Biological Networks: The Pertubation of Genetic and Metabolomic Circuits in Response to and Environmental Contaminant

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At its most fundamental level, Biology is the control and interplay between a vast number coupled chemical reactions. These chemical reactions control the basic processes of life as well as providing rapid response mechanisms to counter a plethora of environmental changes. Our group is working to elucidate the genetic and metabolomic circuits perturbed by the exposure of trace amounts of military explosives. In order to analyze the dynamic relationships between the vast number of biological reactants that may respond to the presence of an environmental contaminant of military interest, powerful techniques must be developed. The United States Army is committed to understanding the biological impact of high explosive ordinance contamination on military ranges. The tools for analyzing these complicated and dynamic networks are evolving but are restricted to the known relationships to the measured values of the gene products and metabolites. New algorithms designed to elucidate heretofore unknown relationships between these measured quantities. We are turning to Network Science techniques to analyze these enormous and complicated data sets.

Objective:

The fundamental questions our research is addressing are: (1) What individual messenger RNA transcripts and metabolites are up- or down-regulated in response to environmental contaminants? (2) What biologics perturbed by the explosives are common among bacteria (*Escherichia coli* and *Bacillus subtilis*), simple eukaryotes (*Dictyostelium discoideum*), and model higher eukaryotes (*Danio rerio*)? (3) How are these transcripts and metabolites connected?

Approach:

Over the two years of the research plan, our efforts will focus on collecting the large and complicated data sets and analyzing them using commercial software and custom algorithms developed by collaborators in the USMA EECS department. The data sets will be made available to the public so researchers from other institutions may benefit from our work. The experiments we conduct take place primarily in labs at USMA although we routinely travel to the Adelphi, Maryland campus of the Army Research Lab to perform the some of the nucleic acids processing for the gene expression microarray work. Further metabolomic work using advanced mass spectrometry methods will rely on collaborators at the University of Washington. Further, the cadets on our team engaging in this course of research will be learning advanced techniques in biotechnology while they plan, conduct and analyze experiments.

Impact:

This research will provide Army leadership and public healthcare officials the specific and useful information about genes and small molecule metabolites affected by high explosives contamination. Further, the analysis of these large and complex data sets using standard and custom designed algorithms will assist the evolution of new computational techniques to study complicated relationships of military importance. Through the analysis of the data generated from our project, the advancement of Network Science techniques over the course of this project will benefit many fields of Army research from the analysis of social networks to the prediction of IED locations in a warzone.