

# Topological analysis and visualization of Potyvirus protein-protein interaction network



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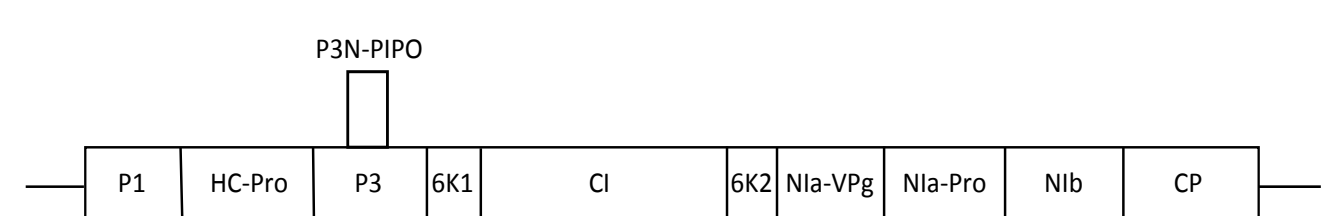
Determine which potyvirus PPIs are more common  
Construct a network with the most important PPIs

## Objectives

Carry out a complete topological analysis of the network  
Study the relation between virus and host proteins

## Data Collecting

Potyvirus represent 30% of all known plant viruses. Their symptoms reduce crop quality and yield. Potyviruses have a 10 kb ss-RNA(+) genome.

