Preparing Data for vContact from Proteins (Cyverse)

Version 4

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ABSTRACT

Preparing data for use in vContact by using VirSorted Ocean Sampling Day (2014) contigs, using tools available in Cyverse. This protocol creates a BLAST DB, BLASTs sequences, and creates a gene-to-contig mapping file. Results from this protocol are suitable for vContact-PCs.

EXTERNAL LINK

https://dx.doi.org/10.7717/peerj.3243

THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

Bolduc B, Jang HB, Doulcier G, You Z, Roux S, Sullivan MB, vConTACT: an iVirus tool to classify double-stranded DNA viruses that infect and . PeerJ doi: 10.7717/peerj.3243

PROTOCOL STATUS

Working

We use this protocol in our group and it is working

GUIDELINES

This is part of a larger protocol *Collection* that involves the end-to-end processing of raw viral metagenomic reads obtained from a sequencing facility to assembly and analysis using Apps (i.e. tools) developed by iVirus and implemented within the Cyverse cyberinfrastructure.

BEFORE STARTING

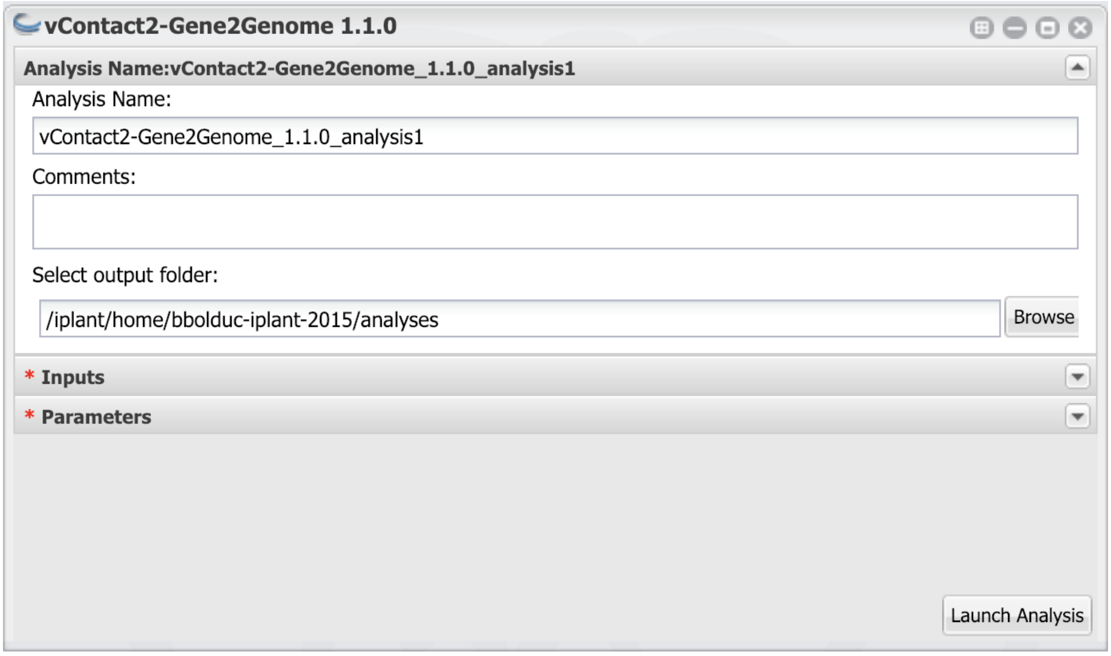
To run this protocol, users must first register for Cyverse account. All data (both inputs and outputs) are available within Cyverse's data store at /iplant/home/shared/iVirus/ExampleData/

Starting at version 4, this method is dramatically simplified, as nearly all steps were integrated into vConTACT2's functionality. This results in a faster, easier-to-use, and less complicated method. Any user wishing to repeat experiments *exactly* as described in the original iVirus manuscript should run version 3 or earlier. However, except for very minor spelling changes, the results files are nearly identical, and the content 100% identical.

Generating Gene-to-Genome Mapping

1 Open vContact2-Gene2Genome

Open "vContact2-Gene2Genome" from the "Apps" menu.


vContact2-Gene2Genome 1.1.0

Analysis Name:vContact2-Gene2Genome_1.1.0_analysis1

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Comments:

