Modeling Gene Transfer and Its Impact on Antibiotic Resistance

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This project addresses the issue of increasing drug resistance of pathogenic bacteria in the post-antibiotic era through mathematical and computational analyses. The analyses were focused on understanding the impact vertical gene transfer (VGT), horizontal gene transfer (HGT), and antibiotic dosing. A mathematical model was built that examined wild-type and mutated (re-sistant) bacterial population growth. The model was built first discretely, but transformed into differential equations to be more faithful to biology existing in current literature. It accounted for time and space, and included growth and different mutations to antibiotics. MATLAB was used to analyze the model quantitatively and using statistical analysis. A sensitivity analysis was performed and showed that HGT was a dominant process in the development of resistance across populations. A computer model was then built that could visually simulate the spatial dy-namics and interactions of wild and mutated bacteria. It was based upon the mathematical model derived in the previous phase and explained why HGT dominated the mutation process, as well as how antibiotic dosing affected popiulations. These results can be used to understand the development of resistance in a number of bacteria strains and show how to optimize current antibiotic usage to delay widespread resistance and prolong time for research of the sustaina-ble alternatives to antibiotics.

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