

VIROME: Downloading libraries of VIROME data

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Abstract

This tutorial explains how to download entire libraries of data from the VIROME web application.

Wommack, K. E., J. Bhavsar, S. W. Polson, J. Chen, M. Dumas, S. Srinivasiah, M. Furman, S. Jamindar, and D. J. Nasko. 2012. VIROME: a standard operating procedure for analysis of viral metagenome sequences. *Standards in Genomic Sciences* 6:427-439 [[PMC3558967](https://pubmed.ncbi.nlm.nih.gov/2258967/)]

[See site](#) for more information.

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Guidelines

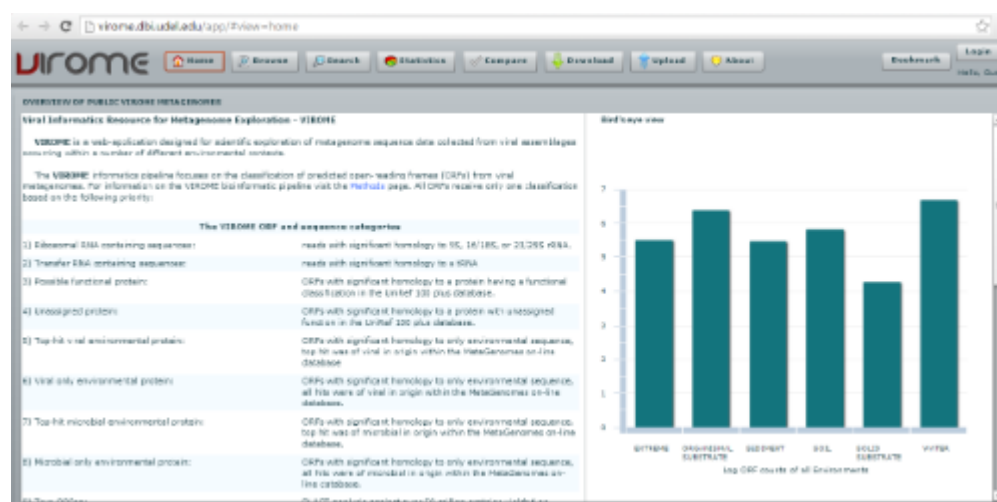
See full video below for more information.

YouTube link: <https://www.youtube.com/watch?v=sVoku4GyK6s>

Protocol

Step 1.

Go to [VIROME web application](#).



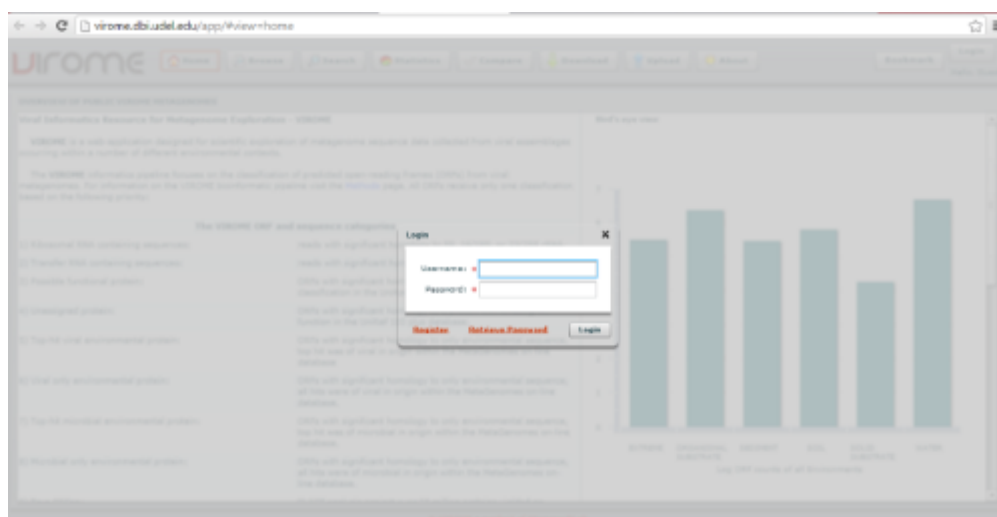
Step 2.

