**Try an assembly!**

This will provide an example of how to assemble reads using **Newbler** aka “GS De Novo Assembler”.

1. Download the reads.
	1. From within your SEA Virtual Machine, go to **phagesdb.org**.
	2. From the **Resources** dropdown menu, select **Documents**.
	3. On the documents page, under the **Sample Files** heading, download the file named **AlanGrant Reads**.
2. Create a new **Newbler** assembly project.
	1. Open Newbler (GS De Novo Assembler) by clicking the icon on the left menu bar within the SEA Virtual Machine.



* 1. Click **New Assembly Project**.
	2. In the window that opens, replace “untitled” with the name of your project. (E.g. “AlanGrant”)
	3. Click **OK**.
1. Add your reads to your project.
	1. Select the project tab from the top of the **Newbler** window.
	2. Select the **FASTA and FASTQ reads** sub-tab.
	3. Click the **+** button to add a reads file.
	4. In the window that opens, navigate to the downloaded file **AlanGrant\_50kReads.fastq**, select it, and click **OK**.

(The location of the file may vary. The default location is in your Downloads folder.)

* 1. In the next window (Set FASTA/FASTQ Read Attributes) just click **OK**.
	2. Now you’ll see a reads file in your project.
1. Set parameters.
	1. Click the **Parameters** tab at the top of the window.
	2. Click on the **Output** sub-tab.
	3. In the right column, click the button to create a “**Complete Consed Folder**”.
	4. Mess with any other parameters you’d like. (The defaults are all good for phage genomes.)
2. Assemble!
	1. Click the **Start** button on the right side of the Newbler window. If prompted, click “yes”.
	2. Wait for the magic to happen! When the status bar in the upper right disappears, and you see “Ready for Analysis” return, it’s done! (Should take < 5 minutes.)
3. Check out the results.
	1. Click on the **Alignment results** tab to see a summary of the contigs created. Click on a contig to see the assembled reads.
	2. Click on the **Project** tab to see how many reads were used and incorporated.
	3. Click on the **Result files** tab to see some of the files that have been created, and click on a file to see its contents.
4. Look at the assembly in consed

If you have some command-line skills, this should be not too bad. If you need some command-line education, you can use the video tutorials here:

<http://phagesdb.org/workflow/videos/consed02/>

<http://phagesdb.org/workflow/videos/consed03/>

* 1. Close Newbler, answering “Yes” if prompted to save the project.
	2. Open a terminal



* 1. Navigate to your newly-created assembly folder.
	2. Go into **assembly/consed/edit\_dir/**
	3. From within the edit\_dir, type **consed** and press enter.
	4. Select the file 454Contigs.ace.1 and click **Open**. Voila!

Some basics of consed can be found in the video tutorial below:

<http://phagesdb.org/workflow/videos/consed04/>