# CALIFORNIA STATE SCIENCE FAIR
# 2010 PROJECT SUMMARY

**Name(s)**
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**Project Number**
**S0999**

**Project Title**
## Autonomous Robot Modeling of Bacterial Motion and Chemotaxis

**Abstract**

**Objectives/Goals**
Some forms of bacteria have flagella to move through water and have two movement phases: straight swim and random tumbling. Certain forms continuously transition between the movement phases, while other bacteria, such as E. coli, employ chemotaxis to decide between movement phases. Chemotaxis is a process in which bacteria direct themselves toward highly favorable areas of food by either straight swimming when conditions are improving or randomly tumbling to reorient themselves when conditions are unfavorable. A comparison between the completely random movement method and chemotaxis movement was made. In addition, an evaluation of how frequently to check food concentrations and decide between transitioning was completed. Finally, the effects of external disturbances on bacteria were explored.

**Methods/Materials**
Due to the complexity of creating a bacterial environment with a wide range of food concentrations, a bacterium was modeled using an autonomous robot created with the Arduino platform and programmed in Python. The modeled environment contained a dynamic gradient of light levels that represented food concentrations in a bacterial environment.

**Results**
Findings show chemotaxis movement performs better than completely random movement by an average of 57 percent. Furthermore, checking food concentration levels every 0.5 seconds was the optimal frequency and resulted in the highest average light level. Additionally, external disturbances caused detrimental effects on collecting light for the chemotaxis movement while having minimal effects on the completely random movement.

**Conclusions/Discussion**
This model demonstrates that random movements are not completely random: there is a clear evolutionary benefit of chemotaxis movement and the frequent checking of concentration levels.

**Summary Statement**
The completely random movement and chemotaxis movement of bacteria were modeled and compared utilizing an autonomous robot programmed in Python.

**Help Received**
Used robotics lab at Harvey Mudd College under the mentorship of Dr. Dodds.