Running VirSorter in iPlant Discovery Environment

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Abstract

This protocol gives an introduction to running VirSorter in the iPlant Discovery Environment.

Guidelines

See the wiki page of VirSorter for a more complete descripton of the result files:

https://pods.iplantcollaborative.org/wiki/display/DEapps/VIRSorter+1.0.2

Before start

To access VirSorter on iPlant, you will first need to create a (free) account. This can be done at this address: https://user.iplantcollaborative.org/register/
Help can found
at: https://pods.iplantcollaborative.org/wiki/display/start/Registering+for+and+Managing+your+iPlant+Account

Protocol

Step 1.
Register an account with iPlant.

🔗 LINK:
https://user.iplantcollaborative.org/register/

Step 2.
Login to the Discovery Environment.

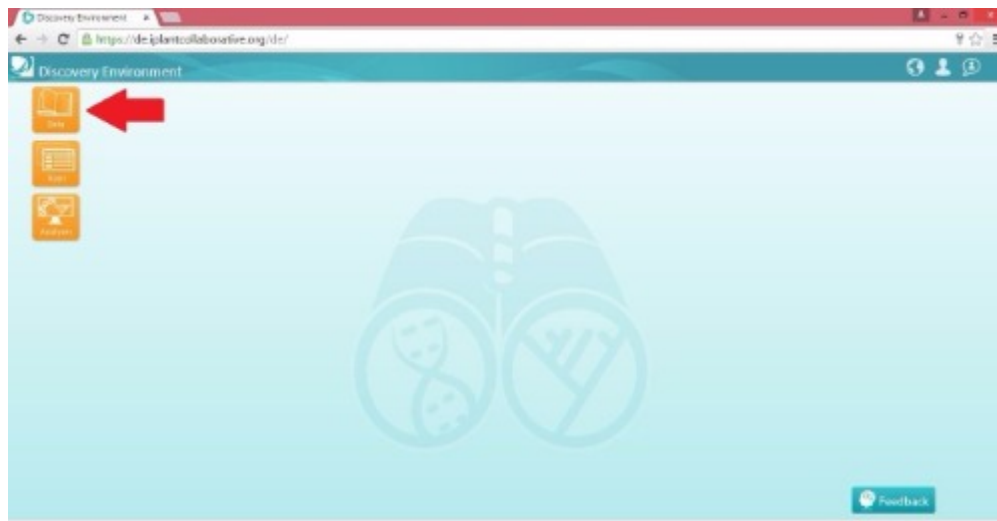🔗 LINK:
https://de.iplantcollaborative.org/de/

➕ NOTES
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The Discovery Environment is the section of iPlant hosting VirSorter.
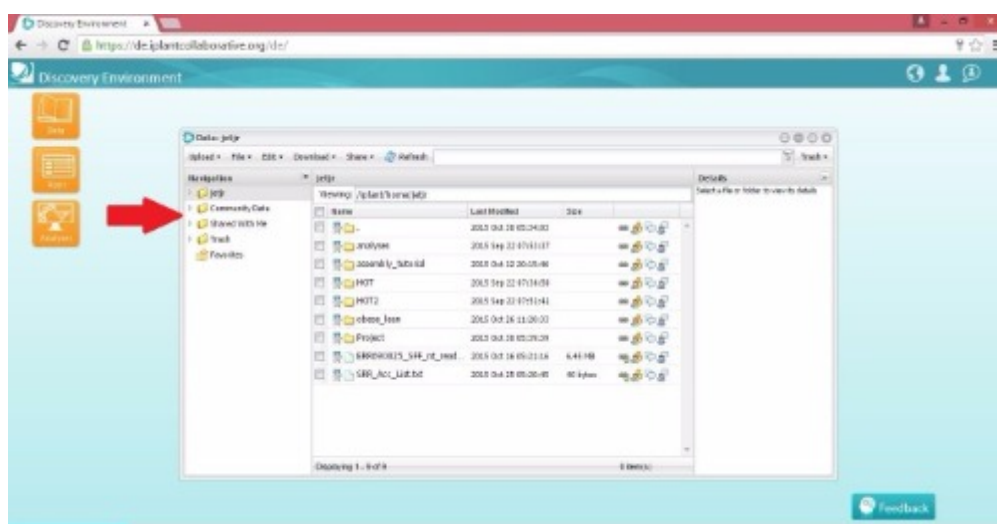
Upload your data

