Infections caused by multidrug-resistant bacteria are a critical problem in healthcare settings and of increasing concern in the community. Traditional surveillance methods that focus on selected organisms do not provide insight into overall patterns of antimicrobial resistance as it emerges in different communities and strategies to track emergence and identify contributing risk factors are needed. The goal of this project is to develop an “antibiotic resistome” map of the distribution of antimicrobial resistance genes across New York City. The map will be used to identify individual and neighborhood level factors that contribute to regional differences in the distribution of these genes. Ultimately, this new approach to infectious disease surveillance could be used to develop new intervention strategies to reduce the spread of multi-drug resistant bacteria in the community.