Select output folder: /iplant/home/bbolduc-iplant-2015/analyses

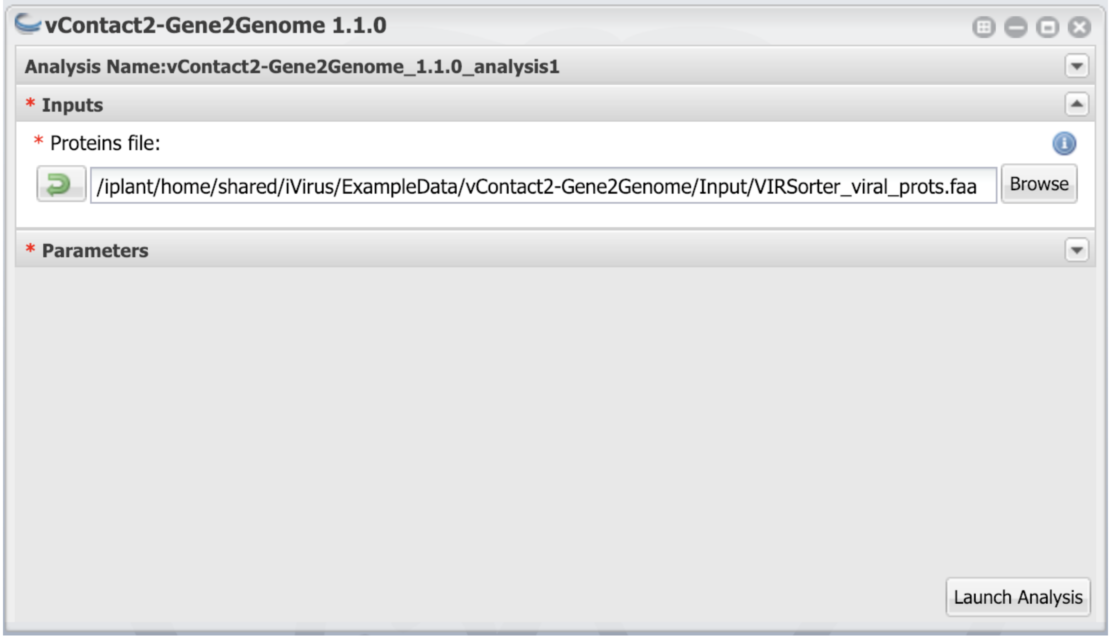
Starting menu for the Gene2Genome app in the CyVerse Discovery Environment.

2 Select Inputs

Select the 'Inputs' tab.

For **Proteins file**:

- Navigate to *Community Data* --> *iVirus* --> *ExampleData* --> vContact2-Gene2Genome --> *Input*. Select *VIRSorter_viral_prots.faa* Alternatively, copy-and-paste the location: /iplant/home/shared/iVirus/ExampleData/vContact2-Gene2Genome/Input into the navigation bar and select the protein fasta file.


vContact2-Gene2Genome 1.1.0

Analysis Name:vContact2-Gene2Genome_1.1.0_analysis1

* Inputs

* Proteins file: /iplant/home/shared/iVirus/ExampleData/vContact2-Gene2Genome/Input/VIRSorter_viral_prots.faa

Inputs section of Gene2Genome

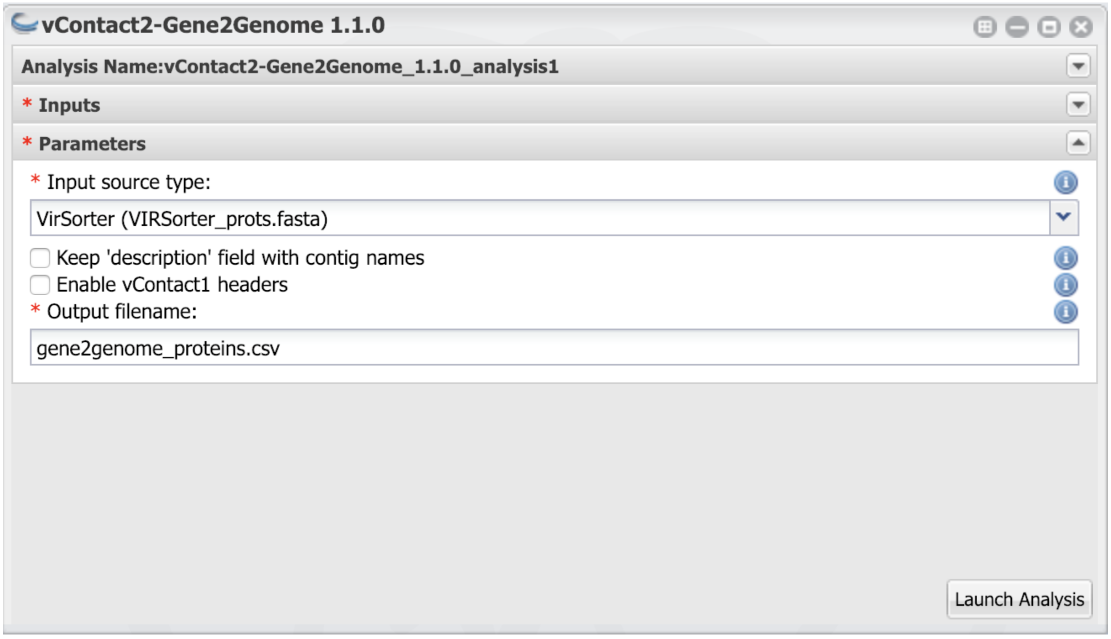
3 Select Parameters

Under "**Input source type**" change to *VirSorter*. Users can select a number of different parsing formats depending on the ORF caller they used to generate their proteins. For this example, everything passed through VirSorter, so we'll use VirSorter's formatting convention to extract the contigs each ORF/gene derives.

