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## Researchers Publish Article on Tracking Infectious Disease

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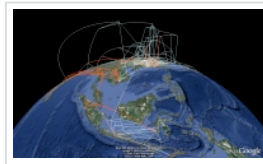
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### **Supramap uses genomics, supercomputer, web to display virus evolution.**

**Columbus, Ohio**— A new web-based application powered by supercomputers has the potential to inform public health decisions by visualizing genetic and evolutionary information about the spread of infectious diseases across time, geography, host animals and humans.



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In a journal article published in the April 2010 online issue of *Cladistics*, [Daniel Janies](#), Ph.D., explains how [Supramap](#) was created to track the avian influenza virus (H5N1) and, more recently, to monitor the H1N1 virus. *Cladistics* refers to the scientific classification of living organisms, based on common ancestry, into evolutionary trees. Evolutionary trees are used by many researchers studying infectious diseases to understand the geographic and host origins of pathogens and how the pathogens change over time. [Supramap](#) puts phylogenies in a geographic context as well.

"The integration of our core phylogenetic reconstruction codes with [Supramap](#) has allowed an entirely new way to view linked evolutionary and geographic information," said [Ward Wheeler](#), a coauthor of the article and curator-in-charge of scientific computing at the American Museum of Natural History (AMNH). "The [Supramap](#) tool set has broad utility not only in tracking human disease in time and space, but historical patterns of biodiversity and global biotic changes."

Janies, an associate professor of Biomedical Informatics at The Ohio State University (OSU), Wheeler and several colleagues created [Supramap](#) to calculate and project evolutionary trees in online geographic information systems, such as Google Earth. The resulting visualizations have been described as "weather maps for disease" that allow public health officials to see when and where pathogens spread, jump from animals to humans and evolve to resist drugs.

"Currently, we are investigating H1N1 cases from around the world – and Ohio – by building evolutionary trees that discover how this strain came to be assembled and jumped from animals to humans. We are also monitoring specific viral genes for mutations that confer resistance to drugs" said Janies, an expert in computational genomics. "Using parallel programming on high performance computing systems at the Ohio Supercomputer Center (OSC) greatly improves the efficiency and accuracy of our work."

Janies and his colleagues used a small cluster computer at OSU to beta-test the [Supramap](#) application, which has been developed through a grant from the Defense Advanced Research Projects Agency (DARPA). The research team also adapted the [Supramap](#) code to function smoothly on the OSC's flagship IBM Cluster 1350 "Glenn" system, which features 9,500 cores and 24 terabytes of memory. They now are working with the Center's staff to finish development of a Web interface to provide easy Internet access to the application by scientists and public health officials.

This material is based upon work supported by, or in part by, the U.S. Army Research Laboratory and Office under grant number W911NF-05-1-0271.

#### Publication:

**"The [Supramap](#) project: Linking pathogen genomes with geography to fight emergent infectious diseases."**

[Daniel Janies](#), The Ohio State University, Biomedical Informatics

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