Software requirement specification V.1.1  
for: Virus-Phage Network  
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1. Introduction  
   A tool to visualize and analyze the results of VHIP 2.0, which is an algorithm to predict virus-host interactions. Visualizations will include heatmaps and network graphs. The results will be compared to a variety of random models.

VHIP 2.0: <https://github.com/DuhaimeLab/VirusHostInteractionPredictor>

Sample data: <https://github.com/ecampau/virus_phage_network/tree/main/Sample_Input>

1. Overall description  
   Input: Results of VHIP 2.0. Columns include pairs (where the virus name is to the left of the colon and the host name is to the right of the colon), GCdiff, k3dist, k6dist, Homology, Predictions, and InfProbabilities.   
   Output: Visualizations for the virus-phage interactions in the dataset, including heatmaps, network graphs, and matrix statistics (e.g. Centrality).
2. Requirements

Input data format: tsv file with a row for each possible virus-phage pair. The values in the predictions column should be either 0 (non-infection) or 1 (infection). The values in InfProbabilities should be between 0 and 1.