

Community Detection in Disease Gene Network

Pre-Thesis Seminar

S. Chatterjee

Supervisor: B. S. Sanjeev

Department of Applied Sciences
Indian Institute of Information Technology, Allahabad

1 June, 2024

Outline

- Introduction
- Previous work and reviews
- Pathogen Host Interactions
- Network Analysis and Centrality Indices
- Network Modularity
- Modularity based Community detection
- Epstein-Barr associated carcinomas
- COVID-19 DisGeNET Analysis
- Conclusions and future work

Introduction

Definition:

Network theory is a useful tool for analyzing complex systems. Applications of network theory include the World Wide Web, Internet, Gene regulatory networks, Metabolic networks, Social networks, etc.

Objective:

Our objective is to introduce the concept of general network biology and elucidate how network analysis can be used to represent and interrogate different aspects of the Pathogen-Host Interactions.

Motivation

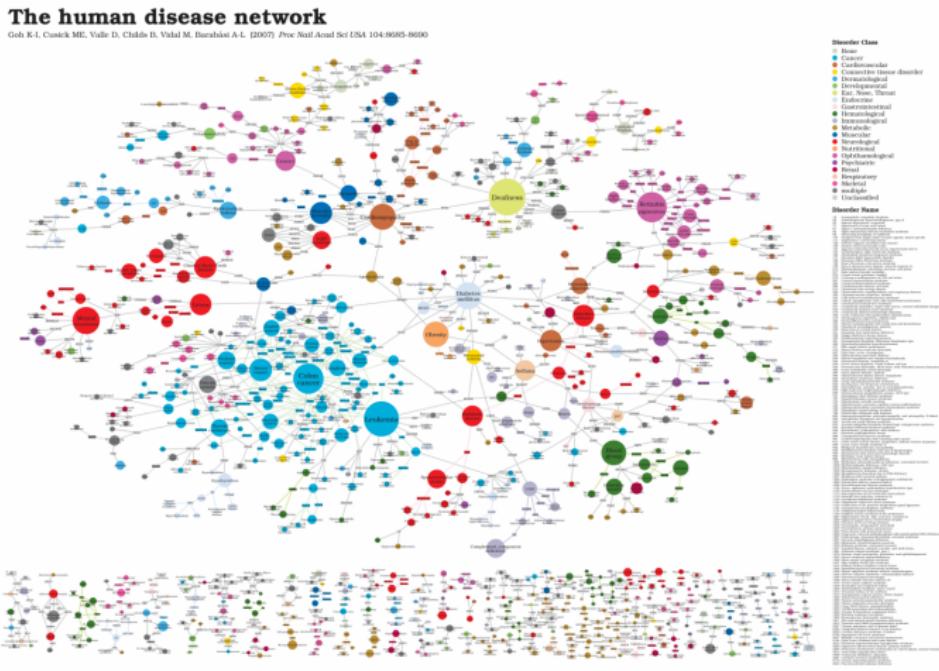


Figure: The Human Disease Network¹.

¹Goh, K.I., Cusick, M.E., Valle, D., Childs, B., Vidal, M. and Barabási, A.L., 2007. The human disease network. Proceedings of the National Academy of Sciences, 104(21), pp.8685-8690.

Introduction - A Complex Network Problem

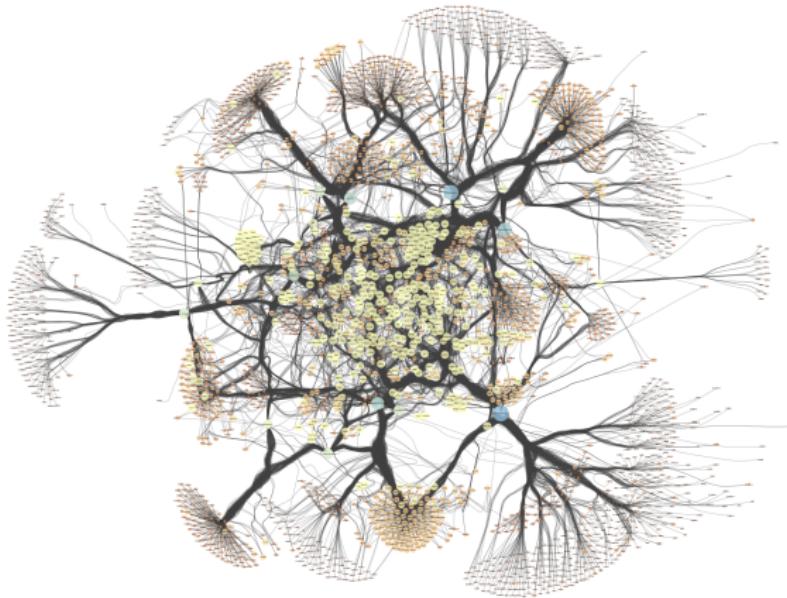


Figure: The Pathogen Host Network².

²Piñero, J., Ramírez-Anguita, J.M., Saúch-Pitarch, J., Ronzano, F., Centeno, E., Sanz, F. and Furlong, L.I., 2020. The DisGeNET knowledge platform for disease genomics: 2019 update. Nucleic acids research, 48(D1), pp.D845-D855.

Introduction

- Nodes and edges are the building blocks of any network, also called a graph, where nodes represent variables and edges represent relationships between the variables. Using this concept, network analysis has been applied to several fields.
- In recent times, network analysis has also been applied extensively in biology, especially in computational and systems biology research.^{3,4}

³Barabasi AL, Gulbahce N, Loscalzo J. Network medicine: a network-based approach to human disease. Nat Rev Genet 2011, 12:56–68

⁴Califano A, Butte AJ, Friend S, Ideker T, Schadt E. Leveraging models of cell regulation and GWAS data in integrative network-based association studies. Nat Genet 2012, 44:841–847

Background - Disease module hypothesis

- The hypothesis states that proteins involved in the same disease have a tendency to interact with each other, forming ‘disease modules’.
- A topological module is a particularly dense area of a network in which the nodes have a higher proportion of links between the components of the module than to components outside that module.
- Functional modules are groups of nodes in a network neighborhood with similar function.
- Disease modules are defined as a group of network components that contribute to a cellular function and, when disrupted, lead to disease.

Types of network-based modules

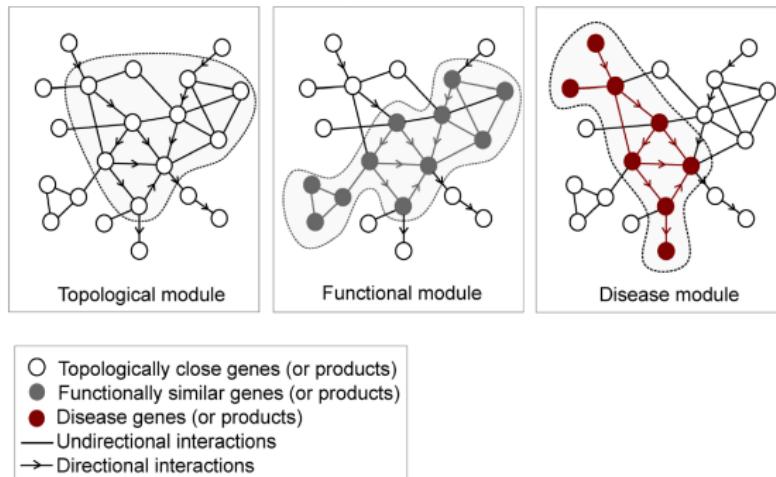


Figure: Review of network-based modules⁵.

⁵Barabási, A.L., Gulbahce, N. and Loscalzo, J., 2011. Network medicine: a network-based approach to human disease. *Nature reviews genetics*, 12(1), pp.56-68.

Network-based methodology

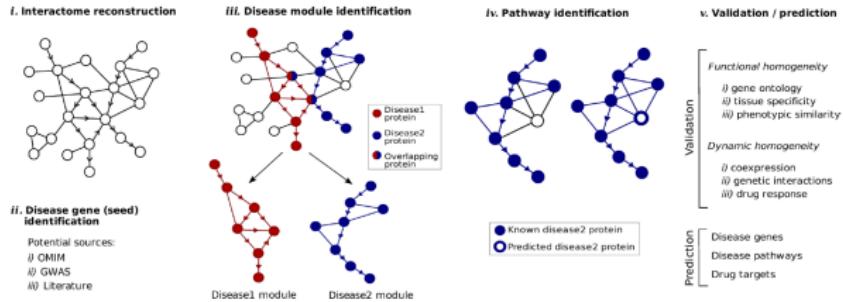


Figure: Schematic representation of methodology⁶.

⁶Barabási, A.L., Gulbahce, N. and Loscalzo, J., 2011. Network medicine: a network-based approach to human disease. *Nature reviews genetics*, 12(1), pp.56-68.

Previous Work and Reviews

- Comprehensive reviews have appeared on molecular networks and their applications.^{7,8,9,10}
- Various studies suggest that interactions between host and pathogen molecular networks are not random but rather well orchestrated, directed events that can influence both host and pathogen behavior.¹¹
- Given the intricate interactions that underlie immune function, the use of networks is not only suitable but also necessary for understanding host immune responses.¹²

⁷Veiga DF, Dutta B, Balazsi G. Network inference and network response identification: moving genome-scale data to the next level of biological discovery. *Mol Biosyst* 2010, 6:469–480

⁸Vital-Lopez FG, Memiševic V, Dutta B. Tutorial on biological networks. *WIREs Data Mining Knowl Discov* 2012, 2:298–325

⁹Chen B, Butte AJ. Network medicine in disease analysis and therapeutics. *Clin Pharmacol Ther* 2013, 94:627–629

¹⁰Barabasi AL, Oltvai ZN. Network biology: understanding the cell's functional organization. *Nat Rev Genet* 2004, 5:101–113.

¹¹Fraser ID, Germain RN. Navigating the network: signaling cross-talk in hematopoietic cells. *Nat Immunol* 2009, 10:327–331

¹²Kidd BA, Peters LA, Schadt EE, Dudley JT. Unifying immunology with informatics and multiscale biology. *Nat Immunol* 2014, 15:118–127

Work-flow of Research

Specifically, we want to concentrate on the following five broad issues:

- Construction, identification and application of network centrality measures in biological networks.
- Topological analysis and community detection in disease gene networks.
- Identification of modules and hierarchical structure of networks.
- Synchronization of network-based modules in the network.
- Statistical validation and conclude our findings.

Introduction to Modularity in Biological Networks

- Modularity is the fraction of the edges that fall within the given groups minus the expected fraction if edges were distributed at random.
- Modularity reflects the concentration of edges within modules compared with random distribution of links between all nodes regardless of modules.
- In general, the term ‘modularity’ refers to the compartmentalization and interrelation of the parts.
- Modularity can be mathematically represented and topologically studied to reveal unexpected structural features.
- Biological networks, including animal brains, exhibit a high degree of modularity.