Keep 'description' field with contig names: Some formats have descriptions in their fasta files. Flagging this option keeps those descriptions.

Enable vContact1 headers: vContact1 and vContact2 fundamentally use the same input information, but are formatted a little differently. *If you use vContact 1* you must select this box. Failure to do so will result in vContact 1, well, failing. If you are using vContact2, then keep this *unchecked*.

Output filename: Anything useful or descriptive.



vContact2-Gene2Genome 1.1.0

Analysis Name:vContact2-Gene2Genome_1.1.0_analysis1

* Inputs

* Parameters

* Input source type:

VirSorter (VIRSorter_prots.fasta)

□ Keep 'description' field with contig names

□ Enable vContact1 headers

* Output filename:

gene2genome_proteins.csv

Parameters section of Gene2Genome

4 Launch Analysis

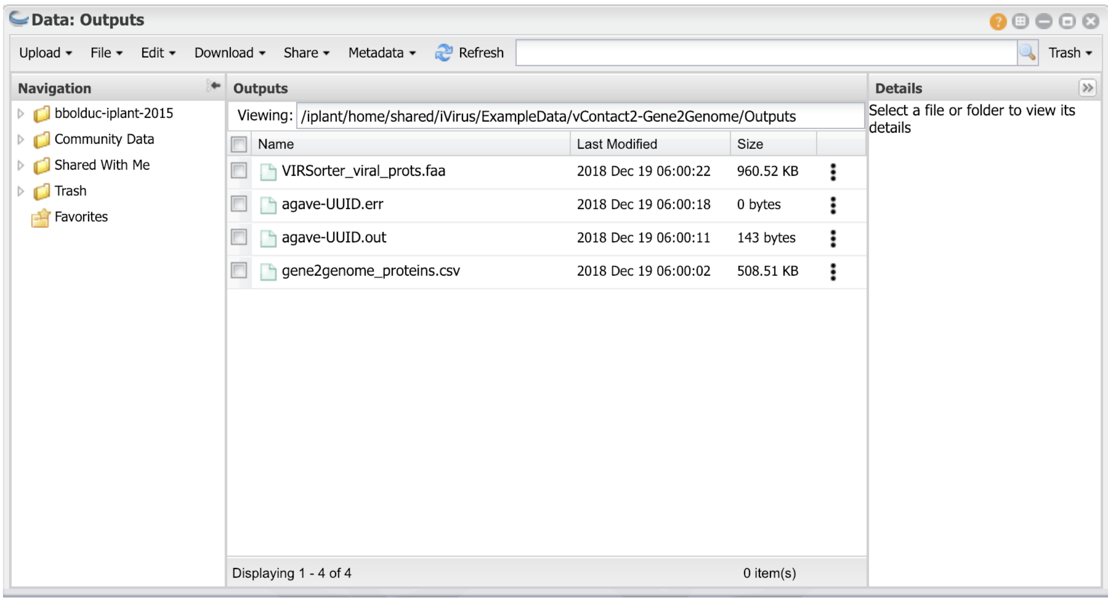
Run the job!

This should take minutes. Depending on the queue in Cyverse, it will likely take longer to submit and start the job than it does to run it!

5 Results

EXPECTED RESULT

Expect results can be found in the vContact2-Gene2Genome 'Outputs' directory. They'll be 4 files: 2 with agave messages (the errors and outputs), the original proteins file (VIRSorter_viral_prots.faa) and the gene-to-genome mapping file.



Viewing: /iplant/home/shared/iVirus/ExampleData/vContact2-Gene2Genome/Outputs

Name	Last Modified	Size
VIRSorter_viral_prots.faa	2018 Dec 19 06:00:22	960.52 KB
agave-UUID.err	2018 Dec 19 06:00:18	0 bytes
agave-UUID.out	2018 Dec 19 06:00:11	143 bytes
gene2genome_proteins.csv	2018 Dec 19 06:00:02	508.51 KB

Displaying 1 - 4 of 4 0 item(s)

Output files produced by the vContact2-Gene2Genome app

From this point, it's off to vConTACT2! *The gene2genome_proteins.csv* file and the *original proteins file* (used as input for this app) are the only hard requirements for vConTACT2.