Jeffrey A. Nichols, Oak Ridge National Laboratory, Oak Ridge, TN, USA Thomas G. Hallam, University of Tennessee, Knoxville, TN, USA William Waldrep, Jr., Undergraduate, University of Chicago, Chicago, IL, USA Paula Federico, Capital University, Columbus, OH, USA Calvin A. Butchkoski, Pennsylvania Game Commission, Harrisburg, PA, USA Gregory G. Turner, Pennsylvania Game Commission, Harrisburg, PA, USA C. David Culver, American University, Washington, DC, USA Rebecca K. Nichols, Homeschool High School Student, Knoxville, TN, USA Gary F. McCracken, University of Tennessee, Knoxville, TN, USA

Modeling the Spread of White-Nose Syndrome, an Emerging Disease of Bats

During the first several years of the White-Nose Syndrome (WNS) epizootic affecting hibernating bats in North America, it and its causative pathogenic fungus *Geomyces destructans* (Gd) exhibited high rates of dispersal averaging about 600 km/year and high virulence with colony mortality frequently exceeding 95%. However, in recent years, regional differences in the spread of the disease and survival of hibernating bats are evidenced in northern versus southern latitudes. Also, it is thus far limited to the eastern half of the United States and Canada. To help understand these differences in WNS dispersal in the United States, and to determine if spread will continue nationwide, we project the spread of the fungus at national, regional, state and local scales by using an agent-based, spatially-explicit, temperature-dependent, dynamic stochastic model developed over two summers.

For nationwide, high-resolution results, serial computation was inadequate to produce the detailed results we required in a reasonable amount of time. The WNS dispersal model began as a student project written in Visual C#. We initially redesigned it into a multi-core computation engine driven by python scripts on an eight-core Mac Pro for regional results, then later a C++, OpenMP model executed on Kraken (kraken.nics.tennessee.edu) for nationwide results. Kraken is a petaflop scale, Cray supercomputer maintained by the University of Tennessee for academic use. Our runs required 18K hours of compute time on Kraken.

For regional and national simulations, we approximate cave locations by county centroid in the contiguous U. S. and utilize karst cave density to determine habitability. The ambient surface temperature of each county centroid is used as a proxy for this cave's temperature. The results of several thousand simulations are summarized to determine robust trends and visualized in Google Earth.

The disease dispersal structure demonstrates regional scale movement towards epicenters followed by local disease expansion around the epicenters. Simulations suggest several robust hypotheses relating to survival at the national level: 1) Warmer temperatures provide a refuge for WNS-susceptible bats in the southern U.S.; 2) There is a spatial bottleneck that could present feasible opportunities to control or delay the western spread of WNS; and 3) The disease is slowed by the Great Plains and Rocky Mountains, but projects to continue to spread into the western U.S.