



# CALIFORNIA STATE SCIENCE FAIR 2015 PROJECT SUMMARY

<b>Name(s)</b> <b>Annette Chang; Daisy Chen</b>	<b>Project Number</b> <b>S1105</b>
<b>Project Title</b> <b>A Multimethod Analysis and Spatial Predictive Modeling of Bacterial Dynamics in Newport Bay</b>	
<div><div><b>Objectives/Goals</b> Our project enumerates and identifies trends in coliform and enterococcus bacteria levels throughout Newport Bay and its surrounding watershed using multiple methods assessed for practical use. In addition we utilize a computational modeling approach to predict the spatial dynamics of bacterial distribution over short time scales that may help identify possible sources of contamination and assist management decisions.</div><div><b>Methods/Materials</b> Field sampling trips were conducted during July/Aug 2014 and Feb/Mar 2015 to collect water samples. Approximately 150 water samples were collected from approximately 10 locations throughout the Newport Bay Watershed which were analyzed for total coliform, E. coli, and bacteroidetes and enterococci bacteria counts. Four different methods (Viable Plate Count, Colilert-18 Assay, Fluorescent Particle Counter, Quantitative PCR) were employed for indicator bacteria enumeration. Data from these methods were correlated to a spatial model produced via the 3D hydrodynamic model ELCOM-CAEDYM.</div><div><b>Results</b> Marine water sites showed low bacterial counts with an average total coliform MPN of 7.9 in August, and these contrasted highly with freshwater inland locations that had an average 5265 MPN. Among all locations, the part of San Diego Creek near Irvine Ranch Water District consistently displayed the highest levels while the Dog Beach at the mouth of the Santa Ana River displayed only low to moderate coliform and enterococci counts. Quantitative PCR indicated much higher quantities of Bacteroides specimens than Enterococci in all samples.</div><div><b>Conclusions/Discussion</b> Our results generally confirmed our postulated sources of bacterial input, with some exceptions, and reflected a relatively well-mixed, dynamic bay system. Freshwater drainage from the marshes around the Upper Newport Bay and Irvine Ranch Water District had the highest consistent levels, while saline locations had reliably low concentrations. ELCOM-CAEDYM modeling indicated spatial, temporal, and seasonal changes in bacterial concentration dynamics. Overall, this study presents a comprehensive view of the distribution and quantity of common indicator bacteria in the Newport Bay watershed based on specific inputs, with implications for public health in the region.</div></div>	
<b>Summary Statement</b> Our project identified trends in coliform and enterococci bacteria levels throughout Newport Bay and developed a computational modeling approach to predict the spatial dynamics of bacterial distribution over time.	
<b>Help Received</b> Used lab equipment at UCI Lander Lab under the supervision of Dr. Felix Grun.	