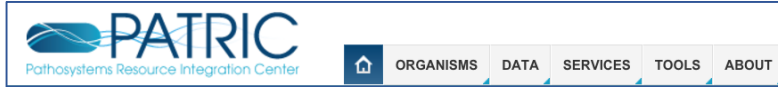
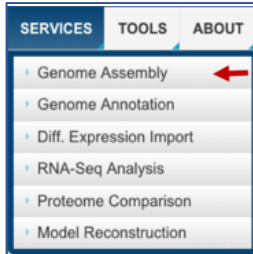


Submitting an Assembly job to PATRIC

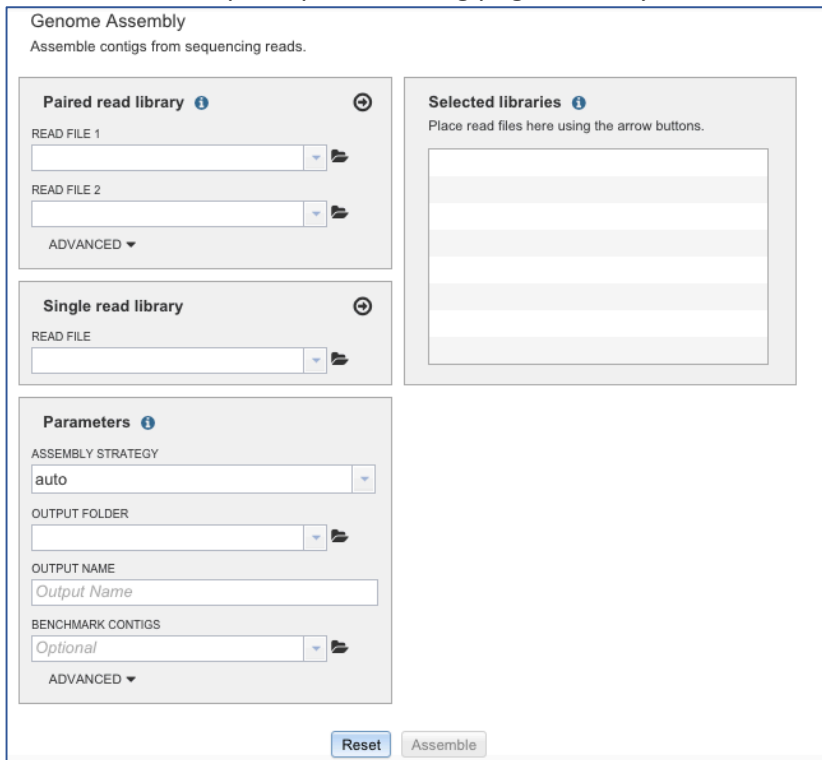
1. At the top of any PATRIC page, find the Services tab.



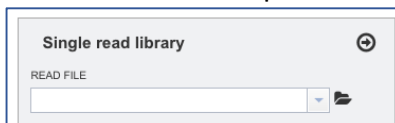
2. Click on Genome Assembly.



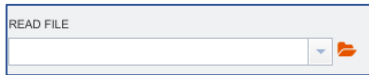
3. This will open up the landing page where you can submit your single or paired read files.

The image shows the "Genome Assembly" submission page. At the top, it says "Genome Assembly Assemble contigs from sequencing reads." Below this are three main sections: "Paired read library", "Single read library", and "Parameters".
- "Paired read library" has two "READ FILE" input fields with file selection icons and an "ADVANCED" dropdown.
- "Single read library" has one "READ FILE" input field with a file selection icon.
- "Parameters" has four dropdown menus: "ASSEMBLY STRATEGY" (set to "auto"), "OUTPUT FOLDER" (with file selection icon), "OUTPUT NAME" (text input with "Output Name" placeholder), and "BENCHMARK CONTIGS" (set to "Optional" with file selection icon). It also has an "ADVANCED" dropdown.
At the bottom right are "Reset" and "Assemble" buttons. To the right of the "Paired read library" section is a "Selected libraries" box with the instruction "Place read files here using the arrow buttons." and a large empty box for file uploads.

