# Virus-host protein co-expression networks reveal temporal organization and strategies of viral infection

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Viral infection is a very complex process where, apart from replication of the viral machinery, many host cell proteins change their abundance, localization and modifications. Traditionally, the global effect of viral infection on the host cell proteome has been investigated using protein-protein interaction networks, which provide only static information of physical interactions between proteins. However, viral infection is a dynamic event, since viruses can hijack different cellular processes at different times of their replicative cycle.

Here, we take advantage of a recent technique to quantify the global proteome of virus and host cells across time, *Quantitative Temporal Viromics*[1], to reconstruct in detail the protein co-expression networks for different virus/host systems. These complex networks reveal that the viral infection can be seen as a dynamical process where a relatively small but strongly connected network (the virus proteome) activates different modular components of a larger network (the host proteome), Fig. 1. We take advantage of a formal framework, the *theory of interacting networks* [2, 3, 4], to describe the viral replicative cycle as a dynamic interaction between complex protein networks, where perturbations induced by viral proteins spread to hijack the host proteome for the virus benefit. Our methodology provides useful insights into the virus and host temporal organization and strategies, key protein nodes targeted by the virus and dynamical bottlenecks during the course of the infection.

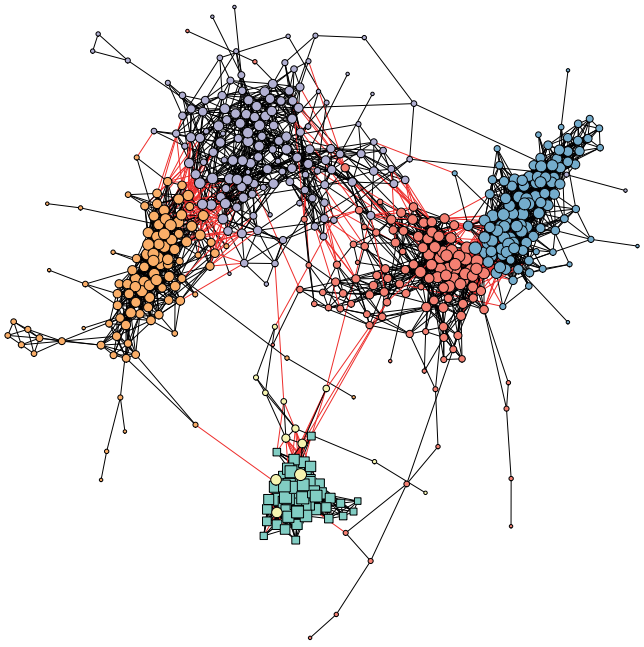

Fig. 1. Protein co-expression network of Epstein-Barr virus infection. Green squares: viral proteins. Circles: Host proteins. Colors correspond to different communities.

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