

# Virtool: Software for Detection of Plant Virus Using Next Generation Sequencing

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## Introduction

National and international movement of propagative plant material requires reliable testing for the presence of harmful viruses. Next generation sequencing (NGS) is rapidly being developed as a tool for diagnostic testing and can be used for the detection of both known and novel viruses. It provides a major improvement over bioassays by dramatically reducing the both the time and cost of testing.

Virtool has been developed to make plant virus detection using short reads more accessible to lab technicians and administrative staff. It presents the analytical process from quality assessment of Illumina libraries to a diagnostic result in a modern and intuitive interface.

Virtool implements many quality control measures that will be necessary as NGS is adopted as a recognized diagnostic testing method.

## Implementation

Virtool is a web application. The server is written in Python and is made to run on the Linux operating system. The browser client has been developed using modern web technologies that allow intuitive real-time monitoring of analytical tasks and clean, navigable result visualization.

Virtool has two primary analytical functions. The first is to identify known viruses within a sample. This is accomplished using fast read mapping and statistical reassignment of ambiguous mappings using a method adapted from Pathoscope (Hong *et al.*, 2014).

The second function is to identify sequences that may be genomic components of potential novel viruses. Reads with no mapping to host or known viral reference sequences are assembled and translated before being scanned for viral motifs using profile hidden markov models (HMM) generated from viral sequences (Skewes-Cox, 2014) and HMMER 3.1b2+ (Eddy, 2012).

## Features

- import, quality assessment, and correction of FASTQ files
- sample management
- user management and permission control
- visualization of sample quality and analytical results
- modifiable and trackable virus reference database
- built-in job manager
- host and contaminant genome screening
- automatic software updates from GitHub repository
- automatic import of virus database and profile HMMs
- complete JSON web API

## Availability

Website: <https://www.virtool.ca>  
 GitHub: <https://github.com/virtool>

## References

- Eddy, S.R. (2012). *PLoS Comput. Biol.*, **7**, e1002195.  
 Hong, C. et al. (2014). *Microbiome*, **2**, 33.  
 Skewes-Cox, P. et al. (2014). *PLoS One*, **9**, 8.

## Screenshots

### Job Manager

#### Jobs

Job Name	Status	Started	By
PathoscopeBowtie	Complete	Started 12 days ago	james
PathoscopeBowtie	Complete	Started 12 days ago	james
PathoscopeBowtie	Complete	Started 11 days ago	james

### Sample Manager

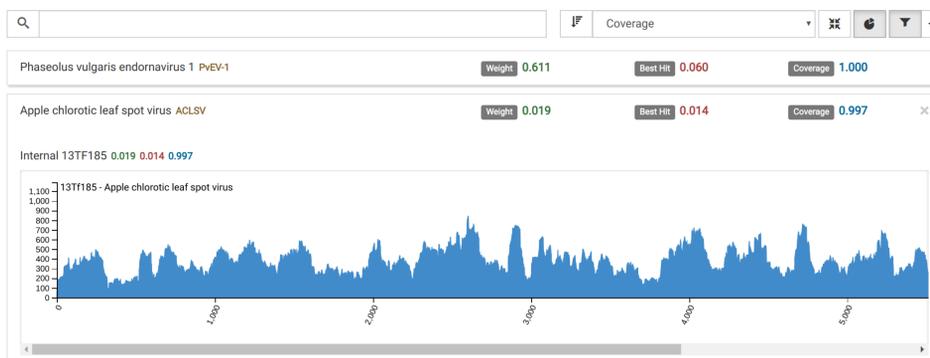
#### Samples 1311

Sample Name	Actions	Created
17SP004	Import Pathoscope NuVs	Created a month ago by tracy
17SP003	Import Pathoscope NuVs	Created a month ago by tracy
17SP005	Import Pathoscope NuVs	Created a month ago by tracy

### Result Viewer

#### 17SP006

Field	Value
Algorithm	PathoscopeBowtie
Index Version	3
Library Read Count	2,555,354
Created	a month ago
Created By	tracy



### Virus Editor

#### Grapevine leafroll-associated virus 2 GLRaV2

Field	Value
Name	Grapevine leafroll-associated virus 2
Abbreviation	GLRaV2
Version	0
Unique ID	7ae12e5b

#### Isolates 5

Isolate Name	Details										
Isolate 93/955	<table border="1"> <tr><td>Name</td><td>Isolate 93/955</td></tr> <tr><td>Source Type</td><td>Isolate</td></tr> <tr><td>Source Name</td><td>93/955</td></tr> <tr><td>Default</td><td>Yes</td></tr> <tr><td>Unique ID</td><td>qjz6w3r0</td></tr> </table>	Name	Isolate 93/955	Source Type	Isolate	Source Name	93/955	Default	Yes	Unique ID	qjz6w3r0
Name	Isolate 93/955										
Source Type	Isolate										
Source Name	93/955										
Default	Yes										
Unique ID	qjz6w3r0										
Isolate GRSLV											
Isolate 3138-07											
Isolate SG											
Strain BD											