Parkinson's Disease (abbreviated as PD) is a long-term, debilitating degeneration of neurons in the central nervous system, often first causing motor symptoms such as tremors or loss of balance before progressing into non-motor symptoms such as insomnia, depression, and other cognitive impairments. Leading to nearly 60,000 new diagnoses per year in the U.S. alone, the disease is common, but its causes are fairly mysterious—the genetic causes of most cases are unknown, and even recent research only identifies about six genes in various dominant and recessive forms where mutations in them have been known to cause PD. Since many of the neurons being damaged by PD are known to produce dopamine, current treatments for PD are largely symptomatic and attempt to compensate for the rapid decline in dopamine production following onset. Beyond that, surgical treatments are currently being explored, but PD overall is still considered largely incurable.

While the cause of PD can rarely be pinpointed to a mutation in a single gene, it is possible that mapping the clusters of genes related to those known to cause PD as a proteinprotein interaction network could help in identifying the functions of nearby genes and their role in causing PD. Since working with my faculty mentor, Professor Lenore Cowen, I have read papers in computational biology on how proteins with related functions can be mapped onto graphs, which are then used in turn to predict the functions of other proteins located nearby on the graph. A common strategy to doing this—an algorithm known simply as "majority vote"—was then further refined in "Majority Vote Cascading: A Semi-Supervised Framework for Improving Protein Function Prediction" by Lazarsfeld et al. The new variety of majority vote algorithm that is introduced improves the methods by which relations between protein functions within a protein-protein interaction network are identified.

My research would seek to answer whether or not applying this refined algorithm to the protein network where PD-causing genes are known could help identify and quantify the role of other genes in causing PD. This could potentially help make earlier diagnoses of PD, helping patients to begin lifestyle changes designed to alleviate the disease's effects sooner rather than later in the degeneration. Furthermore, additional discovery in the genetics behind PD could aid in developing more genetically customized treatments that could be increasingly effective in managing the symptoms and causes of PD than the general management strategies currently employed by most PD patients. Although this is my first independent research project, I hope to learn a lot about how researchers think about and begin to solve the major problems of the modern world. I still have a lot to learn about being a leader, but I am confident that my problem-solving, communicative abilities, and capability to quickly learn new skills will all allow me to make the project a success that could one day contribute to major breakthroughs in curing an incurable, yet debilitating disease.