

A Bioinformatics Study of Hepatitis C(HCV) Virus Hub Proteins

Introduction:

Clinical Overview of Hepatitis

(<https://www.cdc.gov/hepatitis-c/hcp/clinical-overview/index.html>)

HCV Life Cycle:<https://www.hepatitisc.uw.edu/biology/lifecycle>

HCV Proteins:<https://www.hepatitisc.uw.edu/biology/proteins>

HCV

Structure:<https://www.hepatitisc.uw.edu/biology/structure> [Optional]

Data Acquisition

- Obtain the raw protein-protein interaction (PPI) data.
- Key Information to Gather:
 - Identify and use a reputable, publicly available database, such as STRING or BioGRID.
 - Perform a search for interactions between HCV viral proteins and *Homo sapiens* (human) proteins.
 - Download the interaction data in a simple, organized file format (e.g., a text or CSV file containing protein pairs).

Network Construction

- **Action:** Build the protein-protein interaction network from the raw data.
- **Key Information to Gather:**
 - Use a dedicated bioinformatics software for network visualization, such as **Cytoscape**.



- Import the downloaded data file into the software to create a visual graph where proteins are **nodes** and their interactions are **edges**.
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Network Analysis (Hub Identification)

- **Action:** Apply computational methods to identify hub proteins.
 - **Key Information to Gather:**
 - Calculate **centrality measures** for each protein in the network.
 - Focus on these two key metrics:
 - **Degree Centrality:** To find local hubs with a high number of direct interactions.
 - **Betweenness Centrality:** To find global hubs that act as bridges connecting different parts of the network.
 - Rank the proteins based on their scores to identify the top candidates for viral and host hubs.
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Interpretation and Conclusion

- **Action:** Connect your computational findings back to the biological context.
- **Key Information to Gather:**
 - Interpret Findings:** Discuss the roles of the viral hub proteins you identified (NS3, NS5A and Core). Explain *why* their functions make them highly connected in the network.
 - Biological Significance:** Hypothesize about the functions of the top host hub proteins you discovered. Are they involved in key cellular pathways that the virus needs to survive?
 - Conclusion:** Summarize your findings and discuss the implications for understanding HCV pathogenesis and for identifying new therapeutic targets.

Key Takeaway: STRING is for finding the data, and Cytoscape is for a deep, quantitative analysis of that data. You need both to successfully complete your project.