Step 3.
Click on the "Data" button on the left.
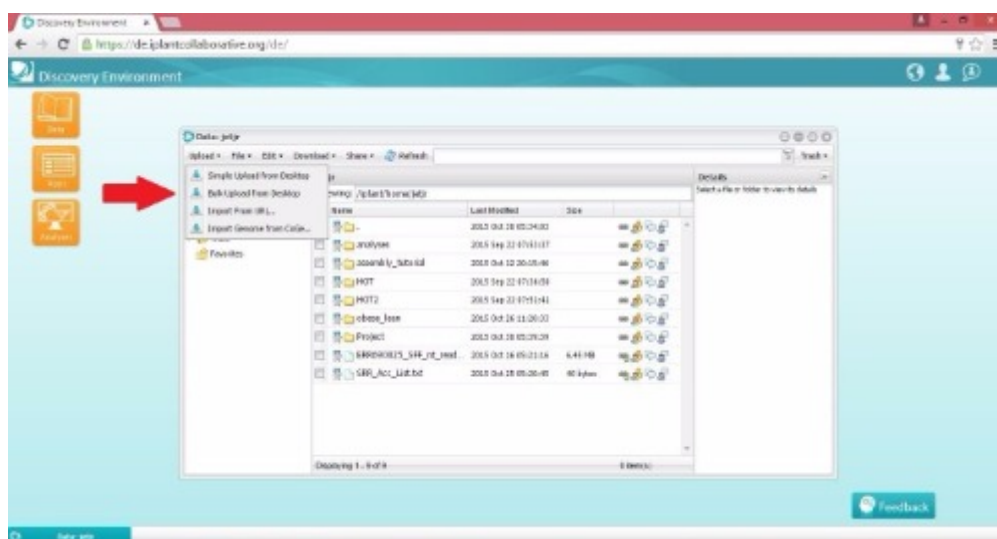
Upload your data
Step 4.
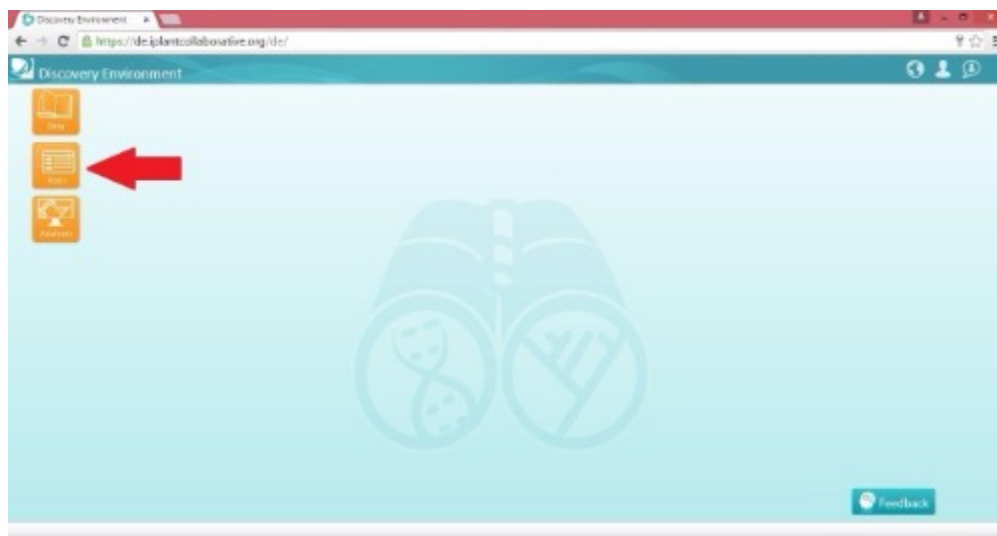Select a directory to work in.