Introduction to Topological Communities

- Larger topological structures within networks are commonly explored in terms of communities (or modules).¹³
- A community is loosely defined as a subgraph with high local link density, so that nodes within the community have a higher number of links to each other than to nodes outside the community. A large number of definitions of communities appear in the literature, as well as algorithms to detect them.¹⁴
- Various algorithms can also reveal hierarchical community structures.^{15,16}

¹³Ravasz, E., Somera, A.L., Mongru, D.A., Oltvai, Z.N. and Barabási, A.L., 2002. Hierarchical organization of modularity in metabolic networks. *science*, 297(5586), pp.1551-1555.

¹⁴Fortunato 2010

¹⁵Girvan, M. and Newman, M.E., 2002. Community structure in social and biological networks. *Proceedings of the national academy of sciences*, 99(12), pp.7821-7826.

¹⁶Ahn, Bagrow, et al. 2010

Table: Modularity Optimization Methods Comparison.^{17,18}

-	Karate	Arxiv	Internet	Web nd.edu	Phone	Web uk-2005	Web WebBase 2001
Nodes/links	34/77	9k/24k	70k/351k	325k/1M	2.6M/6.3M	39M/783M	118M/1B
Newman	.38/0s	.772/3.6s	.692/799s	.927/5034s	-/-	-/-	-/-
Pons and Latapy	.42/0s	.757/3.3s	.729/575s	.895/6666s	-/-	-/-	-/-
Wakita and Tsurumi	.42/0s	.761/0.7s	.667/62s	.898/248s	.56/464s	-/-	-/-
Louvain Method	.42/0s	.813/0s	.781/1s	.935/3s	.769/134s	.979/738s	.984/152mn

¹⁷Blondel, V.D., Guillaume, J.L., Lambiotte, R. and Lefebvre, E., 2008. Fast unfolding of communities in large networks. Journal of statistical mechanics: theory and experiment, 2008(10), p.P10008.

¹⁸Aynaud, T., Blondel, V.D., Guillaume, J.L. and Lambiotte, R., 2013. Multilevel local optimization of modularity. Graph partitioning, pp.315-345.

Network modularity based Louvain method

The Louvain method¹⁹ based on network modularity (Q) is defined as:

$$Q = \frac{1}{2m} \sum_{ij} \left[A_{ij} - \frac{k_i k_j}{2m} \right] \delta(c_i, c_j) \quad (1)$$

where A_{ij} represents the edge weight between nodes i and j ; k_i and k_j are the sum of the weights of the edges attached to nodes i and j respectively; m is the sum of all of the edge weights in the graph; c_i and c_j are the communities of the nodes; and δ is Kronecker delta function ($\delta(x, y) = 1$ if $x = y$, 0 otherwise).

Modularity is a measure of the structure of networks or graphs which measures the strength of division of a network into modules.

¹⁹Blondel, V.D., Guillaume, J.L., Lambiotte, R., Lefebvre, E., 2008. Fast unfolding of communities in large networks. *Journal of statistical mechanics: theory and experiment* 2008, P10008

Brief outline of Louvain Algorithm

- The algorithm is based on 2 components applied alternatively:
 - ▶ local moving
 - ▶ contraction
- Each node u randomly checks for each of its neighbors v and how much the modularity would (+) or (-) when moving from u to v community.
- If an improvement is possible, u is moved into neighbor's community v that gives maximum modularity.
- After this local moving phase, the graph is contracted such that each community becomes a node in the contracted graph.

Louvain Algorithm

Algorithm 1: Louvain Algorithm for Community Detection

Input: Set of nodes and edges in the Graph

Output: Hierarchical layout of modular communities

```
1 G the initial network for Community Detection
2 repeat
3     Place each node of G in its own community
4     Save the modularity of this decomposition
5     while some nodes are moved do
6         for all nodes n of G do
7             c ← neighboring community maximizing modularity
8             if c results in a strictly positive increase then
9                 move n from its community to c
10            endif
11        endfor
12    endwhile
13    if the new modularity is greater than the initial then
14        end ← false
15        G = the network between communities of G
16    else
17        end ← true
18    end
19  endif
20 until;
```

Title:

Identification of Human Proteins vulnerable to Multiple Organisms. ^a ^b

Keywords: Centrality analysis, IIPs, Graph theory, Host pathogen interaction, Hubs.

^aWBSB-2016

^bS. Chatterjee and B.S. Sanjeev, Department of Applied Sciences, Indian Institute of Information Technology, Allahabad, 211012, UP, India

Overview

Table: Overview of PHI Networks²⁰

Parameters	Nos.
Total no. of pathogens	182
No. of human proteins (H_p)	668
No. of pathogen proteins (P_p)	1,188
Total no. of proteins (H_p) + (P_p)	1,856
Total no. of interactions	3,905

²⁰S. D. Tekir, T. Çakır, E. Ardiç, A. S. Sayılıbaşı, G. Konuk, M. Konuk, H. Sarıyer, A. Uğurlu, İ. Karadeniz, A. Özgür, F. E. Sevilgen, K. Ö. Ülgen, PHISTO: Pathogen-Host Interaction Search Tool, Bioinformatics., (Databases and ontologies):1357-1358, 2013.

Method

In our network analysis, we make use of several indicators of centrality to identify the most important vertices within a graph^{21, 22}. Herein, for our undirected graph Γ , such that $\Gamma_p = (V_p, E_p)$, V_p is the set of all nodes (proteins) of H_p (Human) and P_p (Pathogenic) and E_p is the set of corresponding edges (interactions) wherein $E_p \subseteq [V_p]^2$.

²¹N. T. Doncheva, Y. Assenov, F. S. Domingues, M. Albrecht, Topological analysis and interactive visualization of biological networks and protein structures, *Nature Protocols* 7:670-685, 2012

²²Y. Assenov, F. Ramírez, S. E. Schelhorn, T. Lengauer, M. Albrecht, Computing topological parameters of biological networks, *Bioinformatics*, 24(2):282-284, 2008

Our PHI Network

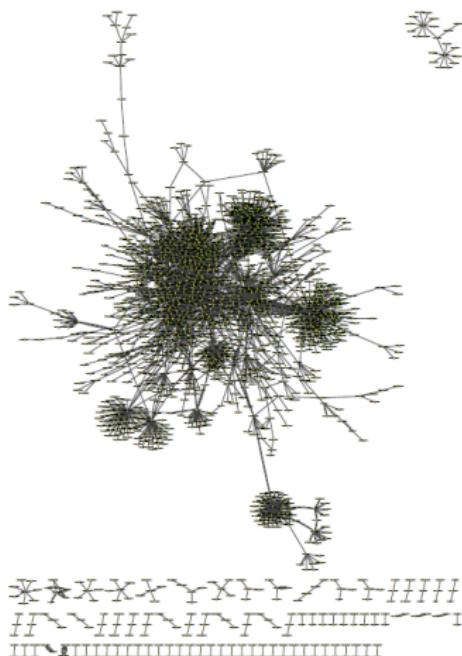
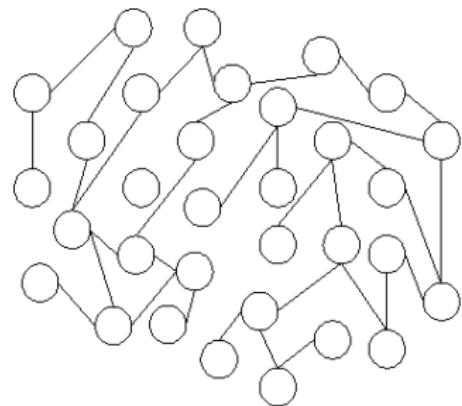


Figure: Pathogen Host Interactome Network.

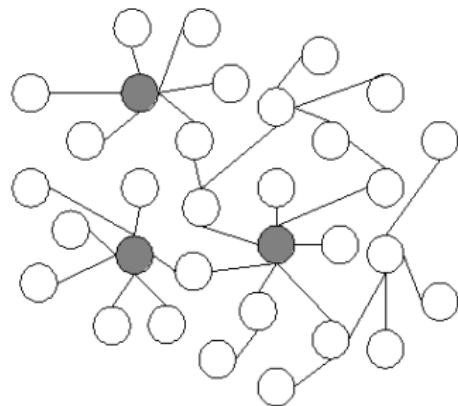
Random v/s Scale-free graphs

Erdős-Rényi random graphs



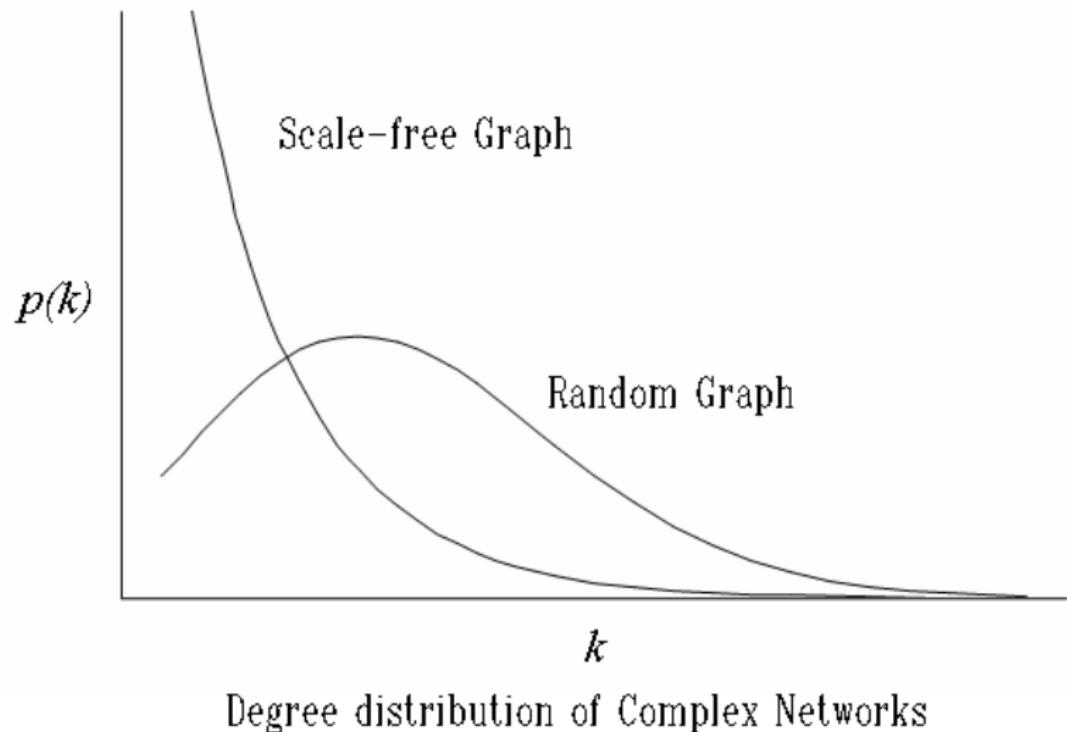
(a) Random network

Barabási-Albert scale-free graphs



(b) Scale-free network

Degree of distribution



Node Degree Distribution

Definition: The node degree distribution is an indicator of the number of nodes with a degree of k . In undirected networks, the node degree of a node n is the number of edges linked to n .

