# Running VirSorter in iPlant Discovery Environment

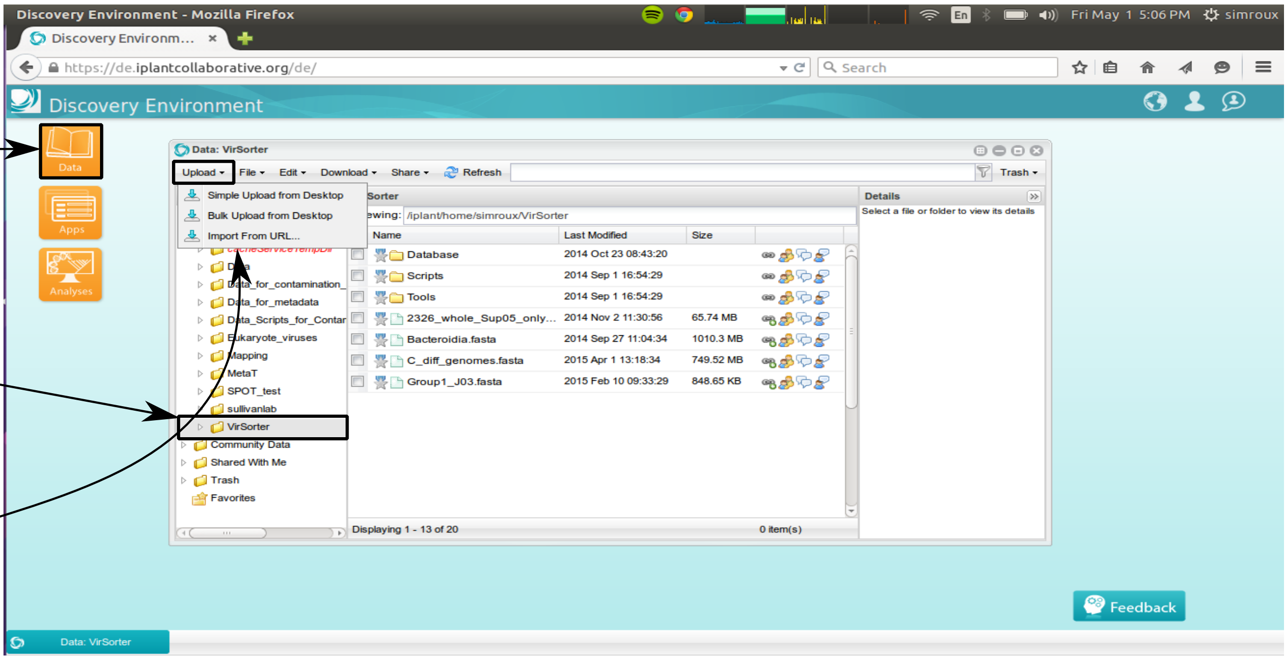
## 1. iPlant Registration

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 be found at https://pods.iplantcollaborative.org/wiki/display/start/Registering+for+and+Managing+your+iPlant+Account).

## 2. Login to the Discovery Environment

The Discovery Environment is the section of iPlant hosting VirSorter, and can be found at https://de.iplantcollaborative.org/de/

## 3. Upload your data



Viewing: /iplant/home/simroux/VirSorter

| Name | Last Modified | Size |
|---|---|---|
| Database | 2014 Oct 23 08:43:20 | |
| Scripts | 2014 Sep 1 16:54:29 | |
| Tools | 2014 Sep 1 16:54:29 | |
| 2326_whole_Sup05_only... | 2014 Nov 2 11:30:56 | 65.74 MB |
| Bacteroidia.fasta | 2014 Sep 27 11:04:34 | 1010.3 MB |
| C_diff_genomes.fasta | 2015 Apr 1 13:18:34 | 749.52 MB |
| Group1_J03.fasta | 2015 Feb 10 09:33:29 | 848.65 KB |