Upload your data
Step 5.
Click on "Upload" to place your data in the current directory.
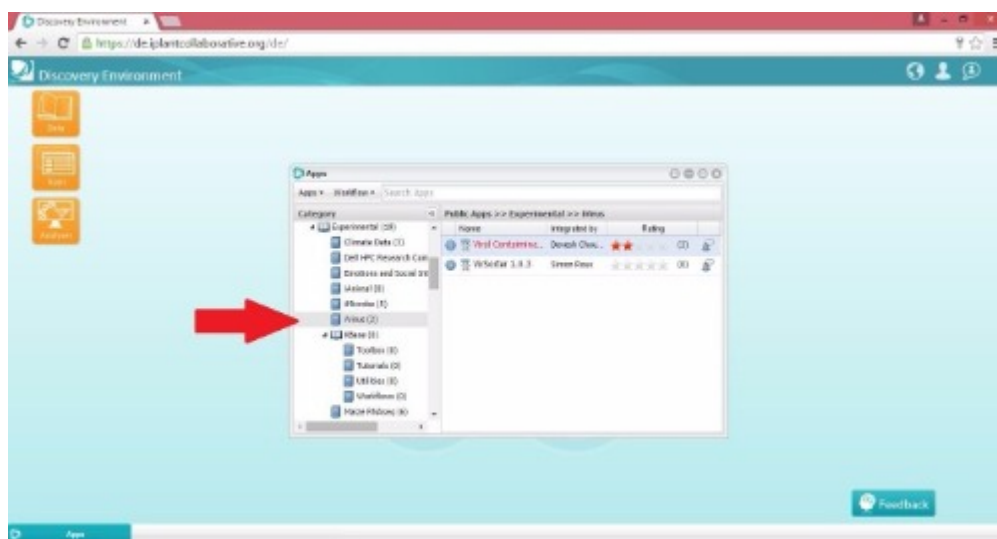
Step 6.

Click on the "Apps" button.

Select VirSorter parameters and launch computation
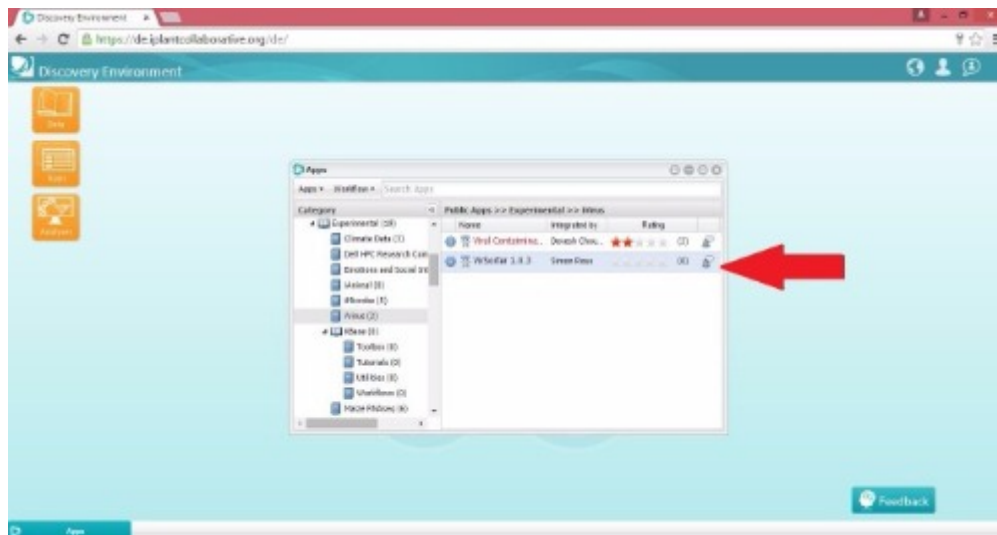
Step 7.

Select iVirus category.