Node Degree Distribution

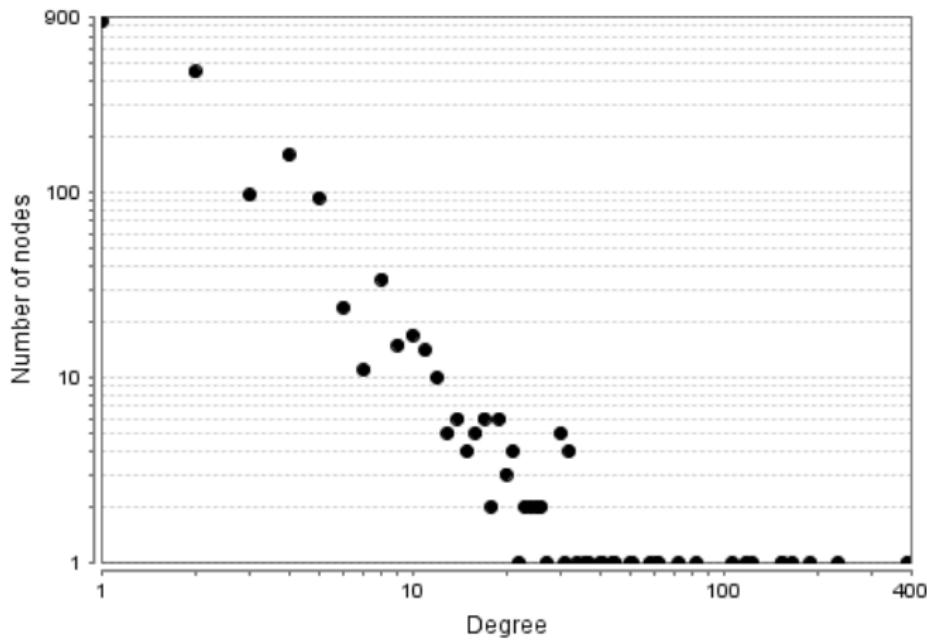


Figure: Node Degree Distribution

Topological Coefficient

Definition: Topological coefficient $T(n)$ of a node n with k_n neighbors is defined as the number of neighbors shared between a pair of nodes, k_n and k_m , divided by the number of neighbors of node k_n :

$$T(n) = \frac{\text{avg}(J(n, m))}{k_n} \quad (2)$$

where the value of $J(n, m)$ is the number of neighbors shared between the nodes n and m , plus one if there is a direct link between n and m and is defined for all nodes m that share at least one neighbor with n . It gives a relative measure for the extent to which a node shares its neighbors with other nodes.

Topological Coefficient

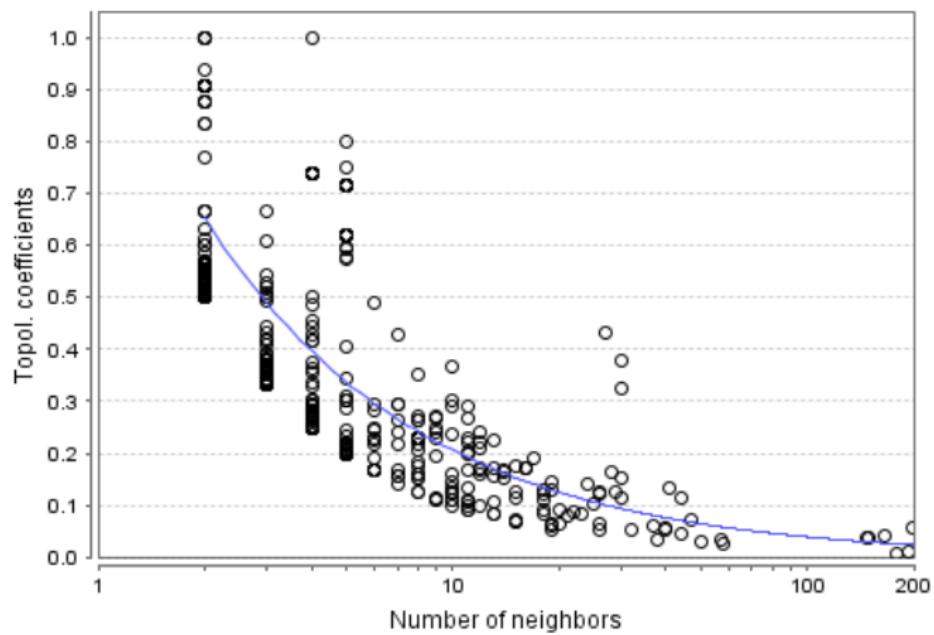


Figure: Topological Coefficients

Stress Centrality

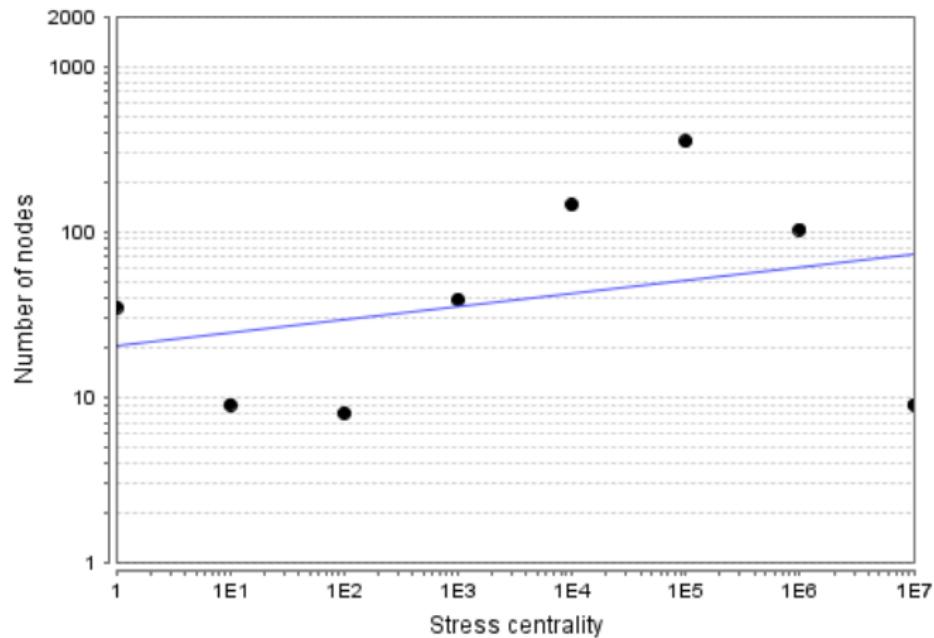


Figure: Stress Centrality Distribution

Results and Discussions

Table: Summary of Network Statistics of PHI Networks

Parameter	Statistics
Connected Components	82
Network Diameter	17
Shortest Paths	2,610,796 (75%)
Avg. number of Neighbors	3.357
Multi-edge node pairs	496

Results and Discussions

Table: Overview of Important Interacting proteins (IIPs)

Human Protein	Uniprot ID	Deg.	No. of Path.	
			Virus	Bact.
P53_Human	P04637	193	35	5
NFKB1_Human	P19838	180	6	4
GBLP_Human	P63244	40	17	3
TOX4_Human	O94842	23	12	3
PDIA1_Human	P07237	22	9	3
MYH9_Human	P35579	13	6	3
RAC1_Human	P63000	41	3	7
CCAR2_Human	Q8N163	18	13	2
ILF3_Human	Q12906	30	23	1

Summary

- The purpose of this study is to perform topographical analysis of large scale pathogen host interaction networks (PHI Networks) in order to identify proteins important for network topology and integrity.
- Various *graph theoretical* approaches were implemented to identify highly interacting hub and central proteins that are crucial for network integrity.
- We could list out 9 highly interacting hubs present in the human host that were involved with 560 pathogenic proteins.

Conclusions

- Topological analyses of bacterial PPI networks have revealed that they follow power-law distributions, i.e., they have few hubs and many peripheral proteins²³ and similar to bacterial PPI networks.²⁴ also follow scale-free distribution.
- Topological analysis of proteins involved in interaction of host and pathogen networks indicates that both bacterial and viral pathogens in general target hub and bottleneck proteins in host networks²⁵.

²³Barabasi AL, Albert R. Emergence of scaling in random networks. *Science* 1999, 286:509–512.

²⁴Guiguemde WA, Shelat AA, Bouck D, Duffy S, Crowther GJ, Davis PH, Smithson DC, Connelly M, Clark J, Zhu F, et al. Chemical genetics of *Plasmodium falciparum*. *Nature* 2010, 465:311–315.

²⁵Durmus Tekir SD, Ulgen KO. Systems biology of pathogen-host interaction: networks of protein-protein interaction within pathogens and pathogen-human interactions in the post-genomic era. *Biotechnol J* 2013, 8:85–96.

Introduction

Title:

Community detection in Epstein-Barr virus associated carcinomas and role of tyrosine kinase in etiological mechanisms for oncogenesis. ^{a b}

Keywords: Epstein-Barr Virus, Community Detection, Biological Process, Louvain method.

^aMicrobial Pathogenesis, 180 (106115), pp. 1-7, July 2023. doi: 10.1016/j.micpath.2023.106115

^bS. Chatterjee and B.S. Sanjeev, Department of Applied Sciences, Indian Institute of Information Technology, Allahabad, 211012, UP, India

Introduction

Background:

The Epstein–Barr virus (EBV) is the first herpesvirus associated with human cancers known to infect majority of the world population ^a. Epstein-Barr virus (EBV) is a ubiquitous human herpes virus associated with the development of many lymphoid and epithelial tumors.

^aEpstein, M.A., 1964. Virus particles in cultured lymphoblasts from burkitt's lymphoma. Lancet 1, 702–703.

EBV infection:

Epstein-Barr virus (EBV) is the primary cause of infectious mononucleosis (IM) and is associated with several malignancies. About 200,000 cancer cases globally per year are thought to be attributable to EBV. These oncogenic viruses have many complicated strategies that disrupt biological pathways in the infected host cells.