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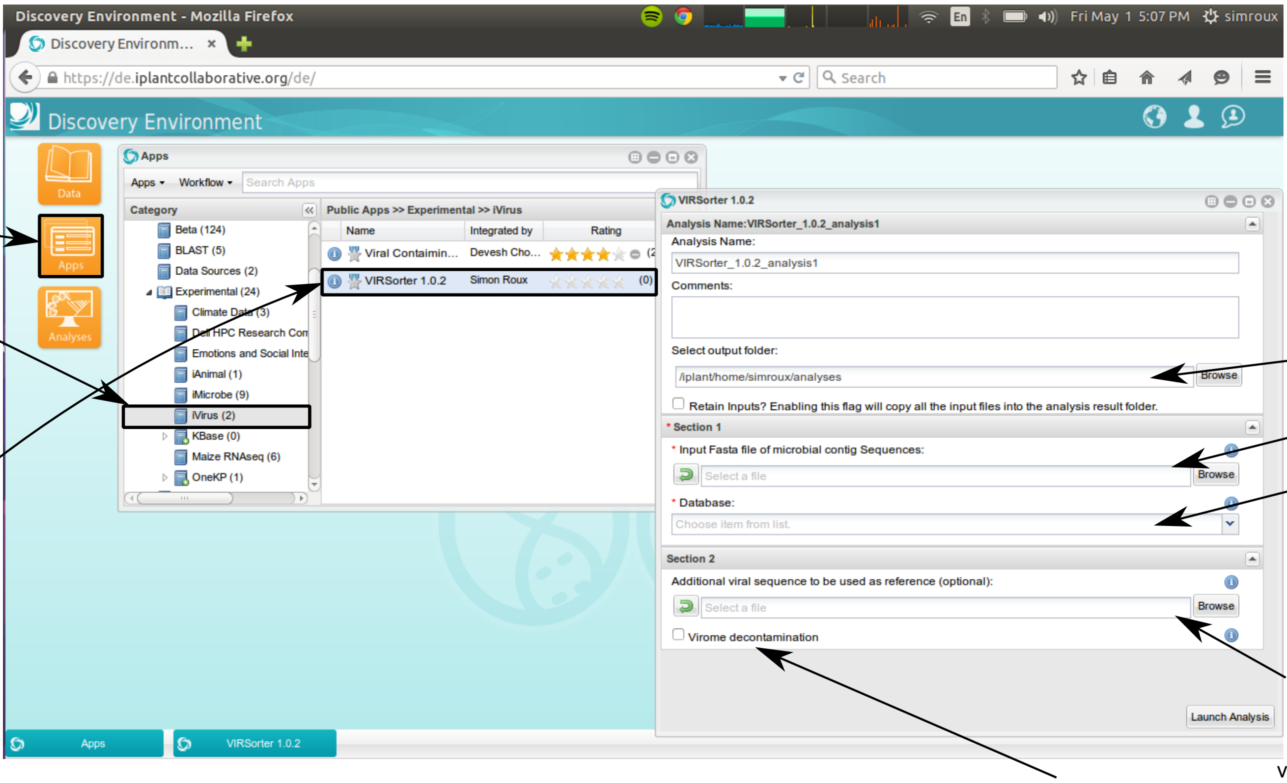
In the data tab

select a directory to work into

and upload your genome(s) / metagenome(s) in fasta format

## 4. Select VirSorter parameters and launch the computation



| Name | Integrated by | Rating |
|---|---|---|
| Viral Contaimin... | Devesh Cho... | (2 |
| VIRSorter 1.0.2 | Simon Roux | (0) |

VIRSorter 1.0.2

Analysis Name:VIRSorter_1.0.2_analysis1

Analysis Name: VIRSorter_1.0.2_analysis1

Comments:

Select output folder: /iplant/home/simroux/analyses

☐ Retain Inputs? Enabling this flag will copy all the input files into the analysis result folder.

* Section 1

* Input Fasta file of microbial contig Sequences: Select a file

* Database: Choose item from list.

