Bacteriophage and their hosts are locked in an age-old arms race. Successful bacteria are subject to "kill-the-winner", or frequency-dependent selection, allowing strains that have acquired or evolved strategies for resistance to prevail. Similarly, phage are also quick to adapt tactics for infecting these potential hosts. Sampling of closely related bacterial strains with differing phage infection profiles can further elucidate the mechanisms of infection. The Polz lab maintains the Nahant Collection, a rich dataset of 277 *Vibrio* strains that have been challenged by 260 unique phage, all with sequenced genomes. This is the largest phylogenetically-resolved host range cross test available to date. Gleaning mechanistic insights from this data is a complex statistical problem, as infection specificities involve interacting proteins between organisms. With approximately 1000 phage protein clusters and 10,000 bacterial protein clusters, there are 10,000,000 possible interactions for the 72,000 observations. Here, we propose using alternative minimization in order to utilize these interaction terms without directly working with this matrix. Our approach aims to set up a framework for analyzing high dimensional cross test data and may be generalizable down the line to additional problems such as screening drugs with various chemical properties/functional groups against cell types with various expression patterns.