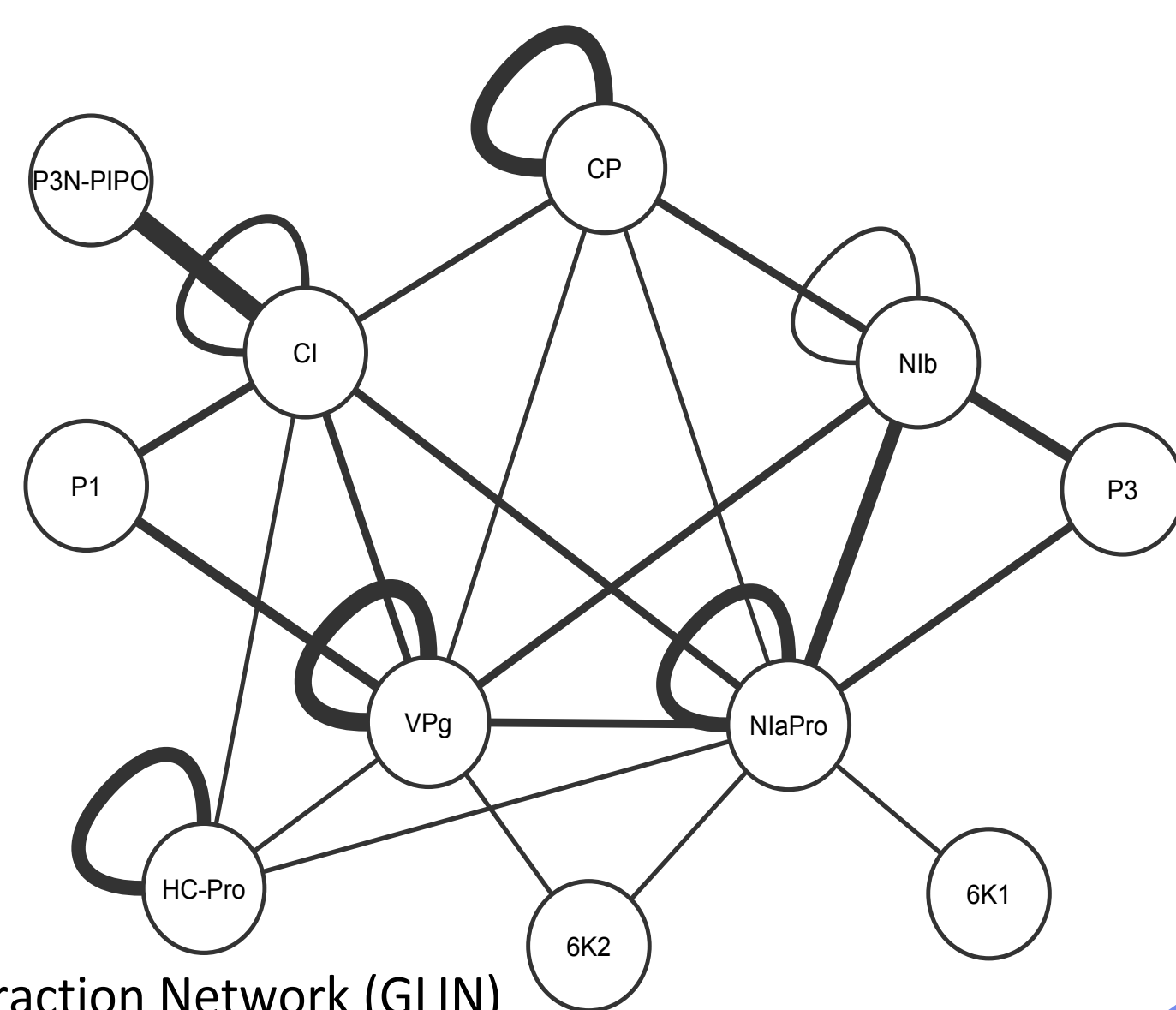


It contains 11 viral proteins in 2 ORFs.

Protein-protein interactions (PPI) are established between them. PPI are physical contacts that take place in cells through molecular docking.

	2	3	2	1	8	2	9	10	6	6	1
2	P1										
5	HC-Pro	78%			44%		44%	44%			
2	P3						56%	44%	67%		
1	6K1						44%				
8	CI				37%		56%	56%	50%	100%	
2	6K2						44%	44%			
9	VPg						80%	56%	56%	44%	
10	Nla-Pro							78%	78%	44%	
6	Nib								44%	56%	
6	CP										88%
1	P3N-PIPO										

Global Interaction Matrix



Global Interaction Network (GLIN)

Potyvirus PPI data was collected from bibliography.

681 PPIs tested, 194 detected among 11 viral proteins in 8 different viruses.

Relevance coefficient (RC) was developed to represent core interactions.

