



# CALIFORNIA SCIENCE & ENGINEERING FAIR 2019 PROJECT SUMMARY

<b>Name(s)</b> <b>Sasha Ronaghi</b>	<b>Project Number</b> <b>S1523</b>
<b>Project Title</b> <b>Using Machine Learning and Surface Enhanced Raman Spectroscopy to Analyze the Effects of Antibiotics on P. aeruginosa</b>	
<p style="text-align: center;"><b>Abstract</b></p> <p><b>Objectives</b> Every year, there are 6,700 multidrug resistant Pseudomonas aeruginosa infections and 440 deaths. Yet, medical professionals have no immediate way of determining the best antibiotic treatment for patients with P. aeruginosa because pathogen identification and antibiotic susceptibility tests take 3-5 days. Physicians must either prescribe broad spectrum antibiotics with harmful side effects or a combination of antibiotics that may increase antibiotic resistance. This problem inspired the design goals of this method: determine the identity of the pathogen, differentiate susceptibility and resistance to antibiotics, and determine minimum inhibitory concentration of an antibiotic in a time and cost efficient way.</p> <p><b>Methods</b> After P. aeruginosa is exposed to the antibiotic, cell lysis is performed to obtain the metabolites inside of the cell. Thereafter, Surface Enhanced Raman Spectroscopy (SERS) is used to provide a chemical fingerprint of the sample. While most SERS studies analyze a single metabolite, this method examines the entire profile of metabolites at 1011 wavenumbers. The large extent of this data is simplified using the machine learning algorithm t-distributed stochastic neighbor embedding (t-SNE). t-SNE is an unbiased machine learning algorithm that reduces the 1011 dimensions of SERS spectra to 2 dimensions for simplification and evaluation. In a susceptibility differentiation test, P. aeruginosa is exposed to Rifampicin (resistant) and Carbenicillin (susceptible) for 30 minutes. In a minimum inhibitory concentration test, P. aeruginosa is exposed to varying concentrations of Gentamicin (susceptible) for 30 minutes. In a time optimization test, P. aeruginosa is exposed to the same concentration of Gentamicin (susceptible) for varying time periods.</p> <p><b>Results</b> A support vector machine learning algorithm confirms that t-SNE can differentiate susceptibility versus resistance with 99% accuracy and differentiate concentration and time exposed with 90% accuracy. The time optimization test shows that changes in metabolites after just 5 minutes of exposure can be detected. Results showed similar trends found in colony forming unit analysis, the gold standard.</p> <p><b>Conclusions</b> Instead of waiting 3-5 days for identification and antibiotic sensitivity results, doctors can see results after 1-2 hours of suspecting infection, which is the total time necessary to inoculate, perform cell lysis, analyze using Surface Enhanced Raman Spectroscopy, and run through the t-distributed stochastic neighbor embedding. Additionally, this method provides a new analysis method the scientific community can use to analyze the effect of antibiotics on bacteria while taking account of the full profile of metabolites.</p>	
<b>Summary Statement</b> Instead of taking 3-5 days to learn which antibiotic treatment is best, I created a method to determine susceptibility and identity of pathogen after 2 hours.	
<b>Help Received</b> I worked on this project at Dr. Allon Hochabum's lab. The only aspect of this project that I didn't do was taking the Surface Enhance Raman Spectroscopy pictures. However, I shadowed the entire process.	