EBV-affecting B-cells and Epithelial cells

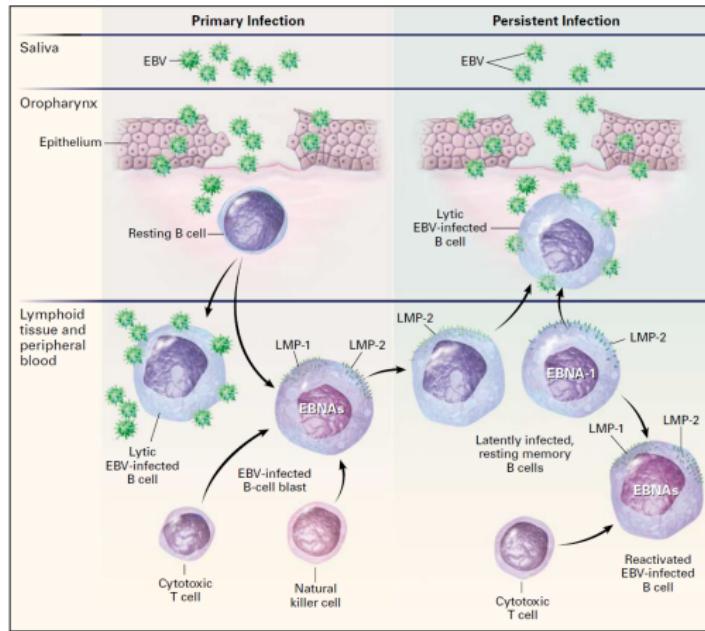


Figure 1. Model of Epstein-Barr Virus (EBV) Infection in Humans.

Figure: Epstein Barr Virus mostly affecting B-cells and Epithelial cells.²⁶

²⁶Cohen, J.I., 2000. Epstein-Barr virus infection. New England journal of medicine, 343(7), pp.481-492.

EBV-associated carcinomas

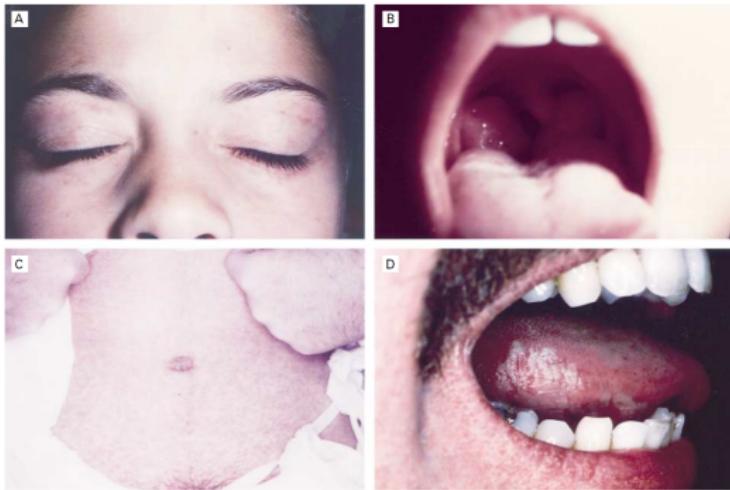


Figure 3. Clinical Findings in Epstein–Barr Virus (EBV) Infection.

Panel A shows petechiae of the eyelids with periorbital edema, and Panel B shows tonsillar enlargement in a patient with infectious mononucleosis. Panel C shows macular rash after ampicillin therapy in a patient with infectious mononucleosis. Panel D shows oral hairy leukoplakia in a patient with AIDS. Photographs courtesy of Maria Turner, M.D.

Figure: Epstein Barr Virus mostly affecting B-cells and Epithelial cells.²⁷

²⁷Cohen, J.I., 2000. Epstein–Barr virus infection. New England journal of medicine, 343(7), pp.481-492.

Review of EBV Vaccine Development

nature medicine

Explore content ▾

About the journal ▾

Publish with us ▾

Subscribe

[nature](#) > [nature medicine](#) > [research highlights](#) > article

RESEARCH HIGHLIGHT | 19 May 2022

Finding a vaccine for Epstein-Barr virus

Nanoparticle vaccines show promise in preclinical models; clinical evaluation is warranted to assess whether they could help reduce the burden of disease associated with EBV in humans.

[Karen O'Leary](#)✉

Figure: Finding a vaccine for EBV.²⁸

²⁸O'Leary, K., 2022. Finding a vaccine for Epstein-Barr virus. *Nature medicine*.

Problem definition

Problem:

Epstein-Barr virus (EBV) is associated with several malignancies. Potential drug targeted therapies/EBV vaccine affecting critical biological processes/pathways can reduce the rate of infectious mononucleosis (IM) in various carcinomas.

Current status:

Trials to reduce the incidence of Hodgkin lymphoma, Burkitt lymphoma and other associated carcinomas are currently under development.

Objective:

Our objective is to implement network theory approaches and elucidate how community detection and functional enrichment can be used to represent and interrogate different aspects of EBV-associated carcinomas and find out which critical processes are being affected.

Types of cancer associated with Epstein-Barr virus

Table: Types of cancer associated with Epstein-Barr virus through DisGeNET (v7).

Sl.	Category	Associated Cancer Type	Reference [PMID]
1	GC	Malignant neoplasm of stomach	1342957
2		Stomach Neoplasms	1342957
3		Stomach Carcinoma	1342957
4		Benign neoplasm of stomach	1342957
5		Carcinoma in situ of stomach	1342957
6		Neoplasm of uncertain / unknown behavior of stomach	1342957
7	HL	Lymphoma, Non-Hodgkin	9547991
8		Hodgkin Disease	9547991
9		Lymphoma, Non-Hodgkin, Familial	9547991
10		Adult Hodgkin Lymphoma	9547991
11		Hodgkin lymphoma, lymphocyte depletion	9547991
12		Lymphocyte Rich Classical Hodgkin Lymphoma	10505767
13		Mixed Cellularity Hodgkin Lymphoma	10505767
14	BL	Nodular Lymphocyte Predominant Hodgkin Lymphoma	10505767
15		Burkitt Lymphoma	2824192
16		Burkitt Leukemia	2824192
17	NPC	African Burkitt's lymphoma	2824192
18		Cancer of Nasopharynx	8732865
19		Malignant neoplasm of nasopharynx	8732865
20	Syndrome	Lymphoproliferative Syndrome, Ebv-Associated, Autosomal	22409825
21		Chronic Lymphoproliferative Disorder of NK-Cells	6158759
22		X-linked immunodeficiency with magnesium defect	25313976

EBV-associated carcinomas

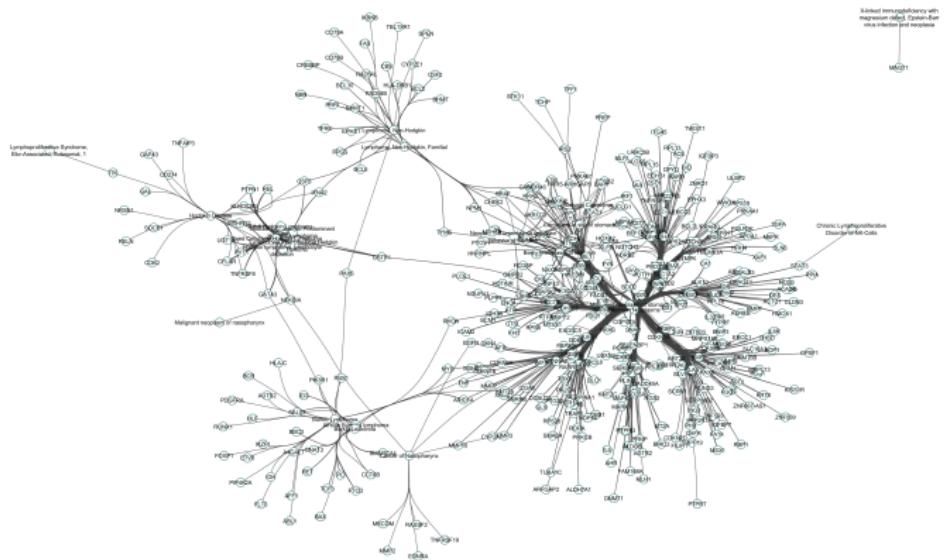


Figure: The Disease Gene Network of Epstein Barr Virus in various neoplastic processes (Gastric cancer (GC), Nasopharyngeal cancer (NPC), Hodgkin's lymphoma (HL) and Burkitt Lymphoma (BL))

Node degree distribution

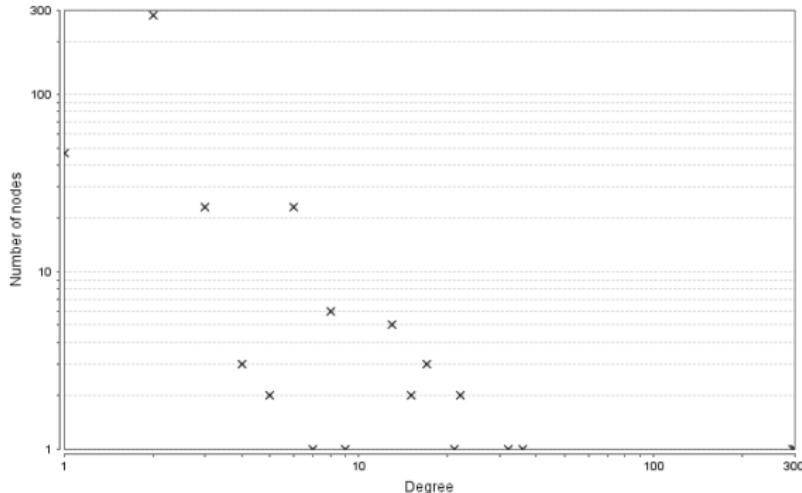


Figure: The node degree distribution of the EBV-associated cancers. Malignant neoplasm of stomach (in GC category) was the most affected carcinoma associated with EBV.

Network Modularity in EBV-linked Carcinoma Network

- Modularity is defined as the fraction of edges that fall within the given groups minus the expected fraction, if edges were distributed at random.²⁹
- A positive modularity signifies that the number of edges connected to nodes in a network within a community exceeds the expected value by chance randomly (range between -1/2 to 1). To identify significant communities Louvain method-based community detection was implemented, and critical processes were selected based on p-values representing their significance.³⁰
- The network modularity of the disease-gene network was found to be 0.359 which depicted a positive modular network structure.

²⁹Brandes Ulrik, Delling Daniel, G.M.G.R.H.M.N.Z., Dorothea, W., 2008. On modularity clustering. IEEE Transactions on Knowledge and Data Engineering 20, 172–188.

³⁰Sham, P.C., Purcell, S.M., 2014. Statistical power and significance testing in large-scale genetic studies. Nature Reviews Genetics 15, 335–346.