Section 2

Additional viral sequence to be used as reference (optional): Select a file

☐ Virome decontamination

In the app tab

select iVirus category

then select VirSorter

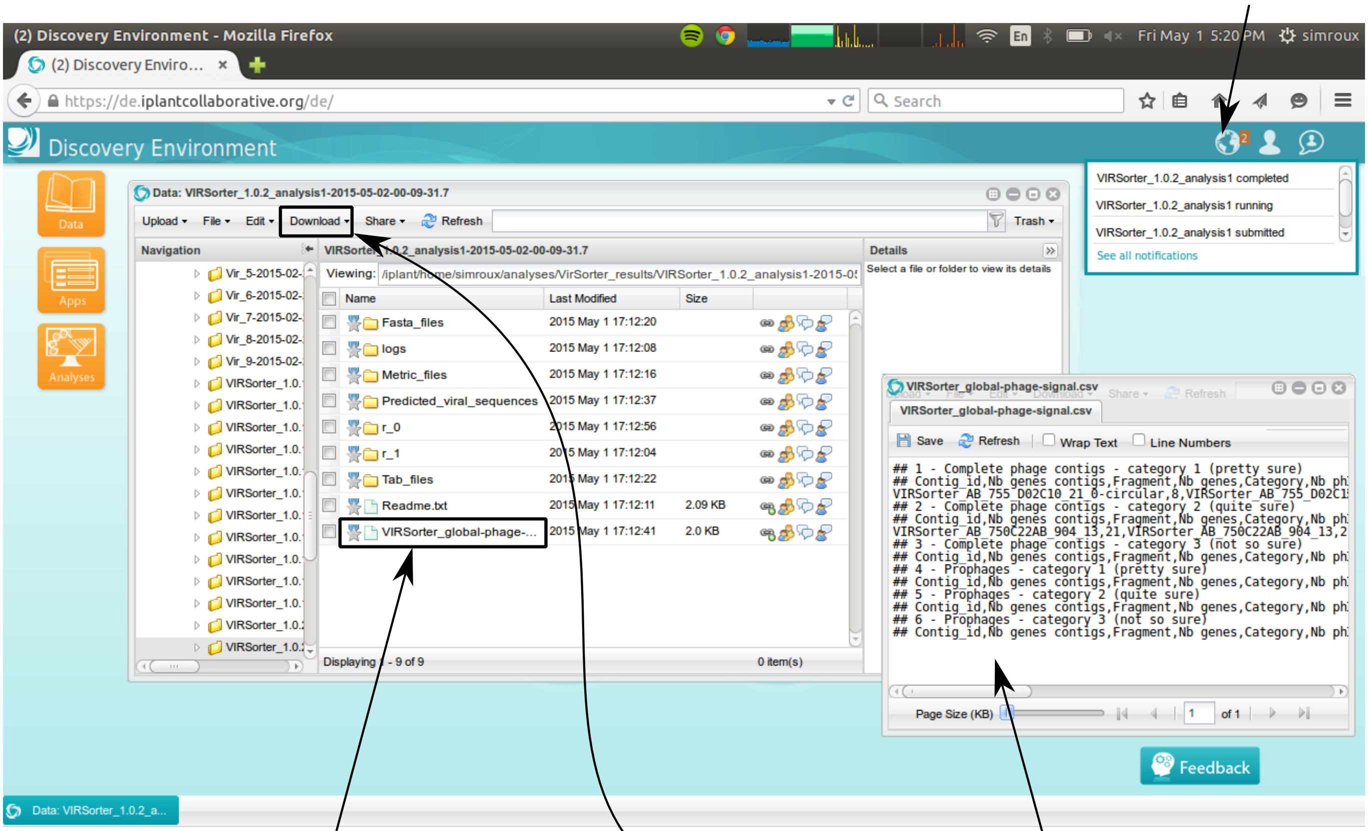
Select an **output folder** then select an **input file** and a **database** (i.e. with or without viromes)

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 the mining of viral signal in microbial genomes or metagenomes)

## 5.Retrieve VirSorter results

Notifications will indicate when the job is
(i) submitted, (ii) running, and (iii) completed



VIRSorter_1.0.2_analysis1 completed
VIRSorter_1.0.2_analysis1 running
VIRSorter_1.0.2_analysis1 submitted
See all notifications

VIRSorter_1.0.2_analysis1-2015-05-02-00-09-31.7

Viewing: /iplant/home/simroux/analyses/VirSorter_results/VIRSorter_1.0.2_analysis1-2015-0

| Name | Last Modified | Size |
|---|---|---|
| Fasta_files | 2015 May 1 17:12:20 | |
| logs | 2015 May 1 17:12:08 | |
| Metric_files | 2015 May 1 17:12:16 | |
| Predicted_viral_sequences | 2015 May 1 17:12:37 | |
| r_0 | 2015 May 1 17:12:56 | |
| r_1 | 2015 May 1 17:12:04 | |
| Tab_files | 2015 May 1 17:12:22 | |
| Readme.txt | 2015 May 1 17:12:11 | 2.09 KB |
| VIRSorter_global-phage-... | 2015 May 1 17:12:41 | 2.0 KB |

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VIRSorter_global-phage-signal.csv

Save Refresh ☐ Wrap Text ☐ Line Numbers

```
## 1 - Complete phage contigs - category 1 (pretty sure)
## Contig_id,Nb genes contigs,Fragment,Nb genes,Category,Nb ph
VIRSorter_AB_755_D02C10_21_0-circular,8,VIRSorter_AB_755_D02C1
## 2 - Complete phage contigs - category 2 (quite sure)
## Contig_id,Nb genes contigs,Fragment,Nb genes,Category,Nb ph
VIRSorter_AB_750C22AB_904_13,21,VIRSorter_AB_750C22AB_904_13,2
## 3 - Complete phage contigs - category 3 (not so sure)
## Contig_id,Nb genes contigs,Fragment,Nb genes,Category,Nb ph
## 4 - Prophages - category 1 (pretty sure)
## Contig_id,Nb genes contigs,Fragment,Nb genes,Category,Nb ph
## 5 - Prophages - category 2 (quite sure)
## Contig_id,Nb genes contigs,Fragment,Nb genes,Category,Nb ph
## 6 - Prophages - category 3 (not so sure)
## Contig_id,Nb genes contigs,Fragment,Nb genes,Category,Nb ph
```

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Once 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 result files stored into different sub-directories.

Result files can be opened in the Discovery Environment or downloaded for further processing

See the wiki page of VirSorter for a more complete description of the result files:
https://pods.iplantcollaborative.org/wiki/display/DEapps/VIRSorter+1.0.2