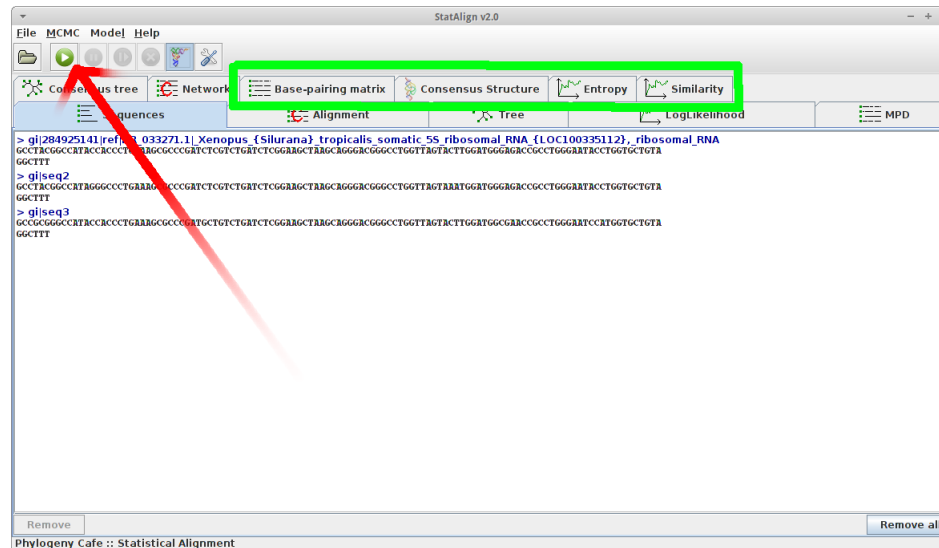
If that went well you should see "*Burn-in:* some number which increases rapidly" in the lower left corner. To see the consensus structure you can click on the tab which the red arrow points to.
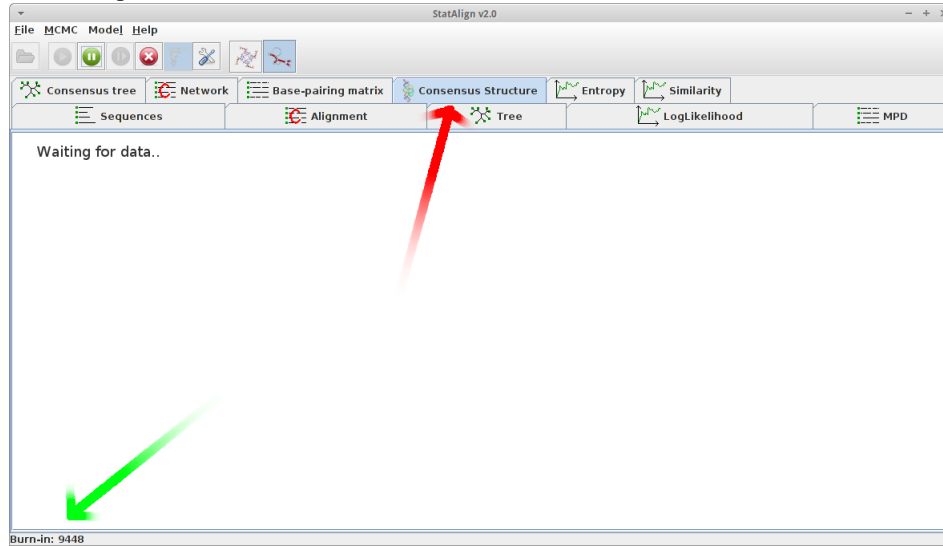
When the burn-in has finished the folding starts and you should see the current consensus structure from the samples we have already taken . The number of samples taken can be seen in the lower left corner.
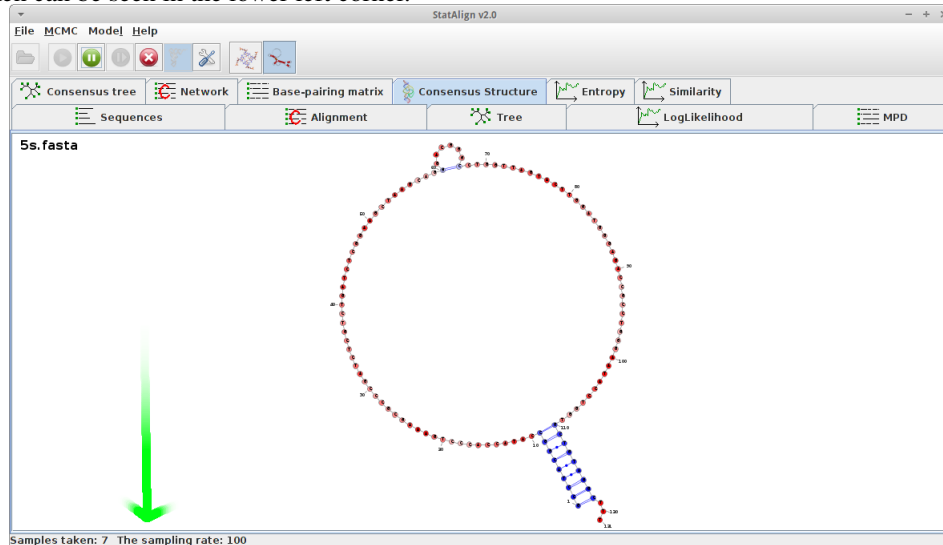
This is the get started tutorial. For a more detailed usage of StatAlign, please visit this website.