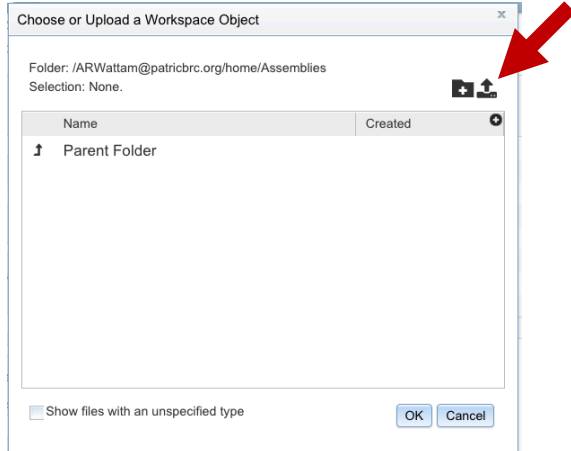
4. In this example we will upload a fastq file that contains single reads.

This is a close-up of the "Single read library" section. It shows the "READ FILE" label above a text input field with a file selection icon to its right.

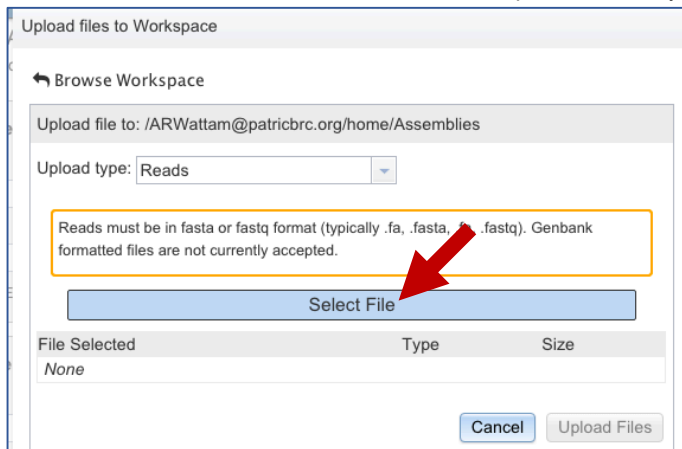
5. If you have not yet uploaded the file to PATRIC, you will need to do so now. First click the folder icon (colored orange in the screenshot below).



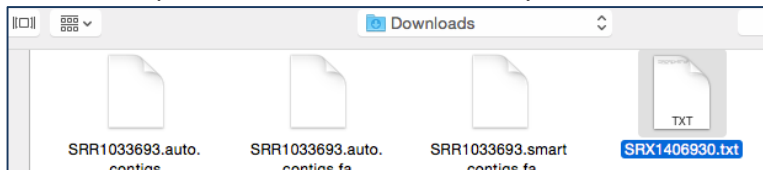
6. This opens up a window where you upload the files. To do this, click on the icon with the arrow pointing up, indicated by a red arrow in the screenshot below.



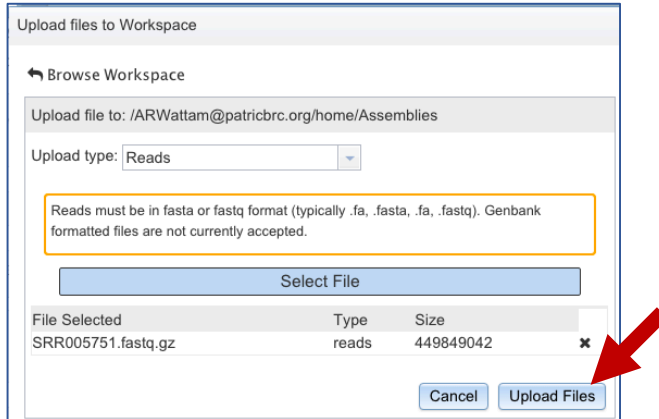
7. This will open up a window where you can select the file you want to upload. Click on the "Select File" in the blue bar (indicated by the red arrow).



