

Public Abstract

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Graduation Term:SP 2015

Department:Computer Science

Degree:PhD

Title:ANALYSIS OF HOST-PATHOGEN INTERACTIONS VIA CLUSTERING, STATISTICAL ANALYSIS, AND DATA VISUALIZATION

Infectious diseases are caused by a variety of agents: viruses, bacteria, parasites, or even proteins. I studied the evolution of the influenza virus, pathogenic bacterial proteins, and resistance in soybeans to soybean cyst nematode using existing and self-developed bioinformatics methods. Using clustering and structural analysis, I determined the overall pattern of evolution for all pandemic subtypes – H1N1, H2N2, H3N2, and H5N1 – of influenza. For bacterial proteins, however, I focused on making data available to biologists everywhere by creating a database, BacPaC, to hold predicted pathogenic proteins, called effectors, as well as data relevant to those proteins. In conjunction with a group of experimental biologists, I determined protein structures for genes that have shown to cause resistance in soybeans and used those structures to find the effects of mutations on binding of various ligands and proteins.