Click the login button.



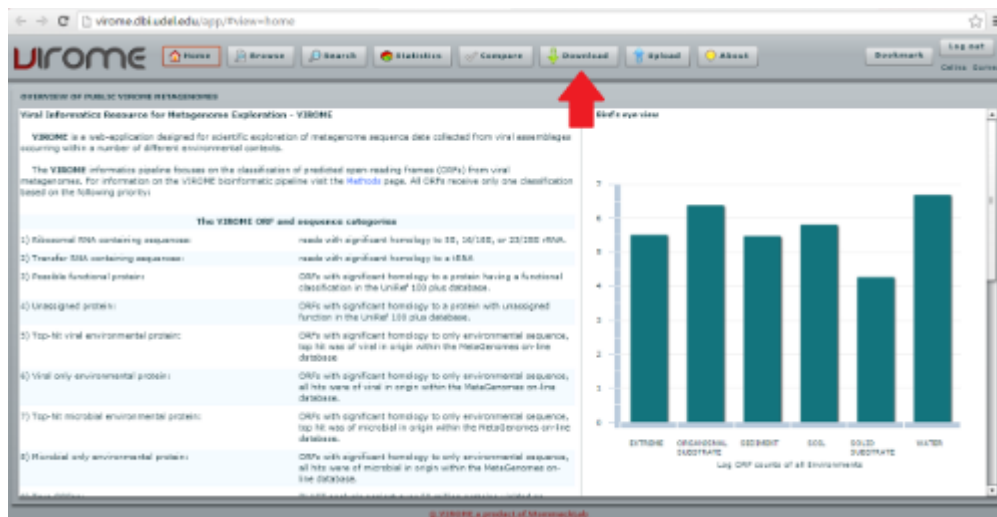
Step 3.

Enter username and password to authenticate into the application.

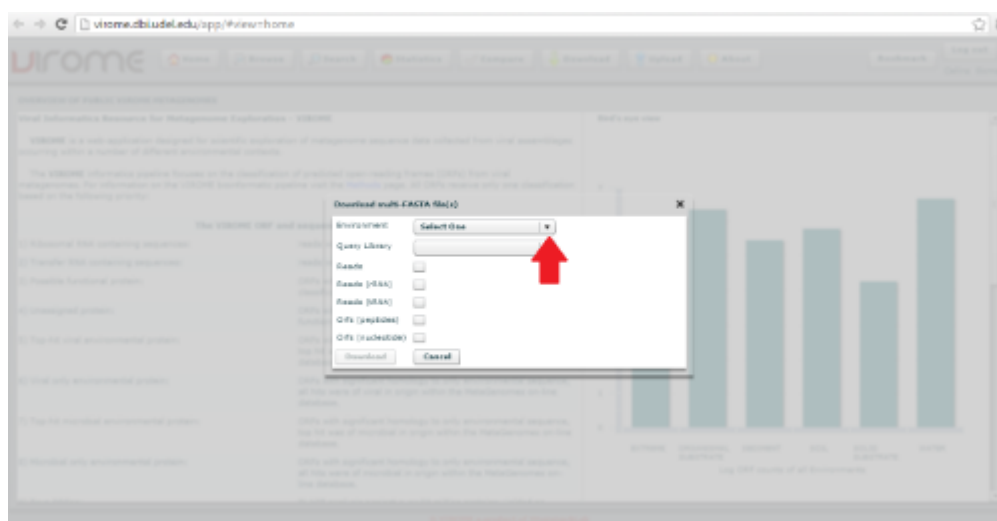


Step 4.