## VVPI network analysis

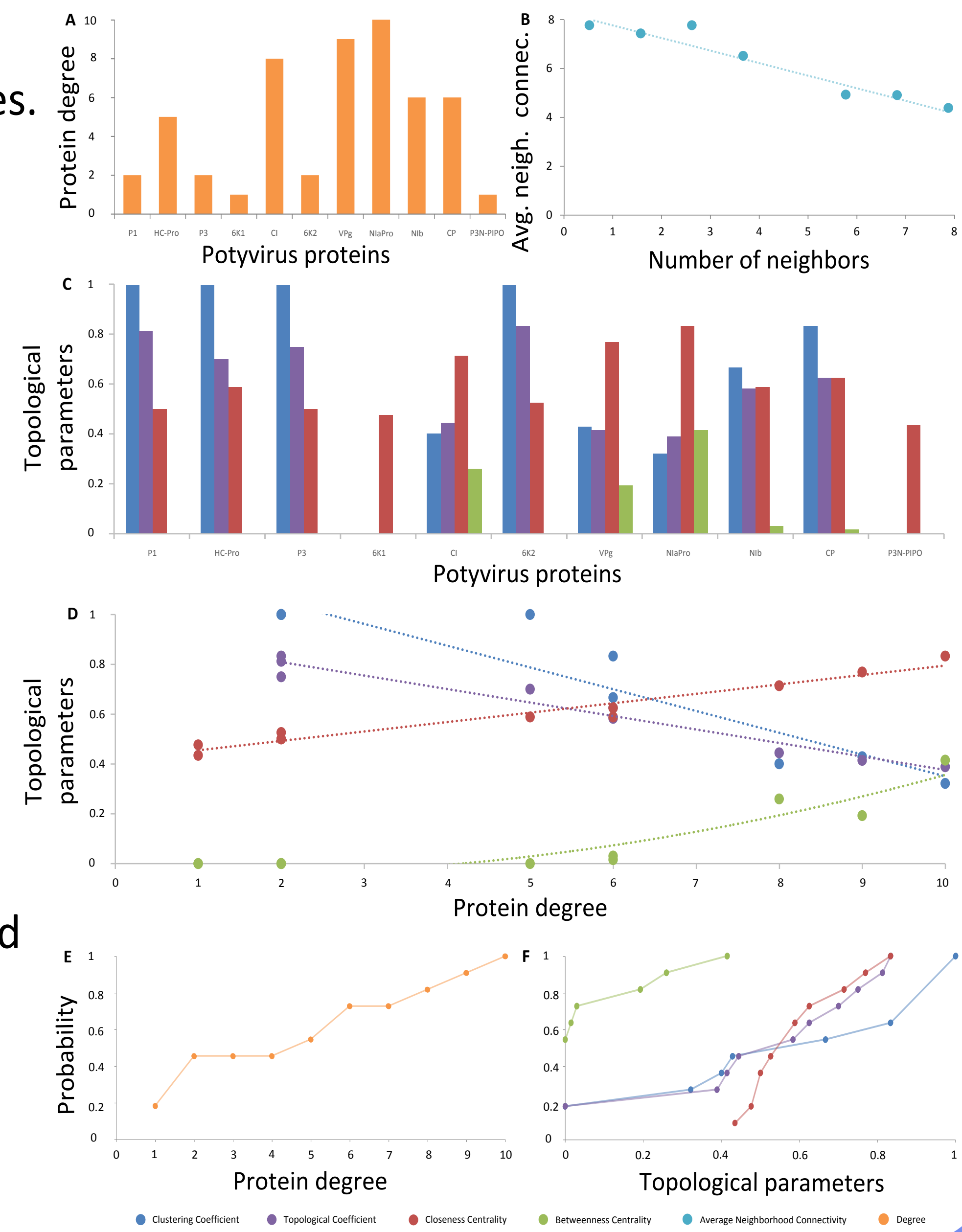
The protein degree shows the interactions it establishes.

Network assortativity study was carried out.

Complete topological analysis of the GLIN.

Some of these parameters are strongly influenced by the degree.