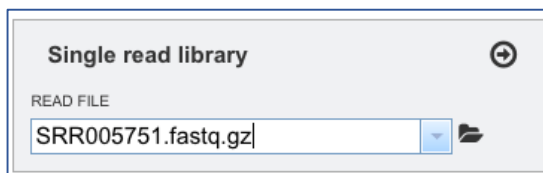
8. This will open a window that allows you to choose files that are stored on your computer. Select the file where you stored the fastq file on your computer.



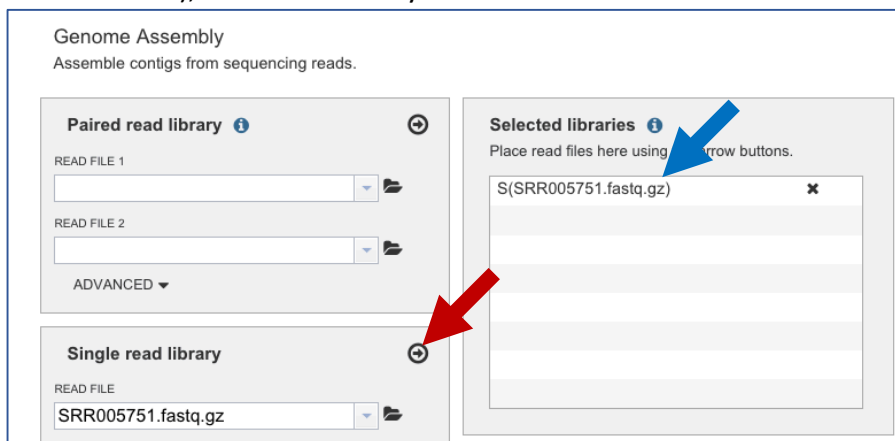
9. Once selected, it will autofill the name of the file. You can see it in the screenshot below. Click on the Upload Files button (red arrow in screenshot below).



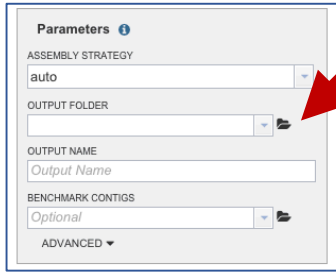
10. This will fill the name of the document into the text box as seen below.



11. Now you must click on the icon of an arrow within a circle (red arrow in screenshot below). This will move your file into the Selected libraries box (blue arrow in screenshot below), where it is ready to be assembled



12. The last step of the assembly process is filling in the parameters that define where the assembled contigs are placed in your workspace, and what you want them to be called. If you do not already have a folder in your PATRIC workspace for assemblies, you will need to create one now. To do this, click on the folder icon under Output Folder (indicated by the red arrow).



Parameters ⓘ

ASSEMBLY STRATEGY
auto

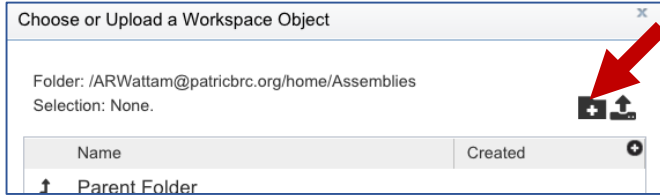
OUTPUT FOLDER
[Folder icon]

OUTPUT NAME
Output Name

BENCHMARK CONTIGS
Optional

ADVANCED ▾

13. In the window that pops up, click on the folder icon (indicated by the red arrow).



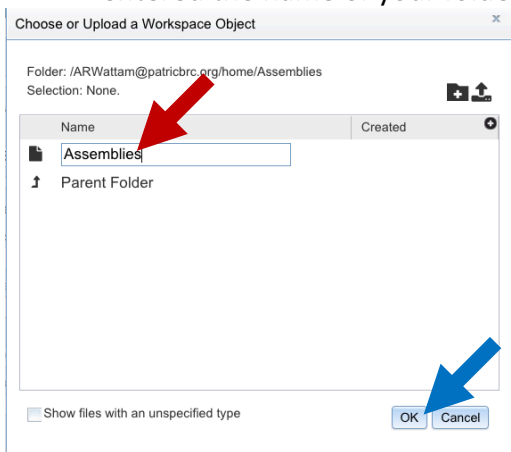
Choose or Upload a Workspace Object

Folder: /ARWattam@patricbrc.org/home/Assemblies
Selection: None.

