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October 4, 2007

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Testimony to the U.S. Senate Committee on Homeland Security and Governmental Affairs
Subcommittee on Oversight of Government Management, the Federal Workforce, and the
District of Columbia

Hearing Title: Forestalling the Coming Pandemic: Infectious Disease Surveillance Overseas

Testimony Title: Geographic and genetic mapping of the emergence and spread of infectious
disease, the Supermap project, supermap.bmi.ohio-state.edu

Thank you Chairman Akaka, Ranking Member Voinovich, and members of the subcommittee.

I am an Assistant Professor in the Department of Biomedical Informatics at The Ohio State University. My current research concerns the global spread of emergent infectious diseases. This work involves the use of large-scale computations on genetic and geographic data derived from viruses and their hosts, both animal and human. I received a Bachelor of Sciences degree in biology from the University of Michigan and a Ph.D. in zoology from the University of Florida. I worked as a postdoctoral fellow and a principal investigator at the American Museum of Natural History in New York City where with funding from NASA and the City we built one of the largest computers used in biological research.

At Ohio State we are working at local, state, and international levels. Our students come from every county in Ohio, every state in the nation, as well as over 100 countries. I am an active member of the Columbus Ohio Health Intelligence Team, a local initiative of Columbus Public Health and the Franklin County Board of Health to prepare for and respond to pandemic influenza. On the international level, I have taught in Brazil, Argentina, and just yesterday I worked with a representative of the Indonesian Ministry of Health.

At Ohio State and the Museum we are using public databases of genetic sequences from viruses isolated from human and animal hosts. Just as deciphering an enemy code can provide warning of an attack, we are decoding the genetic sequences of emergent viruses in order to protect our citizens and food supplies.

We are interested in genetic codes such as mutations that confer drug resistance among viruses and permit viruses that were once restricted to animal hosts to infect humans. With funding from DARPA, we have created a computational system to rapidly compare genetic sequences and return a global map depicting the spread of viruses carrying key mutations over various hosts, time, and geography.

As demonstrated by the success in stopping SARS, the rapid collection and dissemination of sequence data throughout the research community are key components in the fight against emergent diseases. Decision makers and the research community must work together to

translate raw data into actionable knowledge. Once a virus is sequenced, the next step is to put the raw data in the context of known, related viruses. This context allows researchers to apply biomedical background knowledge as to whether pharmaceutical interventions are warranted or other means will be necessary to avert a pandemic. However the biomedical context alone does not inform decision makers about the movement of dangerous viruses.

The next step is what makes our disease mapping system so special. We have developed the information technology to track the stepwise movement of diverse strains of viruses over different countries and among various hosts. We monitor the spread of dangerous strains of viruses that are resistant to drugs and or are able to infect human and animal populations. Regional threats are forecast based on the distribution of these dangerous strains with respect to their proximity to population centers, farms, and areas of military deployment.

As we scale our computational infrastructure and staff, we are able to rapidly add new data on a wide variety of agents of infectious disease and generate knowledge on which preemptive measures are important.

Our maps are also useful for understanding the complex mixture of processes that spread disease in various regions. For example, in Indonesia it is clear that chickens are responsible for spreading avian influenza whereas in other areas, such as Central China, migratory birds are important. However illegal trade is also a concern. There was an interesting case in 2004, where an eagle infected with avian influenza was smuggled from Thailand to Belgium. While this infected eagle was quickly confined and the virus did not spread at that point, that case appears as a clear anomaly in our map, betraying an instance where illegal trade allowed avian influenza to make a huge geographic leap. Furthermore, using methods we have developed we can detect and visualize gaps in the available data that represent under surveyed regions or under reporting.

Even though we have made tremendous analytical advances, a significant portion of the data on avian influenza remains in private hands. Among the reasons for the lack of data sharing include the career aspirations of scientists who want first crack at the data and the interests of nations to assure that their citizens will have access to vaccines.

In light of the severity of the health and economic issues surrounding influenza, we have tried to change the model for data sharing via collaboration and co-authorship with international colleagues who work in the field and are providers of key viral strains for sequencing. These efforts have been exemplified by the Influenza and Coronavirus Genome Sequencing Projects, who are funded by the NIH under a mandate to share data within 45 days of collection.

I realize that data sharing issues are complex and that a balance of competition and collaboration is natural in science and international relations. We will use the data security concepts that have been developed to protect the privacy of patients while allowing clinical research to move forward in the context of data sharing on emergent diseases. For example, cancer research is currently being accelerated by a data sharing and analysis initiative of the NCI the Cancer Biomedical Informatics Grid. We will apply the same underlying software for analysis and mapping of infectious diseases.

Mr. Chairman and members of the subcommittee, I am pleased to have had a chance to discuss these issues with you today and welcome questions. I also would welcome an opportunity demonstrate our system to you.