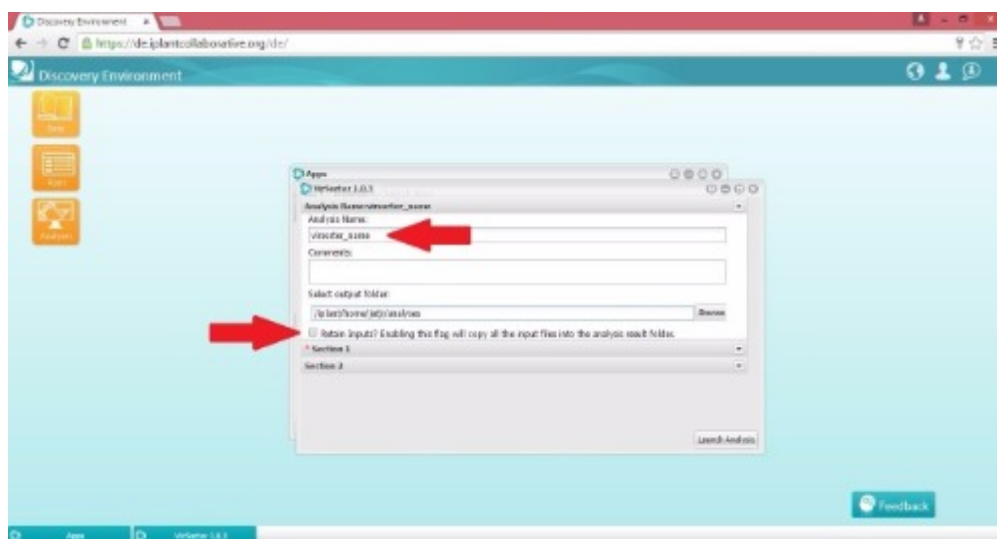Select VirSorter parameters and launch computation

Step 8.

Select VirSorter.

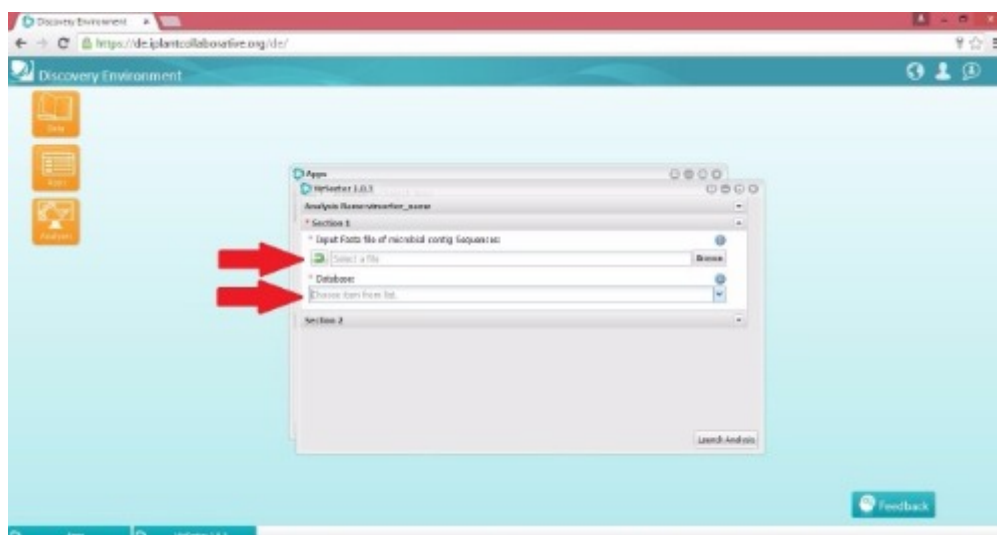Select VirSorter parameters and launch computation

Step 9.

Enter a name and select the output directory for the analysis.

