# Uncovering Strategies of Viruses for Selection of Targets for Infection of Human Cells

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**Abstract:**

The mechanism underlying a viral infection involves the manipulation of host cellular process for propagation. This involves interactions between viral and host proteins leading to a disruption of the host protein network [1] . A recently developed database Viruses.STRING [2] was added to the STRING repository that consists of a comprehensive set of virus-host protein-protein interaction (PPI) networks for more than 239 viruses. This opens up the possibility of analyzing viral-host protein interactions as a biological network problem. In this study, the viral-host networks for all the 77 human infecting viruses in the database will be analyzed. These viruses span the 6 basic classes of human viruses according to the Baltimore classification of viruses [3] . The objective of this study is to understand the following key points for all the classes of viruses.

1. The network characteristics of the identified human proteins that interact with viral proteins in the host PPI network. [4]

2. The network characteristics of the human protein nodes in the viral-host protein interaction networks of Epstein-Barr virus (EBV) [5] and Herpes Simplex Virus (HSV-1) upon infection by the virus.

3. Comparison of viral proteins that interact with host proteins to uncover insights into reasons for certain viral proteins being more suitable for interactions with human proteins in comparison to others.

4. Comparison of strategies based on the above results for understanding differences and similarities between RNA [6] and DNA viruses while infecting human host cells. [7]

## 1. Methodology:

1. Classification of viruses into broad categories of DNA and RNA viruses followed by cleaning and retrieval of viral-host PPI data.

2. Identification of human proteins that interact with viral proteins for all the viruses in each category from the Viruses.STRING database.

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3. Identification of network properties such as the various measures of centrality for the identified interacting proteins in the human PPI database from STRING.

4. Identification of significant network properties of human proteins that can be computed in the virus-host interaction network.

## References

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