Network modularity of Carcinoma Network



Figure: The network modularity of the disease-gene network in EBV-associated carcinomas was 0.359 signifying a positive structured modular network. The figure depicts the size distribution of the 7 modularity classes.

Community detection in modular networks

- Community detection is fundamental to biological network analysis for protein function annotation, disease gene prediction and studies based on targeted drug therapies.³¹
- Such techniques have successfully been implemented for the identification of critical genes based on modularity, network modules and drug targeted therapies.³²
- We implemented Community Detection Application and Service framework (CDAPS) based on the integrated approach to identify and visualize large-scale multi-scale network communities.
- Community detection methods build hierarchical representations directly from the graph structure and we used Hierarchical community Decoding Framework (HiDeF), for network community detection in biological networks.³³

³¹ Singhal, A., Cao, S., Churas, C., Pratt, D., Fortunato, S., Zheng, F., Ideker, T., 2020. Multiscale community detection in cytoscape. PLoS computational biology 16, e1008239.

³² Gulbahce, N., Lehmann, S., 2008. The art of community detection. BioEssays 30, 934–938.

³³ Zheng, F., Zhang, S., Churas, C., Pratt, D., Bahar, I., Ideker, T., 2021. Hidef: identifying persistent structures in multiscale ‘omics data. Genome biology 22, 1–15.

Network community detection methodology

- We performed community detection using the Louvain algorithm in the CDAPS framework with a maximum resolution parameter of less than 50 to gain insights even from relatively smaller communities.
- The community persistence threshold was kept at 5, to remove unstable clusters.

Result

This resulted in a hierarchical network with communities as nodes and their hierarchical relationships as edges. We fetched significant communities in the form of hierarchical modules in the overall network.

Over-representation Analysis

Table: Significant biological processes and the list of genes in each community based on their degree of distribution.

Sl.No	Biological process	Degree	Genes
1	Pathways in cancer	70	ABL1 APC AXIN2 BAX BBC3 BCL2 BCL2L1 BCR BID BIRC2 BIRC5 BMP2 BRAF CASP8 CCND1 CDH1 CDK2 CDK4 CDKN1A CDKN1B CDKN2A CREBBP CTNNAA2 CXCL8 EDNRA EGFR ERBB2 F2R FAS FGFR2 FLT3 GADD45A GLI3 GNA13 GSTP1 HMOX1 HRAS IFNA2 IKBKB IL6 IL6R JUN KRAS MAPK1 MAPK3 MAPK8 MECOM MET MLH1 MMP2 MSH2 MYC NFKBIA NOTCH2 PDGFRA PIK3CA PIK3R1 PPARG PRKCB PTGS2 RAR β RET RHOA RUNX1 RXRB SMAD4 STAT3 TGFA TP53 TPM3
2	Gastrin signaling pathway	27	BCL2L1 BIRC2 BIRC5 BMP2 CCND1 CD44 CDKN1A CDKN1B CDKN2A CXCL8 EGFR FYN GAST HRAS JUN KRAS MAPK1 MAPK3 MAPK8 MMP7 PPARG PTGS2 RHOA RPS6 SERPINE1 STAT3
3	Endometrial cancer	7	APC AXIN2 BRAF CDH1 ERBB2 FGFR2 PIK3CA
4	Trans-sulfuration and one carbon metabolism	6	BHMT CBS MTHFD2 MTHFR SHMT1 TYMS
5	Antifolate resistance	5	FPGS IKBKB MTHFR SHMT1 TYMS
6	Modulators of TCR signaling and T-cell activation	5	ITK NFKBIA REL SOCS1 TNFAIP3
7	TP53 Network	4	ABL1 BAX BBC3 MYC
8	Imatinib and chronic myeloid leukemia	3	ABL1 BCR PDGFRA
9	Guanine / Thymine mispair binding	2	MLH1 MSH2

Hierarchical Network representation

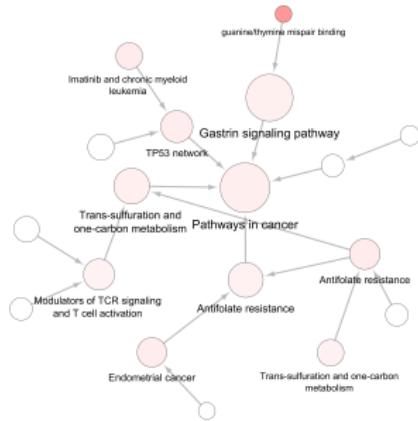


Figure: The figure depicts nodes in the Disease-Gene Network which represents its significance denoted by the size of the node (based on p-values). The respective biological processes and pathways are interlinked in a hierarchical network layout using over-representation analysis.

Over-representation Enrichment Methodology

- We employed the methodology of over-representation analysis to detect statistically significant gene ontology terms.
- Genes were mapped to known functional annotations to detect statistically significant enriched pathways for functional enrichment.³⁴
- The nodes were selected with minimum Jaccard index value³⁵ for overlap greater than 0.05 and the range of p-value³⁶ was kept less than 0.00001.

³⁴Raudvere, U., Kolberg, L., Kuzmin, I., Arak, T., Adler, P., Peterson, H., Vilo, J., 2019. g: Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019 update). Nucleic acids research 47, W191–W198.

³⁵Jaccard, P., 1912. The distribution of the flora in the alpine zone. 1. New phytologist 11, 37–50.

³⁶Storey, J.D., Tibshirani, R., 2003. Statistical significance for genomewide studies. Proceedings of the National Academy of Sciences 100, 9440–9445.

Over-representation Analysis

Table: List of significantly enriched biological processes and pathways along with their corresponding p-values (threshold less than 1.0 E-06).

Rank	Gene Ontology / Biological process	P-value	-log(P)	Reference
1	Pathways in Cancer	4.78E-69	68.32	KEGG:05200
2	Gastrin signaling pathway	8.58E-37	36.06	WP:WP4659
3	Endometrial cancer	3.30E-15	14.48	WP:WP4155
4	Trans-sulfuration and one carbon metabolism	1.58E-11	10.80	WP:WP2525
5	Antifolate resistance	6.82E-11	10.17	KEGG:01523
6	Modulators of TCR signaling and T-cell activation	1.79E-09	8.75	WP:WP5072
7	TP53 Network	1.23E-08	7.91	WP:WP1742
8	Imatinib and chronic myeloid leukemia	3.86E-07	6.41	WP:WP3640
9	Guanine / Thymine mispair binding	2.43E-06	5.61	GO:0032137

Over-representation Analysis

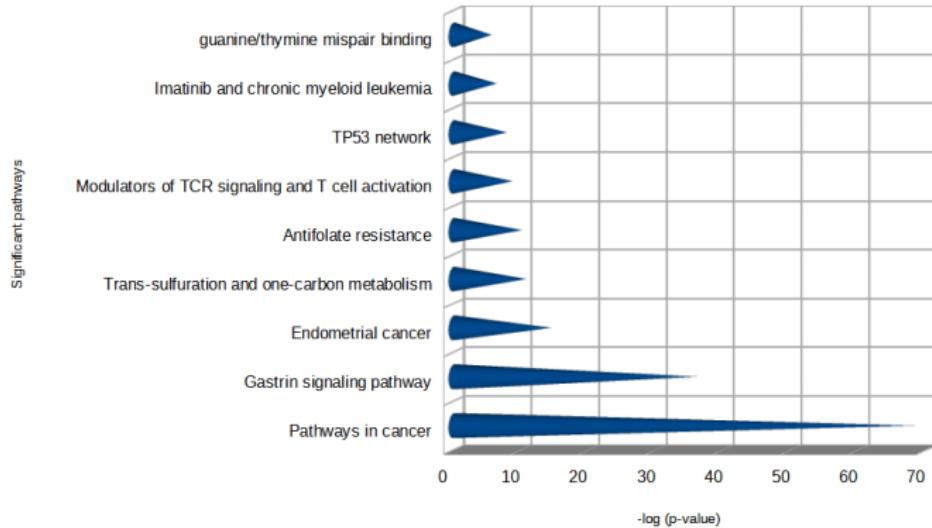


Figure: List of functionally enriched significant biological processes / pathways.

Statistical Validation

- We correlated our findings using the STRING database (experimentally verified) in the form of manually curated function protein interaction network database available for human proteins³⁷ for validation.
- All the 9 significant communities involving gene-ontologies were validated with least False Discovery Rate (FDR), depicting that all of highlighted GO:BP terms are of statistical significance.

Statistical Validation

Table: Functionally enriched biological processes with the total number of genes in the community (G_c) and the False Discovery Rates (FDR).

Rank	Gene Ontology / Biological process	G_c	FDR
1	Pathways in Cancer	70	2.32E-103
2	Gastrin signaling pathway	27	6.69E-57
3	Endometrial cancer	7	3.73E-15
4	Trans-sulfuration and one carbon metabolism	6	2.02E-14
5	Antifolate resistance	5	5.30E-12
6	Modulators of TCR signaling and T-cell activation	5	2.34E-10
7	TP53 Network	4	9.83E-10
8	Imatinib and chronic myeloid leukemia	3	9.62E-07
9	Guanine / Thymine mispair binding	2	0.00017

Results and Discussions

- The top 10 genes that were involved with EBV-associated carcinomas involving GC, NPC, HL and BL were identified as CASP10, BRAF, NFKBIA, IFNA2, GSTP1, CSF3, GATA3, UBR5, AXIN2 and POLE.
- We listed the community of genes involved with 9 key biological processes and critical pathways linked with the Epstein-Barr virus in the overall disease gene network.
- The critical processes mainly involved were associated with pathways in cancer, Gastrin signaling pathway, Endometrial cancer, Trans-sulfuration and one carbon metabolism, Antifolate resistance, Modulators of TCR signaling and T-cell activation, TP53 Network, Imatinib and chronic myeloid leukemia and Guanine / Thymine mispair binding.

Conclusions

- We report 9 key biological processes and disease pathways affected by Epstein-Barr virus (EBV) in the disease gene network. Using community detection algorithm followed by functional enrichment, we identified the community of genes that were involved with respective biological processes involving carcinomas (GC, NPC, HL and BL).
- Further, it was observed that the ABL1 gene plays a vital role in 3 out of 9 biological processes based on over-representation analysis.
- Hence, the linkages between various biological processes infected with Epstein-Barr virus in causing carcinomas from the network of common genes present significant novel insights and therefore, we provide our case for clinical studies.
- Currently, clinical studies (NCT01491763) are under trials (phase IV) to investigate the effectiveness of the combination of chemotherapy and administration of Imatinib in patients and associations (NCT04965649) between BCR-ABL1 and T-cell modulators (CD8+ T-cells).