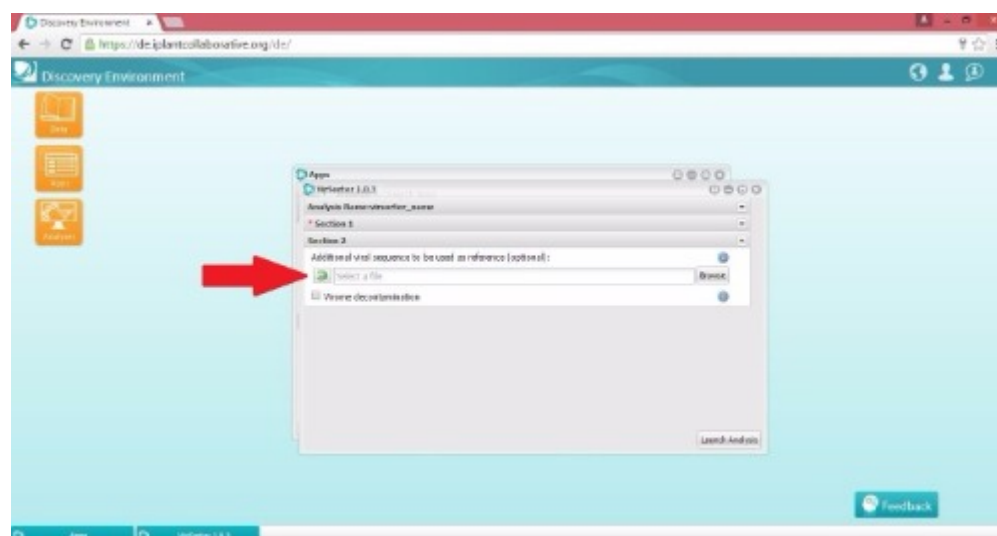Select VirSorter parameters and launch computation

Step 10.

Click section 1, select an input file and a database (i.e. with or without viromes).

Step 11.

You can also select a fasta file of additional viral sequences and select the 'virome decontamination' mode, designed to identify viral sequences in datasets that are mostly viral (as opposed to mining of viral signal in microbial genomes or metagenomes).
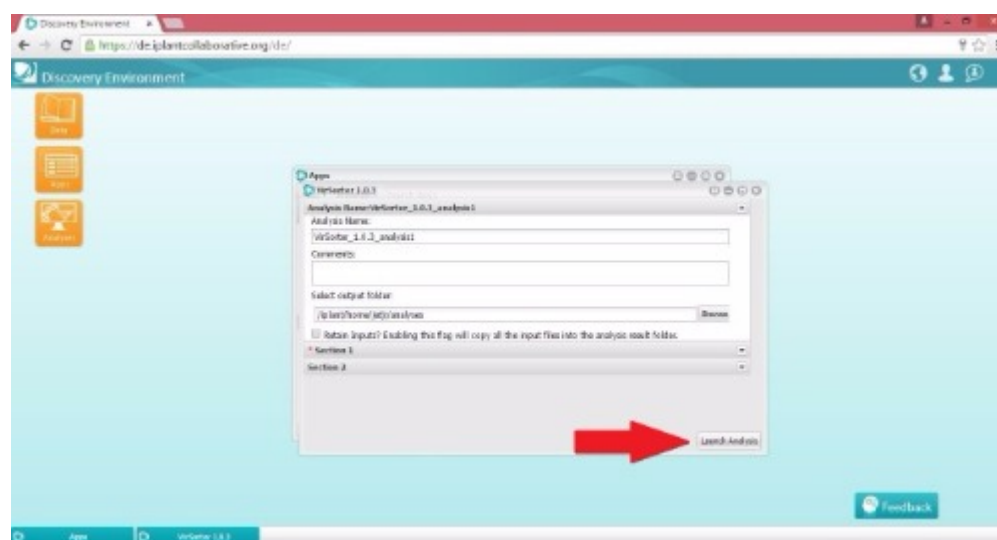

➕ NOTES

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This step is optional.