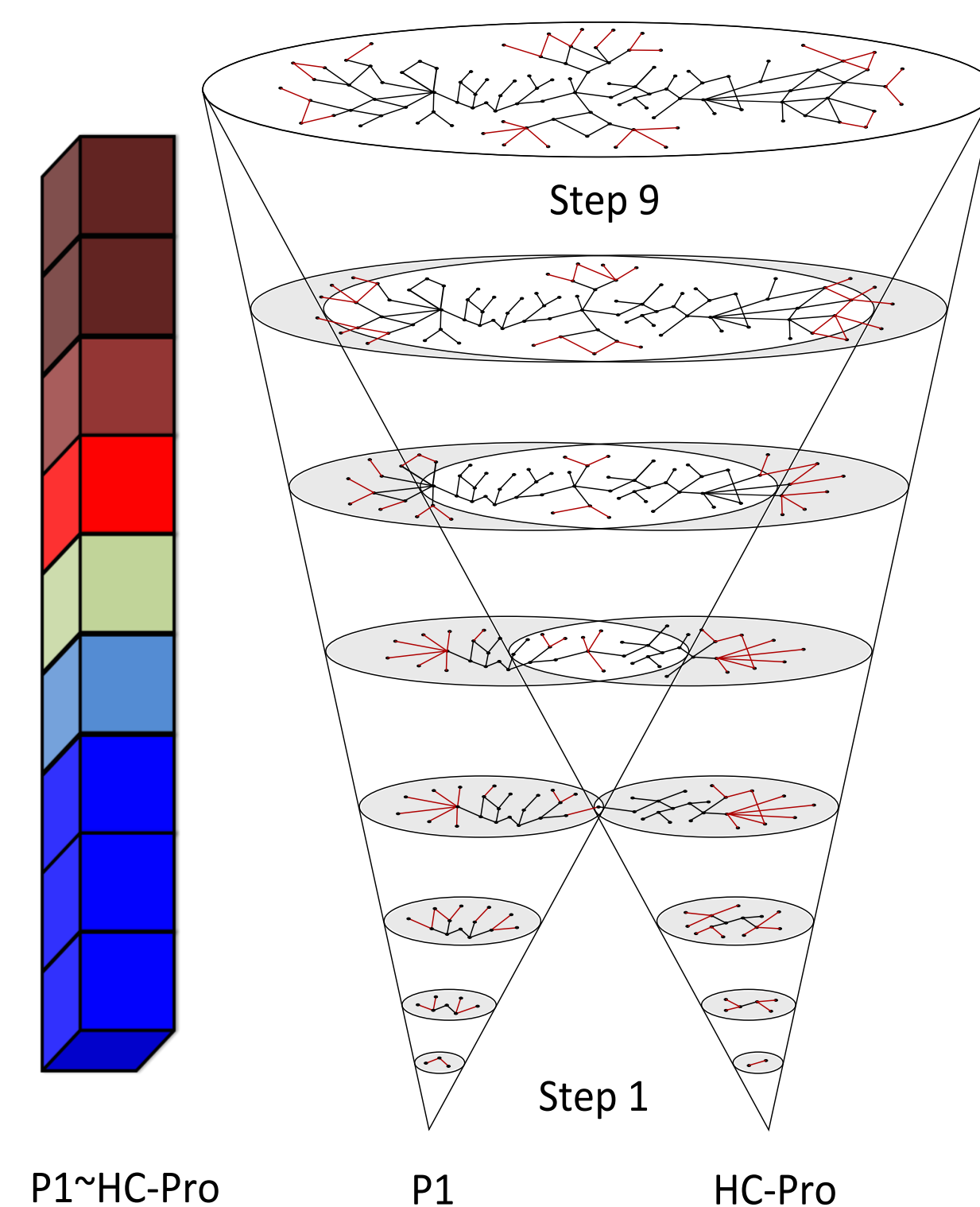
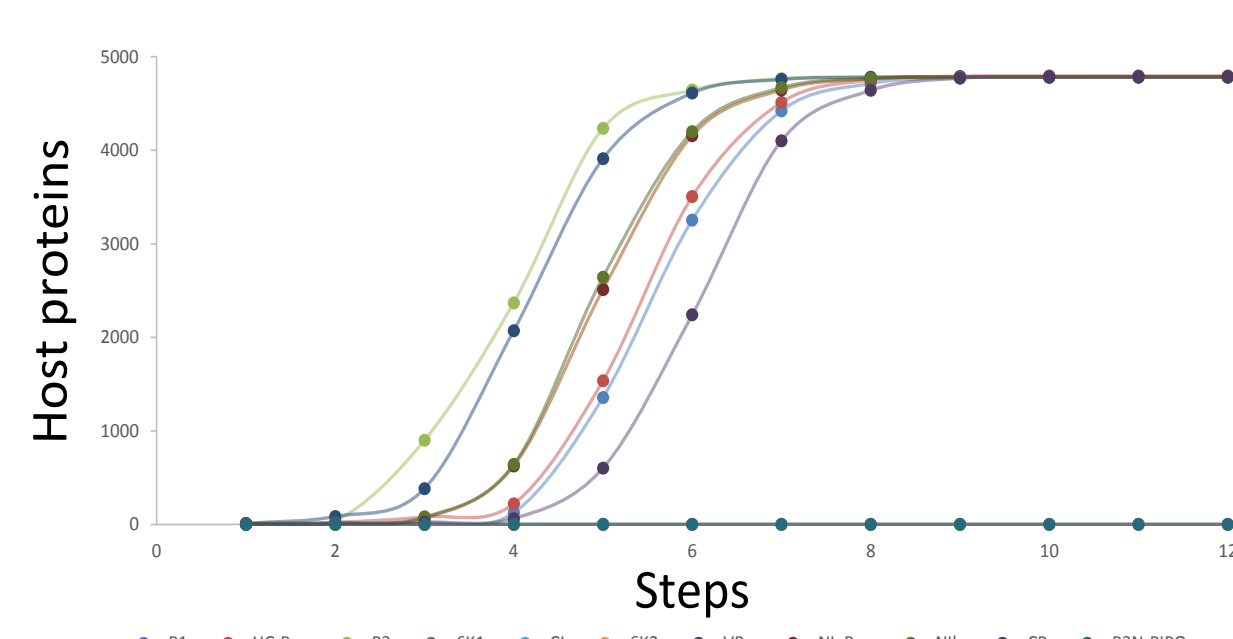
