

Network Analysis of Human Gut Virus & Bacterial Infectious Relationships

Geoffrey D Hannigan
Patrick D Schloss

Introduction

Results

Construction & Validation of Bacteria-Phage Interaction Network

We used Neo4J graph database software to construct the network of predicted interactions between bacteria and bacteriophages. Results from a variety of complementary interaction prediction approaches were layered into a single network (**Figure 1**). *In vitro*, experimentally validated interactive relationships were taken from the existing literature. Clustered Regularly Interspaced Short Palindromic Repeats (CRISPRs) are a sort of bacterial adaptive immune system that serves as a genomic record of phage infections by preserving genomic content from the infectious phage genome. These records were used to predict infectious relationships between bacteria and phages. Infectious relationships were also predicted by identifying expected protein-protein interactions and known interacting protein domains between phages and their bacterial hosts. We finally used nucleotide blast to identify genomic similarity between bacteriophage genomes and sections of bacterial genomes. Such a match is a good predictor of an interaction between the phage and its bacterial host.

Figures

Figure 1