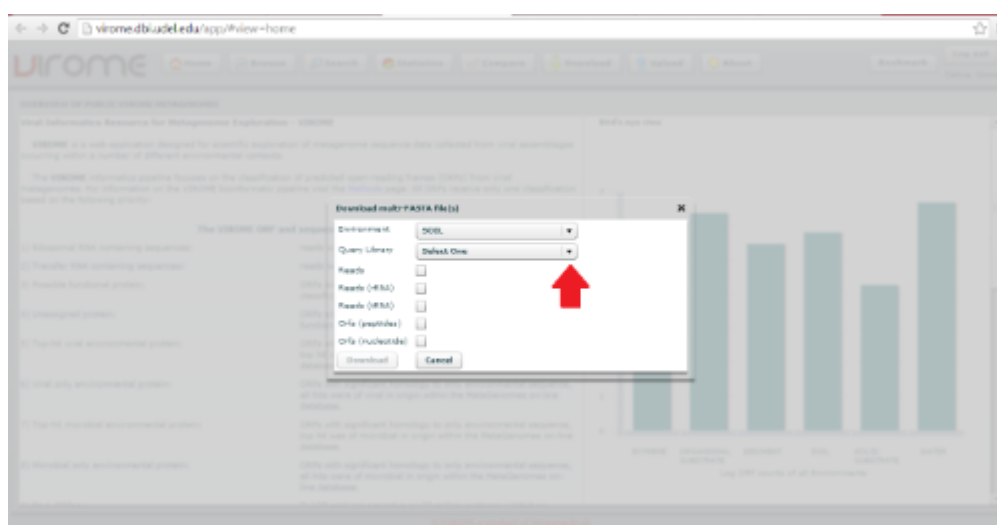
Click the download button.



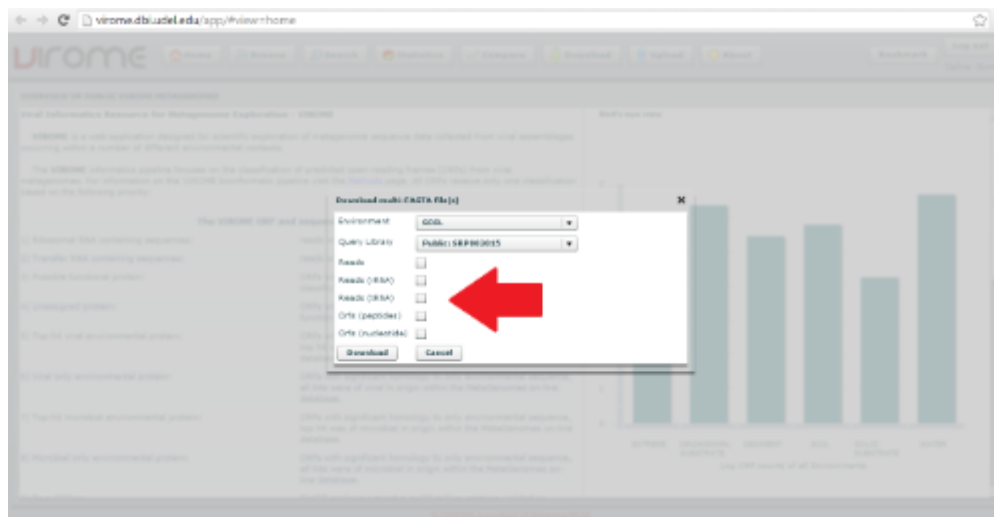
Step 5.
Select an environment.



