# **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

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## 4. Select VirSorter parameters and launch the computation

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n the app tab	Category Category Public Apps >> Experimental >> IVirus Beta (124)	Rating Analysis Name:VIRSorter_1.0.2_analysis1 Analysis Name: VIRSorter_1.0.2_analysis1 Comments: Comments:		*
select iVirus category then select		Select output folder: //iplant/home/simroux/analyses Retain Inputs? Enabling this flag will copy all the input files in Section 1 Input Fasta file of microbial contig Sequences:	nto the analysis result folder.	Select an output folde then select a input file and a
VirSorter		Select a file     Database:     Choose item from list.      Section 2      Additional viral sequence to be used as reference (optional):     Select a file     Utema decembration income	Browse Browse	database (i.e. with or without viromes)
C) Apps	VIRSorter 1.0.2		Launch Analysi	You can also select a fasta file of additional

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)

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

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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

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