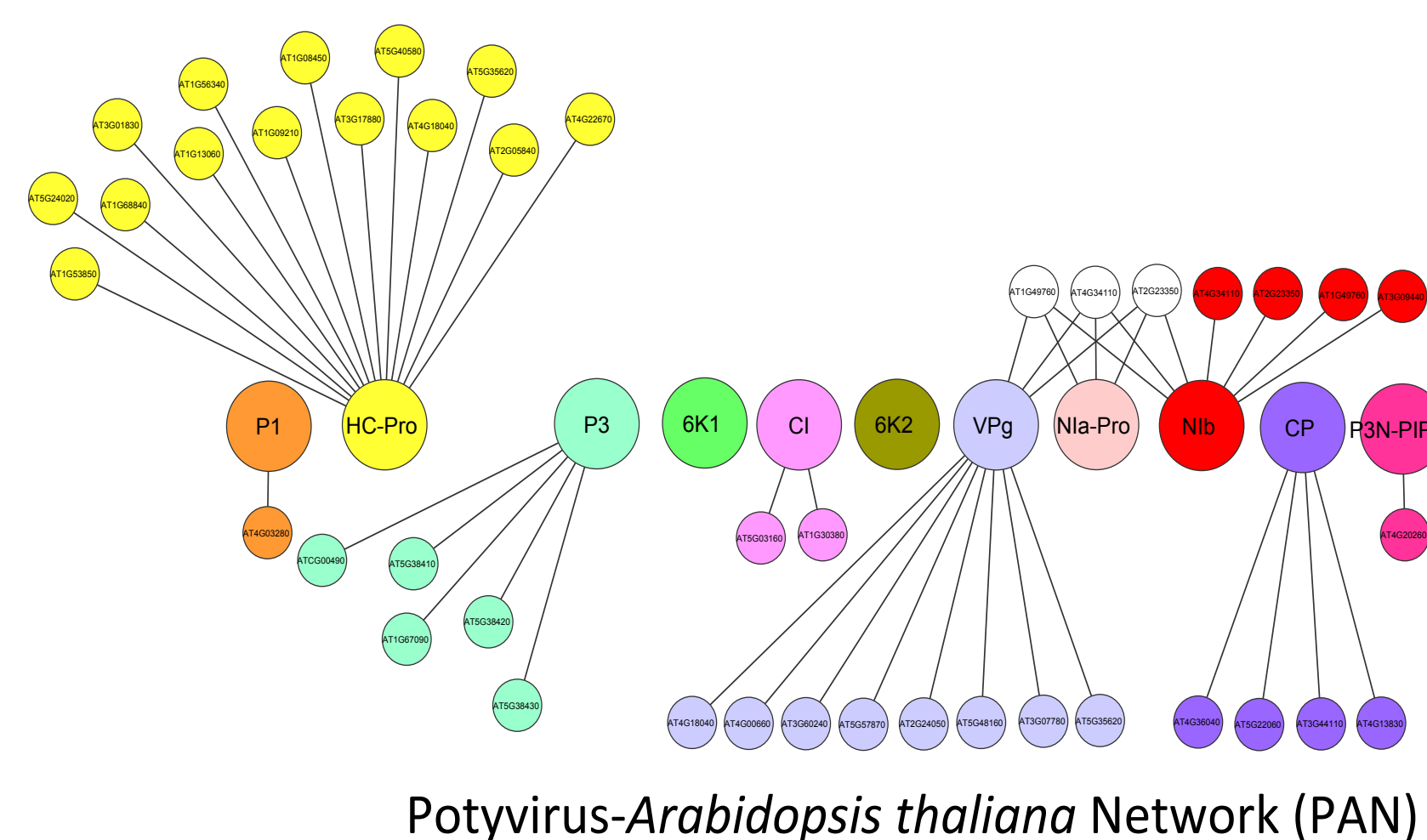
Cumulative topological distributions were calculated and displayed as well.



