

異種ネットワークの構築によりウイルスとホストの関連の解明  
Heterogeneous network construction reveals the virus-host associations

京都大学 化学研究所 バイオインフォマティクスセンター 緒方研究室 欧陽 成州

研究成果概要

The research aims to explore how to build the heterogeneous network in which we can reveal the potential associations among complex biology data in diverse forms.

The plan aims to collect the public data of virus-host interactions including protein sequences, annotations, experiment results and so on. After collecting the data, this research will screen the different forms of data based on the indexes in the reference material, and then trying to standardize the data to build a network. However, when focusing on the NCLDV, the research cannot get enough reliable data to build a network, so it tends to try to use the predicted pairs to build the network.

To begin with, I try to get the protein-protein interaction network (PPI network) to test the feasibility of this project. Unfortunately, it is hard to reveal the potential information of interactions even by using simply formation of organization to build a network like PPI network, as it is difficult to validate node pairs with lack of experiments not to mention the more complex network.

For the further study. I tend to use a simply virus-host system to shrink the scale of interactions so that we have more choices when trying to assess whether a predicted interaction is great or not, even to validate the predicted interaction directly by experiments if the interactions are few but interesting.