Title:

Over-representation analysis of angiogenic factors in
immunosuppressive mechanisms in neoplasms and neurological
conditions during COVID-19. ^a ^b

Keywords: SARS-CoV2, Community Detection, Biological Process, Carcinoma,
Neoplasms.

^aMicrobial Pathogenesis, 185 (106386), pp. 1-9, Dec 2023. doi: 10.1016/j.micpath.2023.106386

^bS. Chatterjee and B.S. Sanjeev, Department of Applied Sciences, Indian Institute of Information
Technology, Allahabad, 211012, UP, India

Introduction

Background:

Evidence from multiple studies has shown that the severity of COVID-19 is enhanced by comorbid and life-threatening diseases, and patients with comorbidities have been affected disproportionately. Such patients are more susceptible to organ failure and mortality.

COVID-19 infection:

Given the global spread of COVID-19, it is vital to investigate biological processes and pathways that are common between COVID-19 and other diseases and comorbid conditions. Such advances would ultimately contribute towards better therapeutic outcomes.

COVID-19 gene associations - An example

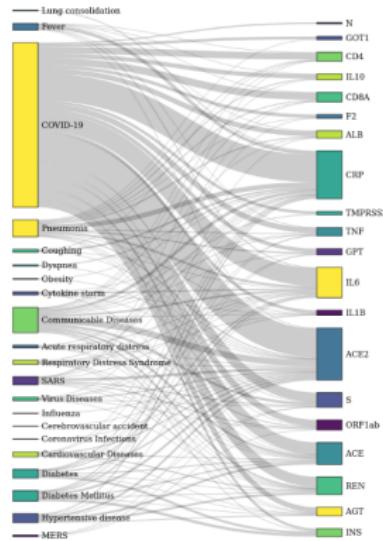


Figure: Genes that are frequently mentioned together with COVID-19.³⁸

³⁸<https://www.ncbi.nlm.nih.gov/research/coronavirus>

Problem definition

Problem:

Treating patients with life threatening diseases during COVID-19 pandemic has been quite challenging and therapeutic clinical applications used in various immunotherapies have led to the worsening of COVID-19 outcomes among patients.

Current status:

The molecular interplay involving overlapping relationships between COVID-19 and other diseases is not yet fully understood and undergoing clinical investigation.

Objective:

Our objective is to implement network theory approaches and elucidate how community detection and functional enrichment can identify biological processes and pathways shared between COVID-19 and other diseases.

COVID-19 IntAct DisGeNET Analysis

(a) High degree genes			(b) High degree diseases		
Rank	Gene	Degree	Rank	Disease Name	Degree
1	VEGFA	1899	1	Neoplasms (unclassified)	535
2	BCL2	1456	2	Malignant Neoplasms	459
3	CTNNB1	1368	3	Primary Malignant Neoplasms	444
4	ALB	1198	4	Malignant Neoplasm of breast	372
5	COX2	875	5	Tumor cell Invasion	368
6	AGT	765	6	Breast Carcinoma	363
7	HLA-A	672	7	Liver Carcinoma	352
8	HMOX1	666	8	Carcinogenesis	347
9	FGF2	635	9	Neoplasm metastasis	344
10	COMT	622	10	Colorectal carcinoma	309
11	MET	594	11	Malignant neoplasm of prostate	284
12	PLG	586	12	Prostrate carcinoma	276
13	PCNA	581	13	Malignant neoplasm of lung	263
14	PARP1	565	14	Carcinoma of lung	262
15	AIMP2	555	15	Primary malignant neoplasm of lung	257
16	FBN1	552	16	Non-small cell Lung carcinoma	241
17	HSPA4	550	17	Tumor progression	235
18	GNAS	536	18	Alzheimer's Disease	226
19	STAT1	531	19	Malignant neoplasm of stomach	221
20	AHSA1	526	20	Stomach carcinoma	209
21	TGFBR2	502	21	Malignant neoplasm of colon	208
22	HSPA1B	502	22	Glioblastoma	198
23	DNMT1	496	23	Glioblastoma Multiforme	195
24	HSPA1A	458	24	Glioma	193
25	DPP4	451	25	Melanoma	188

Degree Distribution

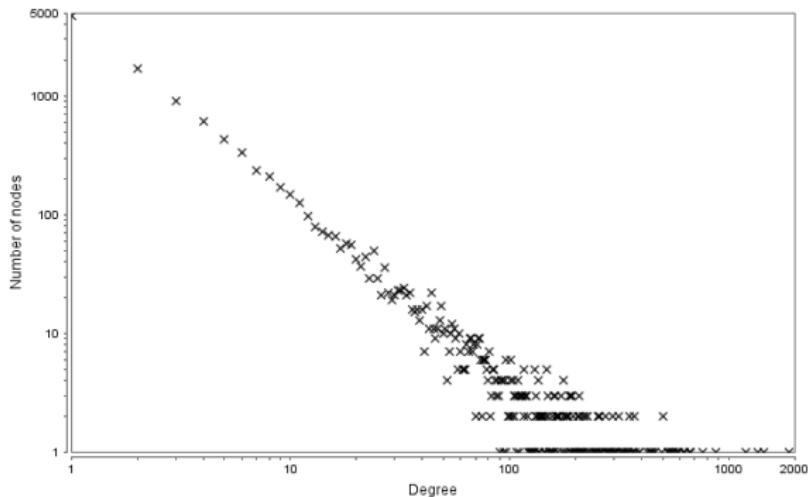


Figure: Very high degrees for only a fraction of nodes shows that only a smaller set of genes and diseases have high interactions with other nodes. For instance, Vascular Endothelial Growth Factor A (VEGFA) is known to be involved in 1899 diseases, while malignant neoplasms are associated with 459 genes. All the genes, taken from COVID DisGeNET data set, are known to be associated with SARS-CoV-2 too.

Network modularity

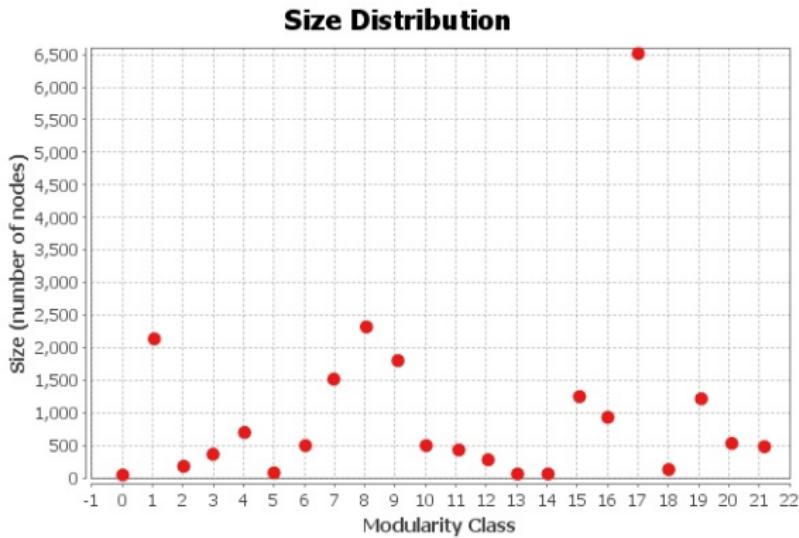


Figure: The network modularity of the disease-gene network was 0.28 signifying a positive structured modular network. The figure depicts the size distribution of the 22 modularity classes.

Over representation Analysis

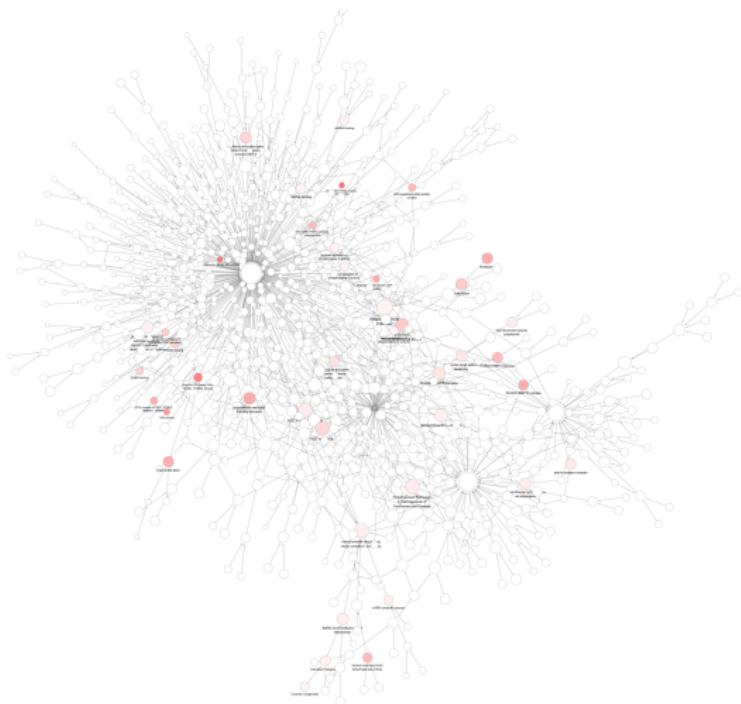


Figure: Hierarchical network layout of biological pathways.

Over-Representation Analysis

Table: Significant biological processes and pathways. p-value threshold is less than 1.09E-06.

