
VirHostNet 2.0: turning virus/host systems biology into a science 2.0 and a reproducible research framework.

Vincent Navratil*¹

¹PRABI (Pole Rhône Alpes de Bioinformatique) – Université Claude Bernard - Lyon I (UCBL) – France

Résumé

Virus/host molecular systems biology, also known as systems virology, is an emerging scientific fields that aims at a better understanding of molecular mechanisms associated to viral infection and infectious diseases. This approach is complementary to more reductionist virology and is based on the mathematical modelling and inference of virus/host molecular interaction networks from the integration of multi -omics data, including transcriptomics, proteomics, metabolomics and interactomics.

This last ten years, the new advances in high-throughput measurement of protein-protein interactions (mainly yeast two hybrid and tap-tag/MS screens) produced first drafts of virus/host interactomes. In this context, we have developed in 2009 the VirHostNet release 1.0, a prototypal knowledgebase system dedicated to centralise literature-curated virus/host ppi. In five years, this resource became one of the highly cited (more than 70 references in google scholar) and used "gold standards" in the fields of virus-host systems biology.

We are now proud to present our brand new VirHostNet release 2.0 (<http://virhostnet.prabi.fr>). In this release, we have performed a second round of manual annotations that leads to a five-fold dataset increase (12.000 newly annotations). This resource is now delivered in PSIMI-tab 2.5 format and is shared through the EBI PSICQUIC REST web-service. This virus/host dataset is also updated monthly by integrating virus/host and host ppi from the most comprehensive data providers available through the EBI PSICQUIC web-service. Finally, we completely re-designed the web 2.0 interface, and focus our application on the interactive reconstruction, drawing and analysis of personalised virus/host molecular interactions networks, based on graph theory models and associated graph metrics (degree, betweenness...). We are convinced that VirHostNet 2.0 will continue to help biologists and virologists to interrogate in a unified way our unique virus/host ppi resource, but also to easily reconstruct and share their own protein interaction network analysis in a more reproducible research framework.

Mots-Clés: virus/host systems biology, network biology, web 2.0, knowledge base

*Intervenant