

VIRBIOHUB: A CENTRAL RESOURCE FOR VIRUS BIOINFORMATICS RESEARCH

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ABSTRACT

Viruses are a major cause of infectious diseases, and they lead to a substantial burden on public health and the global economy. Recently emerged outbreaks such as COVID-19 and monkeypox further emphasize the need for bioinformatics resources supporting research on viral diseases. Estimation of infection capacity for viruses, identifying host shifts, and more importantly predicting virus-host protein-protein interactions (PPIs) that are a prerequisite to viral infections are main topics of interest in virus bioinformatics research. Yet, there is still a shortage of data resources to support such research when compared to alternative research areas in bioinformatics (e.g., cancer bioinformatics). To this end, we developed a web resource for virus bioinformatics, namely VirBioHub.

VirBioHub provides a catalog of viruses and their respective hosts, selected virus-host PPI prediction tools, and a pre-computed set of viral infection predictions for various viral families and hosts. In the catalog of viruses and hosts component, for each pair of viruses and their known host - which corresponds to a known infection-, we provide a dataset of manually curated viral attachment protein(s) and host receptor protein(s) together with their taxonomic data. Currently, VirBioHub has the interacting proteins for virus-host pairs from two viral families (89 pairs for Coronaviridae and 80 pairs for Adenoviridae). Virus-host PPI prediction component enables users to run publicly available PPI prediction tools (currently HVPPI and HOPITOR) using their own choice of virus and host protein sequences. The viral infection prediction component is designed to provide host and host shift predictions based on a previously developed infection prediction pipeline originally developed for adenoviruses, namely ML-AdvInfect. Currently, VirBioHub has the precomputed infection prediction results for two viral families (Coronaviridae and Adenoviridae) along with the PPI data supporting these infection predictions. VirBioHub supports virus bioinformatics research by allowing researchers to export all its query results and datasets.

VirBioHub is developed using React.js for the front-end, Redux Toolkit/PostgreSQL for state & data management, and Django REST for the back-end.

VirBioHub acts as a central resource, providing ease of access to virus bioinformatics researchers. In the future, we plan to extend VirBioHub's coverage in terms of viral families and PPI prediction methods. Furthermore, we intend to improve the accuracy of infection and host-shift predictions as new PPI prediction tools and data become available.

Availability

The website is available at <https://virbiohub.mu.edu.tr>. Please see the figure below for a snapshot of VirBioHub.

Acknowledgment

This project is supported by The Scientific and Technological Research Council of Turkey (Grant number: 119E664) and Muğla Sıtkı Koçman University.

Welcome to VirBioHub

VirBioHub is developed by a group of bioinformaticians from different backgrounds at Mugla Sıtkı Koçman University.

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VirBioHub provides a catalog of viruses and their respective hosts, selected virus-host PPI prediction tools, and a pre-computed set of viral infection predictions for various viral families and hosts. VirBioHub is intended as a central resource, providing ease of access to virus bioinformatics researchers. We are aiming to extend VirBioHub's coverage in terms of both viral families and PPI prediction methods, so stay tuned for the updates.

Catalog of Viruses and Hosts

Virus-Host PPI Predictor

Viral Infection Predictor

Pre-Selected Virus-Hosts

Virus	Host	PPI	Virus-Host PPI Prediction													
			Adenovirus	Bacteriophage	Coronavirus	DNA Virus	Herpesvirus	Parvovirus	Retrovirus	Rhabdovirus	Rotavirus	Tobacco Etch Virus	Unassigned	Virus		
Adenovirus	Human	Adenovirus	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteriophage	Human	Bacteriophage	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Coronavirus	Human	Coronavirus	0	0	1	0	0	0	0	0	0	0	0	0	0	0
DNA Virus	Human	DNA Virus	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Herpesvirus	Human	Herpesvirus	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Parvovirus	Human	Parvovirus	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Retrovirus	Human	Retrovirus	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Rhabdovirus	Human	Rhabdovirus	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Rotavirus	Human	Rotavirus	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Tobacco Etch Virus	Human	Tobacco Etch Virus	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Unassigned	Human	Unassigned	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Virus	Human	Virus	0	0	0	0	0	0	0	0	0	0	0	0	1	0

virus-Host PPI Predictor

Enter the Host Protein Sequence:

Enter the Virus Protein Sequence:

OR

Select FASTA File:

OR

Select FASTA File:

Selected File: Q99Y11.fasta

Selected File: PDIIC2.fasta

TOOLS

Host	Virus	Host	Host	Host	Host
Adenovirus	Human	Adenovirus	Human	Adenovirus	Human
Adenovirus	Human	Adenovirus	Human	Adenovirus	Human

Announcements

Abstract Accepted for Presentation in ISMB2022

Our abstract entitled "A Coronavirus Infection and Host-Shift Predictor" is accepted for presentation at the conference on the Intelligent Systems for Molecular Biology 2022 to be held by International Society for Computational Biology. The abstract will be presented as a poster between July 10-14 2022. 2022-05-31

Abstract Accepted for Presentation in ISMB2021

Our abstract entitled "Assessment of a Novel Feature Selection Algorithm for Virus-Host Protein-Protein Interaction" is accepted for presentation at the conference on the Intelligent Systems for Molecular Biology 2022 to be held by International Society for Computational Biology. The abstract will be presented as a poster between July 25-30 2021.

Pre-Selected Virus-Hosts

Virus	Host	PPI	Virus-Host PPI Prediction													
			Adenovirus	Bacteriophage	Coronavirus	DNA Virus	Herpesvirus	Parvovirus	Retrovirus	Rhabdovirus	Rotavirus	Tobacco Etch Virus	Unassigned	Virus		
Human adenovirus B2	Rattus norvegicus	Adenovirus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Human adenovirus TM2	Rattus norvegicus	Adenovirus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Turkey adenovirus 1	Rattus norvegicus	Adenovirus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Human adenovirus B2	Mus musculus	Adenovirus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bat adenovirus TM	Mus musculus	Adenovirus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Turkey adenovirus 1	Mus musculus	Adenovirus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Human adenovirus B2	Gallus gallus	Adenovirus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bat adenovirus TM	Gallus gallus	Adenovirus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Turkey adenovirus 1	Gallus gallus	Adenovirus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Human adenovirus B2	Homo sapiens	Adenovirus	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Human adenovirus TM	Homo sapiens	Adenovirus	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Turkey adenovirus 1	Homo sapiens	Adenovirus	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Bat adenovirus 1	Rattus norvegicus	Adenovirus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bat adenovirus 2	Homo sapiens	Adenovirus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bat adenovirus 2	Mus musculus	Adenovirus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bat adenovirus 1	Gallus gallus	Adenovirus	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Viral Infection Predictor

Adenovirus

Gallus gallus

Bat adenovirus TM

Gallus gallus, Rattus norvegicus, Mus musculus, Homo sapiens.

Bat adenovirus TM, Turkey adenovirus 1, Bat adenovirus 1, Human adenovirus B2.

Host Entries

Virus Entries