[Folder icon] [Upload icon]

Name	Created
↑ Parent Folder	

14. This will allow you to create a new folder and name it (red arrow). Once you have entered the name of your folder, click the OK button (blue arrow below).



Choose or Upload a Workspace Object

Folder: /ARWattam@patricbrc.org/home/Assemblies
Selection: None.

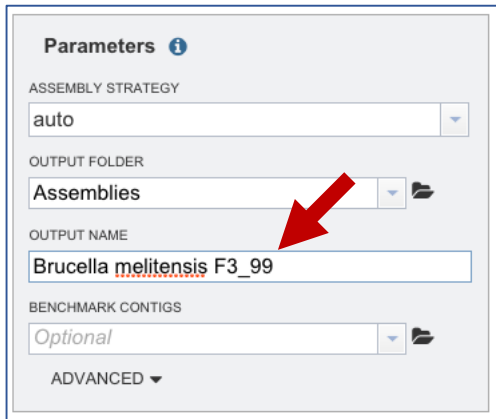
[Folder icon] [Upload icon]

Name	Created
[Folder icon] Assemblies	
↑ Parent Folder	

Show files with an unspecified type

OK Cancel

15. You need to name the assembly. Give it a distinctive name. I prefer genus, species and strain. Enter the name into the text box below Output Name (red arrow below).



Parameters ⓘ

ASSEMBLY STRATEGY
auto

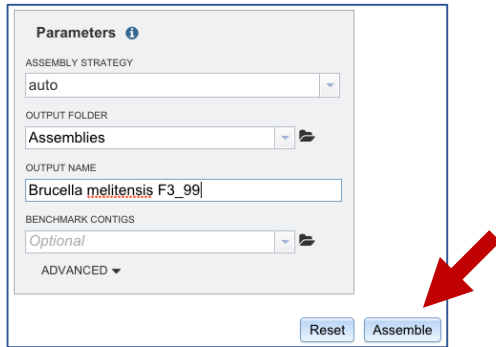
OUTPUT FOLDER
Assemblies

OUTPUT NAME
Brucella melitensis F3_99

BENCHMARK CONTIGS
Optional

ADVANCED ▾

16. To submit the job, click on the Assemble button.



Parameters ⓘ

ASSEMBLY STRATEGY
auto

OUTPUT FOLDER
Assemblies

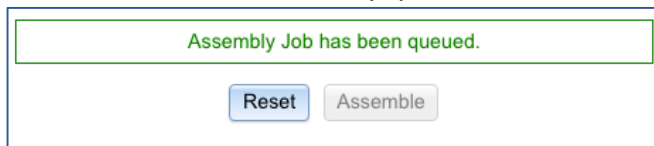
OUTPUT NAME
Brucella_melitensis F3_99

BENCHMARK CONTIGS
Optional

ADVANCED ▾

Reset Assemble

17. If the job was submitted successfully, a message will appear that tells you your job has entered the assembly queued.



Assembly Job has been queued.

Reset Assemble

18. You can check the status of your assembly job by clicking on the Jobs indicator at the bottom of the PATRIC page



Uploads 1·0 Jobs 43·1·0·7

19. Clicking on Jobs will take you to the Jobs Status page, where you can see how your assembly job is progressing. You can also see the status of all the previous service jobs that you have submitted to PATRIC.

Status	Submit	App	Output Name	Start	Completed
● in-progress	11/17/15, 4:04 PM	GenomeAssembly	Brucella suis bv 2 Hungary	11/17/15, 4:04 PM	
● completed	11/13/15, 4:39 PM	GenomeAssembly	Brucella melitensis Bv 1 str F3_99-548	11/13/15, 4:39 PM	11/13/15, 5:41 PM