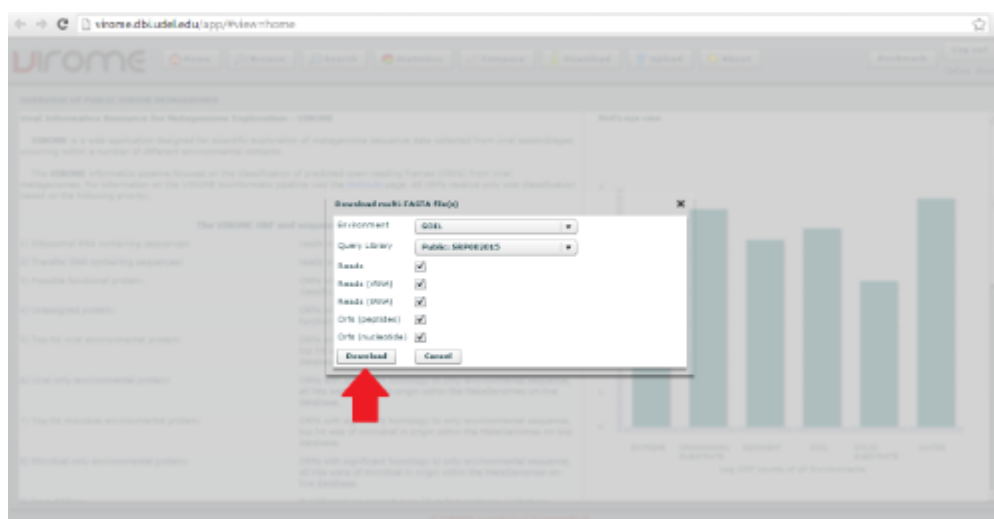
Step 6.
Select a query library.



Step 7.
Select desired data.



Step 8.
Click "download".



Step 9.
Once prompted to save the file, do not change the file name!

Step 10.
Once saved, navigate to the Finder.

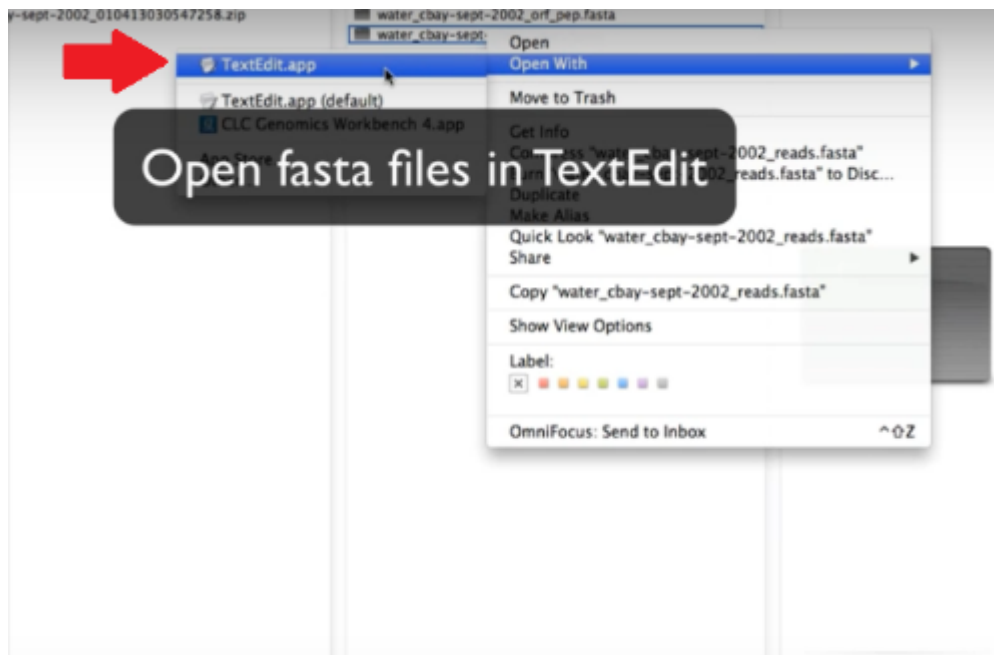


Step 11.

Double click the file to unzip it.

Step 12.

Open fasta files in TextEdit.



Step 13.

For a detailed example please see video in guidelines.

🔗 LINK:

<https://www.youtube.com/watch?v=sVoku4GyK6s>