In 2003 SARS infected over 8,000 people, killing 774. Outbreaks like SARS pose a significant challenge to human health, economic stability, and national security. Existing treatments after often ineffective against outbreaks because outbreaks are typically caused by novel viral strains and because existing drugs and vaccines have narrow specificity. This problem is compounded by the slow timeline of drug development. My long-term goal is to develop the systems biological understanding of viral physiology and infection needed to drive broad spectrum anti-viral development and prospectively manage viral outbreaks. My interest in viral pathophysiology stems from my long-standing commitment to systems biology and human health.

As a graduate student I plan to address a critical and poorly understood aspect of viral infection: how viruses interact with their hosts. All viruses are parasites, dependent on their cellular hosts to produce viral DNA, RNA, proteins, and lipids. This raises two critically important questions: What aspects of host metabolism affect viral synthesis and assembly? Can we exploit viral dependence on host metabolism to fight viral infection?

Currently I am working with Prof. Markus Covert to begin to address these questions by building a comprehensive computational model of bacteriophage T7 replication in the context of its host *Escherichia coli* (*E. coli*). Our model integrates two published models: a genome-scale metabolic model of *E. coli* and an ordinary differential equation model of T7 replication. The hybrid model describes 166 host-virus metabolic interactions and accounts for 1,132 metabolic reactions and 60 T7 proteins and RNA. This level of detail is required to predict *E. coli* metabolic pathways that are required for T7 infection given nutritional and genetic perturbations of *E. coli*’s environment.

Beginning next year I plan to extend the modeling framework we have developed for T7 and *E. coli* to viruses like Influenza A H1N1, SARS coronavirus, and poliovirus infecting human cells. I will integrate models viral replication for these viruses with a genome-scale metabolic model of a human epithelial cell taking into account shared metabolites. These related models will identify viral physiology is be common to many human viral pathogens. I anticipate these models will identify host metabolic pathways critical for viral and potential drug targets.

Beyond graduate school, as an academic systems biologist, I hope to continue to improve our understanding viral infection and collaborate with physicians to develop novel broad-spectrum anti-viral drugs. An NDSEG fellowship will allow me to continue to investigate host-viral interactions and become a leader in the fields of systems biology and virology.