Rank	Gene Ontology / Biological process	P-value	-log(P)	Reference
1	Mitochondrial respiratory chain complex	8.71E-12	11.05998	GO:0032981
2	Ubiquitin E3 ligase	1.63E-10	9.787812	CORUM:622
3	Activin receptor complex	2.82E-10	9.549751	GO:0048179
4	Arylamine N-acetyltransferase activity	1.49E-09	8.826814	GO:0004060
5	Complex I biogenesis	1.49E-08	7.826814	REAC:R-HSA-6799198
6	FK506 binding	3.23E-08	7.490797	GO:0005528
7	HDL assembly	5.21E-08	7.283162	REAC:R-HSA-8963896
8	Integrated Cancer Pathway	3.76E-07	6.424812	WP:WP1971
9	ACE Inhibitor Pathway	5.50E-07	6.258848	WP:WP554
10	Hypothesized Pathways in CVD	5.72E-07	6.242604	WP:WP3668
11	40S ribosomal subunit, cytoplasmic	7.42E-07	6.129596	CORUM:305
12	TIM complex, mitochondrial	8.17E-07	6.087778	CORUM:623
13	EIF3 complex	8.17E-07	6.087778	CORUM:4399
14	VCB complex	8.25E-07	6.083546	GO:0030891
15	Acetylation	1.09E-06	5.962574	REAC:R-HSA-156582
16	SARS-CoV-2 mitochondrial interactions	1.23E-06	5.910095	WP:WP5038
17	snRNA binding	1.30E-06	5.886057	GO:0017069
18	Complex I biogenesis	1.42E-06	5.847712	REAC:R-HSA-6799198
19	Ribosomal small subunit assembly	1.50E-06	5.823909	GO:0000028
20	PLOD2-FKBP10 complex	1.65E-06	5.782516	CORUM:7000
21	Negative regulation of apoptotic pathway	1.73E-06	5.761954	GO:1902042
22	CRD-mediated mRNA stability complex	2.06E-06	5.686133	GO:0070937
23	TIM complex, mitochondrial	2.06E-06	5.686133	CORUM:623
24	ncRNA catabolic process	2.47E-06	5.607303	GO:0034661
25	Acetylation	2.89E-06	5.539102	REAC:R-HSA-156582
26	Angiotensin-mediated drinking behavior	3.28E-06	5.484126	GO:0003051
27	Positive regulation of phospholipase C	4.44E-06	5.352617	GO:0010863
28	DCS complex	4.90E-06	5.309804	CORUM:1288
29	snRNA binding	6.58E-06	5.181774	GO:0017069
30	Ubiquinone and terpenoid-quinone	6.71E-06	5.173277	KEGG:00130
31	Metanephric glomerular capillary formation	7.31E-06	5.136083	GO:0072277
32	CCT complex	7.62E-06	5.118045	CORUM:126
33	Cellular Heat acclimation	8.01E-06	5.096367	GO:0070370
34	Striated Muscle Contraction	8.70E-06	5.060481	REAC:R-HSA-390522
35	Protein N-linked glycosylation via asparagine	9.63E-06	5.016374	GO:0018279
36	Medium-chain-acyl-CoA dehydrogenase activity	9.84E-06	5.007005	GO:0070991
37	Interferon-stimulated gene factor 3 transcription complex	9.90E-06	5.004365	CORUM:60

Over-Representation Analysis

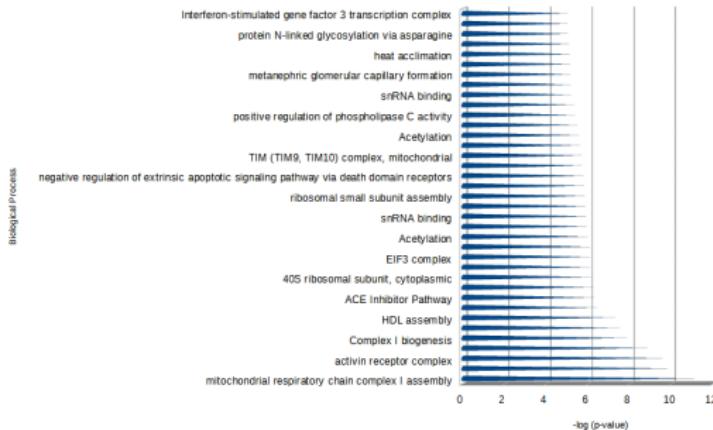


Figure: List of significantly enriched biological pathways.

Over-Representation Analysis

Table: Community of genes from functionally enriched pathways along with their respective overlap representation ratio. The genes that are underlined represent mitochondrial genes.

Community	Genes	Overlap ratio	Community Size
1	ACAD9 AIFM1 BCS1L <u>NDUFA10</u> <u>NDUFAF1</u> <u>NDUFAF2</u> <u>NDUFB9</u>	0.075	426
2	CUL2 ELOB ELOC	0.6	27
3	ACVR2A ACVR2B ACVR1A ACVR1B	0.111	67
4	NAT2 NAT1 AANAT	0.025	230
5	<u>NDUFA10</u> <u>NDUFAF1</u> <u>NDUFAF2</u> <u>NDUFB9</u>	0.067	69
6	FKBP1A FKBP3 FKBP7	0.231	15
7	A2M ABCA1 PRKACA	0.187	310
8	BCL2 CHEK2 MYC PTEN	0.057	816
9	ACE2 AGT KNG1	0.097	295
10	FBN1 FBN2 TGFBR2	0.088	355
11	RPS10 RPS17 RPS27	0.083	63
12	TIMM10 TIMM9	0.667	6
13	EIF3B EIF3J	0.667	5
14	CUL2 ELOB	0.5	8
15	NAT2 NAT1	0.4	72

Statistical Validation

- For validation, we correlated our findings with the STRING database which comprehensively covers human proteins in the form of manually curated function protein interaction network ³⁹.
- 13 out of all the 15 significant communities (86.67%) detected were cross validated and were found to have least False Discovery Rate (FDR), implying that the majority of highlighted GO:BP terms are clinically significant.

Statistical Validation

Table: Functionally enriched biological processes validated using STRING in the community and the False Discovery Rates (FDR) of each GO:BP node.

Community Rank	Gene Ontology / Biological process	FDR
1	Mitochondrial respiratory chain complex I assembly	9.60E-14
2	Ubiquitin E3 ligase	-
3	Activin receptor complex	5.84E-11
4	Arylamine N-acetyltransferase activity	5.18E-08
5	Complex I biogenesis	1.62E-07
6	FK506 binding	0.0007
7	HDL assembly	0.0211
8	Integrated Cancer Pathway	2.16E-08
9	ACE Inhibitor Pathway	6.19E-07
10	Hypothesized Pathways in Pathogenesis of CVD	1.78E-06
11	40S ribosomal subunit, cytoplasmic	1.56E-05
12	TIM complex, mitochondrial	0.00034
13	EIF3 complex	0.0012
14	VCB complex	0.00019
15	Acetylation	-

Conclusions

- Our study strongly suggests that the patients with comorbid conditions such as those with various carcinomas, neoplasms and Alzheimer's disease, are the most vulnerable among all the disease classes infected by SARS-CoV-2 through community detection.
- Functional enrichment through over-representation analysis methodology was used to discover significant biological processes and pathways shared between COVID-19 and other diseases.
- Improving endothelial permeability and vasodilation with VEGF-targeted therapy could allow the repair of damaged vascular endothelium and may have an anti-inflammatory effect and improve oxygenation.
- Strategies involving treatment with anti-VEGF drugs such as bevacizumab besides VEGFR-mediated signaling therapies may deliver favorable outcomes.

Conclusions

- Currently ongoing Phase-III clinical trials that focus on the safety and efficacy of VEGF-targeted therapeutic drug bevacizumab (NCT04822818).
- Currently, clinical studies are under Phase-II trials to assess the potential of anti-VEGF drugs such as Bevacizumab for COVID-19 (NCT04275414)

The potential genes that were involved in multiple diseases involving various carcinomas were identified as VEGFA, BCL2, CTNNB1, COX2, HLA-A, HMOX1 and FGF2.

- VEGF signaling presents itself as a strong therapeutic target. For better outcomes improving endothelial permeability and vasodilation with VEGF-targeted therapy may have an anti-inflammatory effect and improve oxygenation in comorbid conditions with neoplasms and severe neurological conditions.
- As an outcome of our study, we make a strong case for clinical investigations towards anti-VEGF therapies for better therapeutic outcomes.

Title:

Role of Toll-Like Receptors in the interplay between pathogen and damage associated molecular patterns. ^a ^b

Keywords: PAMPs, lipopolysaccharides (LPs), endotoxins, DAMPs, Interleukins, Interferons.

^aarxiv-preprint

^bS. Chatterjee and B.S. Sanjeev, Department of Applied Sciences, Indian Institute of Information Technology, Allahabad, 211012, UP, India

Pathogen Interactions

Table: Number of Pathogens and their Class (Bacteria/ Virus).

Sl.	Pathogens	Class	Degree(Γ)
1	<i>Helicobacter pylori</i>	Bacteria	1150
2	<i>Chlamydia pneumoniae</i>	Bacteria	745
3	<i>Borrelia</i>	Bacteria	660
4	<i>Toxoplasma gondii</i>	Bacteria	378
5	<i>Streptococcus</i>	Bacteria	109
6	<i>Mycobacterium tuberculosis</i>	Bacteria	72
7	<i>Bartonella</i>	Bacteria	56
8	Enteroviruses	Virus	1025
9	Cytomegalovirus	Virus	865
10	Epstein-Barr virus	Virus	477
11	Herpes simplex virus	Virus	404
12	Parvovirus B19	Virus	390
13	Human herpesvirus 6	Virus	386
14	Influenza A	Virus	224
15	Hepatitis C virus	Virus	199
16	HIV	Virus	180
17	Hepatitis B virus	Virus	103

Pathogen Interactions

Table: Overview of Network

Parameters	Nos.(#)
Total no. of pathogens	17
No. of human proteins (H_p)	2,536
Total no. of associations interacting with pathogens	7,019

Important Interacting Proteins

Gene	Degree	Topol. Coeff.	Betw. Centrality.	Protein
SOD2	41	0.16262985	0.00602848	Superoxide dismutase [Mn], mitochondrial
PTGS2	40	0.18507808	0.00330486	Prostaglandin G/H synthase 2
TNF	36	0.16444268	0.00484062	Tumor necrosis factor
TP53	33	0.1629871	0.00404872	Cellular tumor antigen p53
PLAU	31	0.19851805	0.0028075	Urokinase-type plasminogen activator
NOS2	27	0.1847816	0.00412495	Nitric oxide synthase, inducible
PLAT	26	0.2231064	0.00163375	Tissue-type plasminogen activator
IL6	24	0.19647329	0.00346007	Interleukin-6
ACE	22	0.20865038	0.00227199	Angiotensin-converting enzyme
IL1B	22	0.19851805	0.0028075	Interleukin-1 beta
IFNG	22	0.19776016	0.00359721	Interferon gamma
SOD1	21	0.1748717	0.0034557	Superoxide dismutase [Cu-Zn], soluble
STAT3	20	0.19647329	0.00346007	Signal transducer and activator of transcription 3
MTHFR	19	0.19866054	0.00260592	Methylenetetrahydrofolate reductase
CCL2	19	0.18357301	0.003561	C-C motif chemokine 2

Table: Common Sub-group of Human Proteins during the cross-talk of pathogen and damage associated molecular patterns.