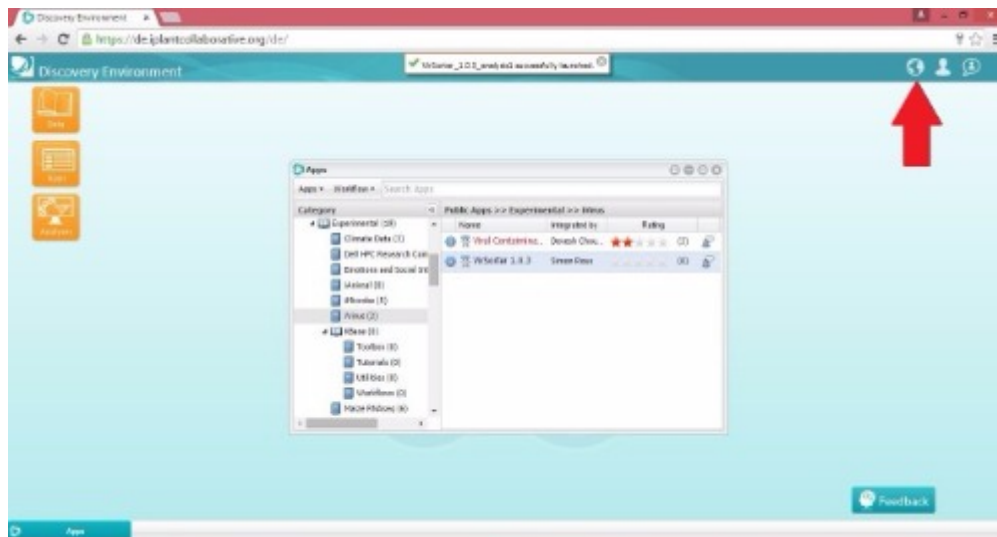Select VirSorter parameters and launch computation

Step 12.

Click "Launch Analysis"
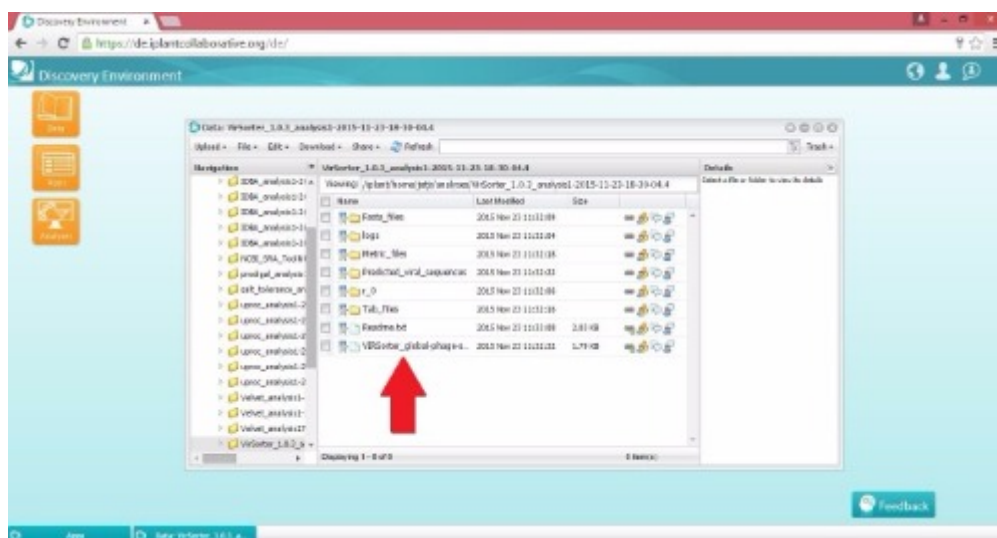

Retrieve VirSorter Results

Step 13.

You will be notified when the job is submitted, when the job is running, and when the job is complete.

Retrieve VirSorter Results

Step 14.

Once the job is completed the output directory will include the main csv output file, listing all sequences detected as viral with their associated category and metrics, alongside the other results files stored into different sub-directories.

Retrieve VirSorter Results

Step 15.

The file can be opened in iPlant or downloaded for further analysis.