ZULFIYA MURADOVA#, HANNAH MCDONALD, PETER HOPKINS, QING WANG, ZHIJUN WANG, and DAVID J. KLINKE, Department of Computer Science, Mathematics and Engineering, Shepherd University, Shepherdstown, WV, 25443, ZHIJUN WANG*, AND DAVID J. KLINKE#, *DEPT. OF COMPUTER SCIENCES, MATHEMATICS, AND ENGINEERING, Shepherdstown, WV, 25443, DEPARTMENT OF CHEMICAL ENGINEERING, AND DEPT. OF MICROBIOLOGY, IMMUNOLOGY & CELL BIOLOGY, WEST VIRGINIA UNIVERSITY, MORGANTOWN, WV . A revised SEIR model for tuberculosis transmission.

Tuberculosis is a complex bacterial infection that can be influenced by many variables. This project attempts to analyze the spread and transmission of tuberculosis using a simplified model. The SEIR (susceptible, exposed, infectious, recovered) model is revised to formulate interactions between the four population groups (S,E,I,R). Equilibrium points and local stability will be discussed with the biological relevance. The model will be calibrated to data collected from the CDC (Center of Disease Control) website pertaining to tuberculosis cases within the United States. The calibrated model may provide insight into strategies that can improve the control of the spread of this infectious disease. The project was supported by NIH Grant P20GM103434 to the West Virginia IDeA Network for Biomedical Research Excellence and the West Virginia Higher Education Policy Commission Division of Science and Research SURE Grant Program.