Significance of TLRs

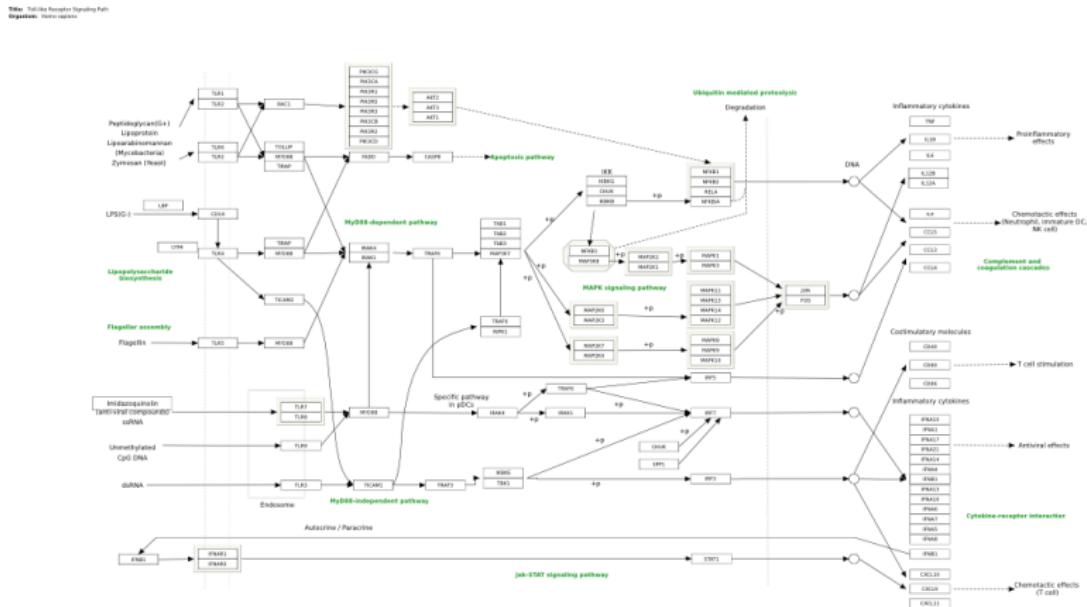
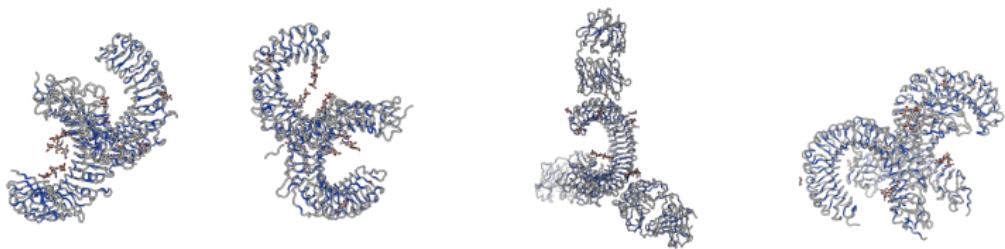


Figure: Toll-like receptor (TLR) Signaling Pathway are membrane-bound host (human) proteins that respond to Gram-positive and Gram-negative bacteria. They induce pro-inflammatory cytokines and are responsible for producing innate immune responses.

Significance of TLRs

Gene	Protein	Uniprot ID	No. of Pathogens	
			Bacteria	Virus
TLR1	Toll-like receptor 1	Q15399	30	4
TLR2	Toll-like receptor 2	O60603	83	18
TLR3	Toll-like receptor 3	O15455	8	29
TLR4	Toll-like receptor 4	O00206	63	22
TLR5	Toll-like receptor 5	O60602	13	5
TLR6	Toll-like receptor 6	Q9Y2C9	19	3
TLR7	Toll-like receptor 7	Q9NYK1	4	16
TLR8	Toll-like receptor 8	Q9NR97	6	13
TLR9	Toll-like receptor 9	Q9NR96	20	20
TLR10	Toll-like receptor 10	Q9BXR5	2	2

Table: Overview of Toll-like receptors (TLRs) and their interactions with bacterial and viral proteins. The number depicted above signifies the number of interactions with bacterial/viral pathogenic proteins.

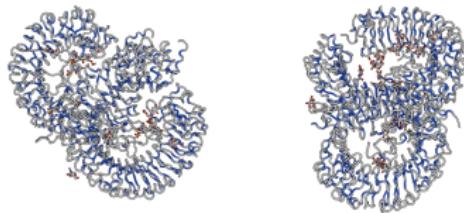


(a) TLR1

(b) TLR2

(c) TLR3

(d) TLR4



(e) TLR7

(f) TLR8

Figure: The blue-colored regions depict Leucine Rich Repeat regions (LRRs) of Toll-like receptors. Based on the number of interactions, Toll-like receptors *viz.* TLR1, TLR2 and TLR4 were found to be more susceptible to bacterial proteins, whereas TLR3, TLR7 and TLR8 were more preferential to viral proteins.

Brief Summary

- In our findings, we found that the TLRs frequently interact with the common subgroup of Human proteins that have higher values of Betweenness Centrality.
- It has also known that the TLRs have a role in stimulating TNF and IL6 production
- No much is known about TLR5, TLR7, TLR9 and TLR10 and their role is still not fully understood.

Conclusions

- Identification and understanding the important interacting proteins can provide insights into key regulatory mechanisms, immune evasion strategies employed by pathogens and potential therapeutic targets.
- We infer that BCR-ABL1 tyrosine-kinase inhibitors (TKI) could be further investigated for clinical studies in EBV associated carcinomas for better prognostic and therapeutic outcomes.
- As an outcome of our study, we propose for clinical investigations towards anti-VEGF therapies for such comorbid conditions affected by COVID-19 for better prognostic and therapeutic outcomes.

Conclusions

- The theory of complex networks holds significance across diverse disciplines, spanning from communications and power systems engineering to molecular biology.
- Network biology approaches can model immune signaling networks that encompass intricate interactions between immune cells, cytokines, and other signaling molecules.
- Analyzing these networks helps to discover the dynamics of host immune responses to infection, including how pathogens evade immune detection and manipulate immune signaling pathways.
- By integrating information on pathogen-host interactions with drug-target networks, we can prioritize candidate targets for drug development.
- This approach facilitates the discovery of novel therapeutic agents that disrupt essential pathways in pathogens.

Publications

- Over-representation analysis of angiogenic factors in immunosuppressive mechanisms in neoplasms and neurological conditions during COVID-19.
S. Chatterjee, B.S. Sanjeev, Microbial Pathogenesis, 185 (106386), pp. 1-9, Dec 2023. doi: 10.1016/j.micpath.2023.106386
- Community detection in Epstein-Barr virus associated carcinomas and role of tyrosine kinase in etiological mechanisms for oncogenesis.
S. Chatterjee, B.S. Sanjeev, Microbial Pathogenesis, 180 (106115), pp. 1-7, July 2023. doi: 10.1016/j.micpath.2023.106115
- Identification of Human Proteins vulnerable to multiple Organisms.
S. Chatterjee, B.S. Sanjeev, In Proceedings of International Conference on Bioinformatics and Systems Biology (BSB), IEEE pp. 1-4, 04-06 March 2016. doi: 10.1109/BSB.2016.7552164
- Role of Toll-like Receptors in the interplay between pathogen and damage associated molecular patterns.
S. Chatterjee, B.S. Sanjeev, In preparation.

Appendix

Tools:

- PHISTO⁴⁰
- DisGeNET⁴¹
- NetworkX
- CDAPS / HiDeF
- Gnuplot
- Cytoscape
- Open Source Community
- Data/codes available on github.com/suprateekchatterjee/

⁴⁰Durmus Tekir S, Cakir T, Ardic E, Sayilirbas AS, Konuk G, Konuk M, Sariyer H, Ugurlu A, Karadeniz I, Ozgur A, et al. PHISTO: pathogen-host interaction search tool. Bioinformatics 2013, 29:1357–1358.

⁴¹Piñero, J., Ramírez-Anguita, J.M., Saúch-Pitarch, J., Ronzano, F., Centeno, E., Sanz, F. and Furlong, L.I., 2020. The DisGeNET knowledge platform for disease genomics: 2019 update. Nucleic acids research, 48(D1), pp.D845-D855.

Community Detection APplication and Service (CDAPS)

The image shows two side-by-side screenshots of the CDAPS framework. On the left is a screenshot of the CDAPS documentation website (<https://cdaps.readthedocs.io>). The header reads "Community Detection APplication and Service v1.12.0". It features a sidebar with "CONTENTS" (Installation, What's New, Quick Tutorial, Tally Attributes on Hierarchy, Columns, Settings) and "LINKS:" (Cytoscape.org, Cytoscape App Store, Idekerlab.ucsd.edu, GitHub). A note at the bottom says "Reach the right audience on a privacy-first ad network only for software devs: [FhirAdz](#)". At the bottom are "Read the Docs" and "v: v1.12.0". On the right is a screenshot of the CDAPS application interface. The title bar says "Docs > CDAPS". The main content area is titled "CDAPS" and contains the text: "Community Detection APplication and Service (CDAPS). CDAPS performs multiscale community detection and functional enrichment for network analysis through a service-oriented architecture. These features are provided by integrating popular community detection algorithms and enrichment tools. All the algorithms and tools run remotely on a dedicated server." Below this is a section titled "Currently supported features:" with a bulleted list: "Community detection algorithms: Louvain, Infomap, OSLOM, CliXO, HiDeF" and "Functional enrichment tools: gProfiler, Enrichr, iQuery". Below the text are two windows showing network analysis results. The left window shows a tree-like structure of network components. The right window shows a complex network graph with nodes and edges, color-coded by community.

Figure: CDAPS framework.⁴²

⁴²<https://cdaps.readthedocs.io>

Hierarchical community Decoding Framework (HiDef)

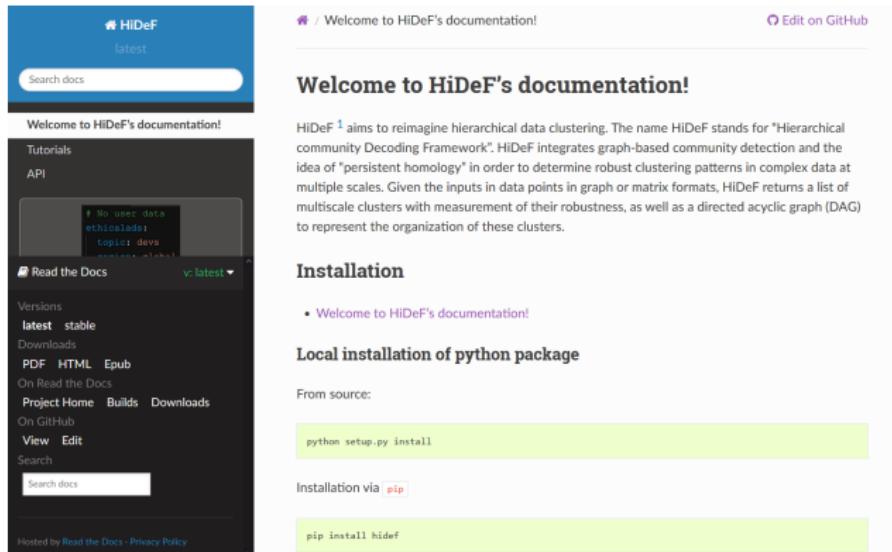


Figure: HiDef framework.⁴³

⁴³<https://hidef.readthedocs.io/>

Questions ??