## VHPI network analysis

Potyvirus establish interactions with the host, disrupting the normal development of the plant. These cross-interactions are extremely important.

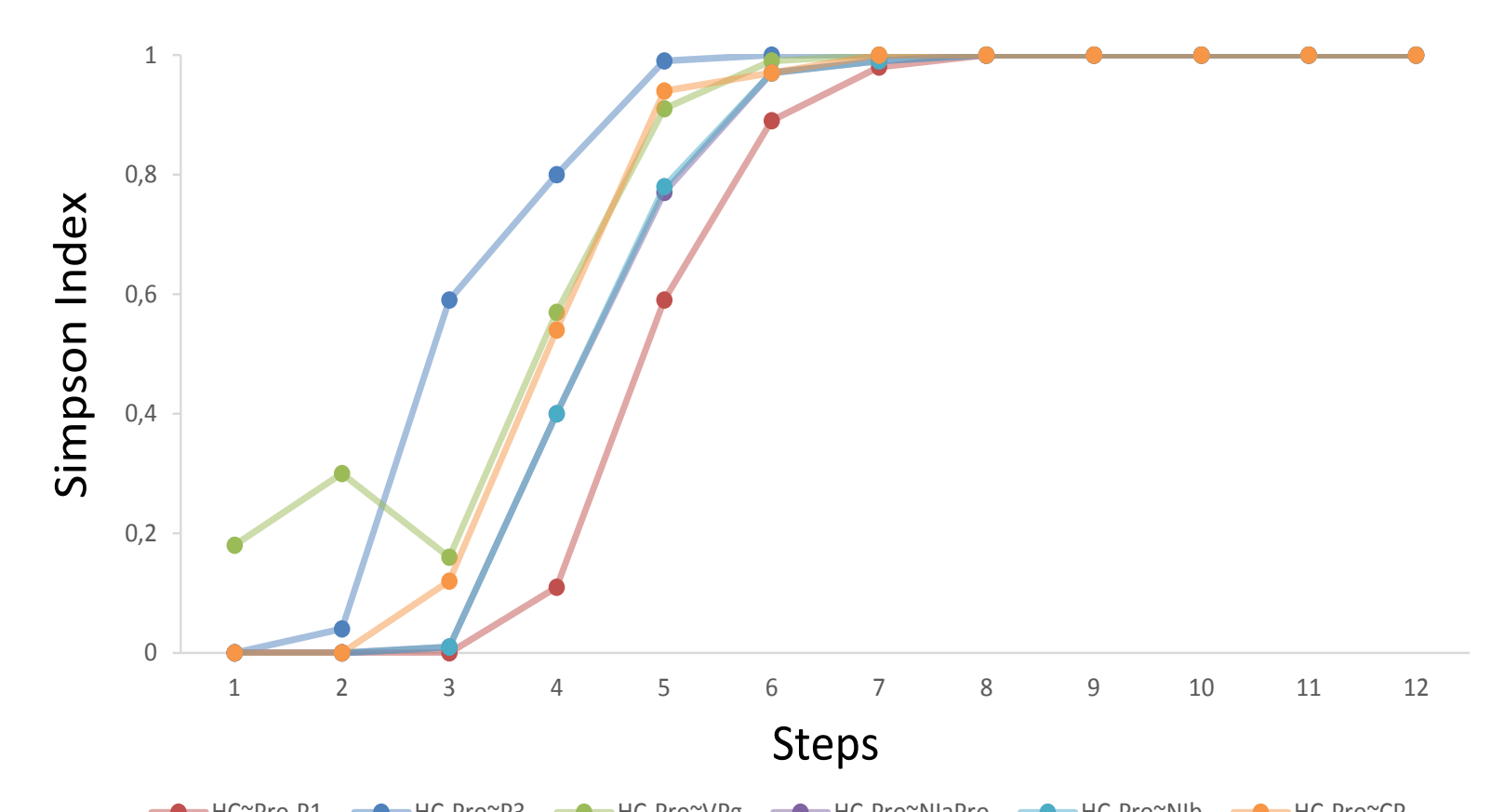
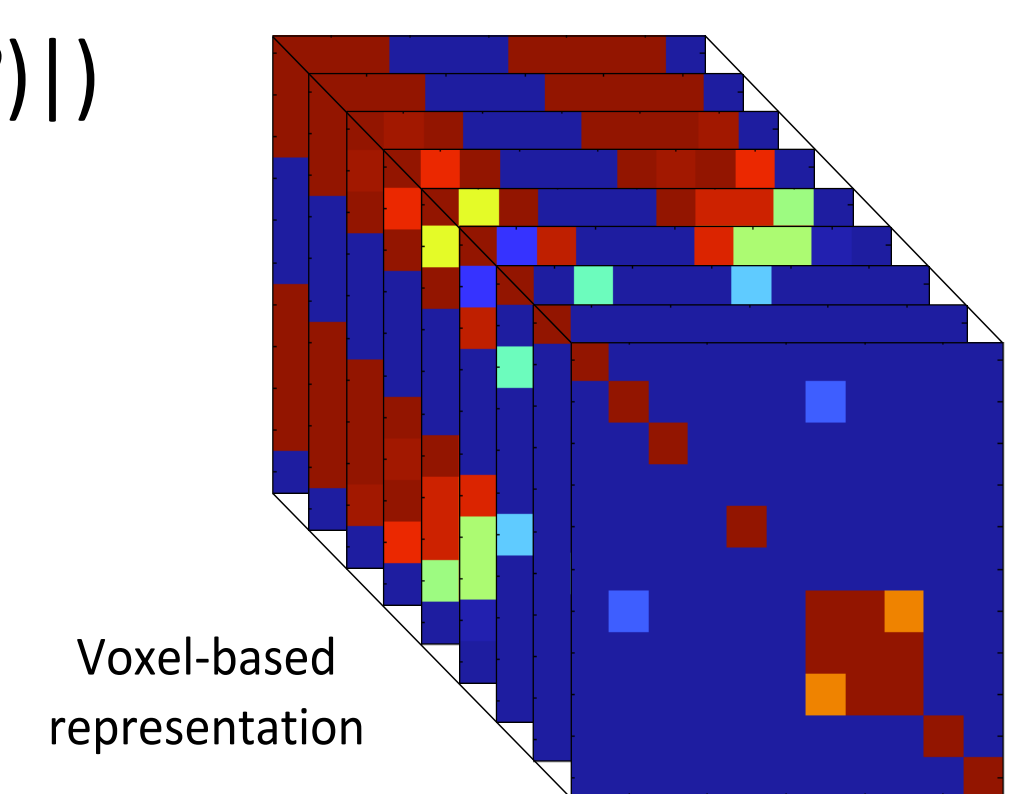
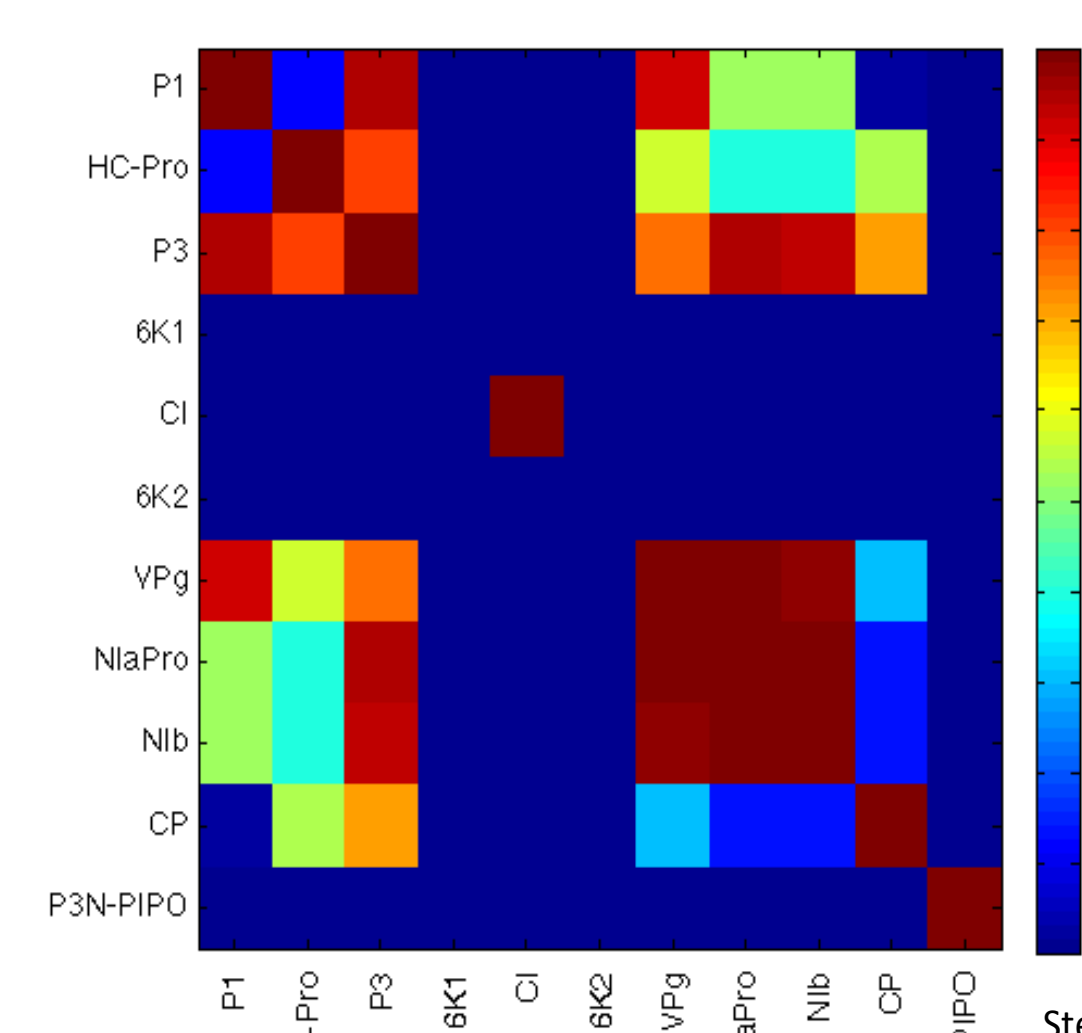
They channel the harmful effect of the virus and point the vital nodes of the network. This effect propagates from those cross-interactions through the network.



Coinciding patterns of propagation through the host network show potential relationships among viral proteins.

Simpson Index parameter:

$$SI(A,B) = |N(A) \cap N(B)| / \min(|N(A)|, |N(B)|)$$



Potential effect that the viral proteins have of the network. Starting from the viral proteins and using the Arabidopsis thaliana interactome as a map, the network coverage was calculated.

## Conclusions:

GLIN is a faithful core representations of potyvirus PPIN.  
Potyvirus PPIN is highly connected, the core proteins are Nib, Nla and CI.  
CI, Nla-VPg and Nla-Pro have the highest control over the network.  
P3 and Nla-VPg effects are the fastest to propagate.  
Common patterns of propagation were indentified in Nla, Nib and P3.

## Acknowledgements:

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